



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 135509

**TO: James Schultz
Location: REM/2D18/2C18
Art Unit: 1635
Tuesday, October 19, 2004**

Case Serial Number: 09/695451

**From: David Schreiber
Location: Biotech-Chem Library
Remsen E01A61
Phone: 272-2526**

david.schreiber@uspto.gov

Search Notes

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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher: O. Schreiber

Searcher Phone #: 272-2526

Searcher Location: Ramsey E01A61

Date Searcher Picked Up: _____

Date Completed: 10/17

Searcher Prep & Review Time: 20

Clerical Prep Time: _____

Online Time: 183

Type of Search

NA Sequence (#) 30

AA Sequence (#) _____

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr. Link _____

Lexis/Nexis _____

Sequence Systems CompuGen

WWW/Internet _____

Other (specify) _____

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SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 65²⁰.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 14:17:38 ; Search time 0.001 Seconds
(without alignments)
0.352 Million cell updates/sec

Title: US-09-695-451-1

Perfect score: 22

Sequence: 1 tgcaggagaacagacacccg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 8 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : rst1-727.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	6.4	29.1	8	1	CF921494
					ACCESSION:CF921494

ALIGNMENTS

RESULT 1
CF921494/c
LOCUS
DEFINITION CF921494 8 bp mRNA linear EST 05-NOV-2003
gmthRw3-10_B07.1_061 Soybean root hair subtracted cDNA library
gmthRw3 Glycine max cDNA, mRNA sequence.
ACCESSION CF921494
VERSION CF921494.1 GI:38192288
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 8)
Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
Expressed sequence tags from soybean root hair subtractive cDNA
library
JOURNAL Unpublished (2003)
COMMENT Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
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/clone_lib="Soybean root hair subtracted cDNA library
gmthRw3"
/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."
Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 734 AGAAACAG 741
Db 8 AAAACAG 1

Search completed: October 18, 2004, 14:17:39
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 14:09:43 ; Search time 0.001 Seconds

(without alignments)
135.608 Million cell updates/sec

Title: US-09-695-451-1

Perfect score: 22

Sequence: 1 tgcaggagaacagacacg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 276 seqs, 3082 residues

Total number of hits satisfying chosen parameters: 552

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 276 summaries

Database : rni1-727.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	15.4	70.0	18	1	US-08-488-214A-45
C 4	15.4	70.0	18	1	US-08-488-208A-45
C 5	15.4	70.0	18	1	US-08-483-211A-45
C 6	15.4	70.0	18	1	US-08-488-223A-45
C 7	15.4	70.0	18	1	US-08-438-431A-45
C 8	13.8	62.7	18	1	US-08-488-225A-45
C 9	13.8	62.7	18	1	US-08-577-081A-67
C 10	12.4	56.4	18	1	US-08-465-095-6
C 11	12.4	56.4	18	1	US-08-179-656A-6
C 12	12.4	56.4	18	1	PCT-US94-00300-6
C 13	12.4	56.4	19	1	US-08-288-140-28
C 14	12.2	55.5	18	1	US-08-422-978-4649
C 15	11.8	53.6	18	1	US-08-912-129A-42
C 16	11.4	51.8	17	1	US-08-329-350-40
C 17	11.4	51.8	17	1	US-08-584-040-5499
C 18	11.4	51.8	17	1	US-08-371-772B-2390
C 19	11.2	50.9	17	1	US-08-584-040-6036
C 20	11.2	50.9	17	1	US-08-371-772B-2873
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C 23	10.4	47.3	12	1	US-08-242-664-12
C 24	10.4	47.3	12	1	US-08-484-138-12
C 25	10.4	47.3	12	1	PCT-US95-06379-12
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C 27	10.4	47.3	14	1	US-08-535-249-125
C 28	10.4	47.3	14	1	US-08-874-601-18
C 29	10.4	47.3	15	1	US-08-291-932A-11
C 30	10.4	47.3	15	1	US-08-363-240A-654
C 31	10.4	47.3	15	1	US-08-081-646-132
C 32	10.4	47.3	15	1	US-08-081-646-867
C 33	10.4	47.3	16	1	US-08-137-024-4
C 34	10	45.5	11	1	US-08-646-695-15
C 35	10	45.5	11	1	PCT-US96-06053-15
C 36	10	45.5	15	1	US-09-081-646-456
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C 38	9.8	44.5	14	1	US-08-442-513A-11
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C 41	9.8	44.5	14	1	US-08-173-489C-198
C 42	9.8	44.5	14	1	US-08-535-249-126
C 43	9.8	44.5	15	1	US-09-049-190-11
C 44	9.8	44.5	15	1	US-08-932-140C-11
C 45	9.8	44.5	15	1	US-09-081-646-460
C 46	9.8	44.5	15	1	US-09-531-000-60
C 47	9.4	42.7	12	1	US-08-560-313A-9
C 48	9.4	42.7	12	1	US-08-611-155B-13
C 49	9.4	42.7	12	1	US-08-916-120A-15
C 50	9.4	42.7	12	1	US-08-507-032-14
C 51	9.4	42.7	12	1	US-09-281-418-162
C 52	9.4	42.7	12	1	US-09-513-783A-73
C 53	9.4	42.7	12	1	US-08-809-513A-9
C 54	9.4	42.7	13	1	US-08-809-513A-4
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C 65	8.8	40.0	12	1	US-09-332-319-10
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Sequence 59, Appl
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Sequence 33, Appl

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125 7.4 33.6 11 1 US-08-435-350-92 Sequence 92, Appl 198
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6.8 30.9 10 1 US-09-916-228-7 Sequence 7, Appl 213
6.8 30.9 10 1 US-09-655-104A-7 Sequence 7, Appl 214
6.8 30.9 10 1 US-08-301-037-7 Sequence 7, Appl 215
6.8 30.9 10 1 US-08-466-539-7 Sequence 7, Appl 216
6.8 30.9 10 1 US-09-394-455-53 Sequence 53, Appl 217
6.8 30.9 10 1 US-09-508-753B-37 Sequence 37, Appl 218
6.8 30.9 10 1 US-09-508-753B-51 Sequence 51, Appl 219
6.8 30.9 10 1 US-09-508-753B-76 Sequence 76, Appl 220
6.8 30.9 10 1 US-09-508-753B-79 Sequence 79, Appl 221
6.8 30.9 10 1 US-09-508-753B-82 Sequence 82, Appl 222
6.8 30.9 10 1 US-09-508-753B-126 Sequence 126, Appl 223
6.8 30.9 10 1 US-09-508-753B-131 Sequence 131, Appl 224
6.8 30.9 10 1 US-09-508-753B-133 Sequence 133, Appl 225
6.8 30.9 10 1 US-09-508-753B-157 Sequence 157, Appl 226
6.8 30.9 10 1 US-09-508-753B-160 Sequence 160, Appl 227
6.8 30.9 10 1 US-10-042-111-42 Sequence 42, Appl 228
6.8 30.9 10 1 US-10-042-111-43 Sequence 43, Appl 229
6.8 30.9 10 1 US-09-394-467-7 Sequence 7, Appl 230
6.8 30.9 10 1 US-10-104-818-7 Sequence 7, Appl 231
6.8 30.9 10 1 US-09-989-789-1332 Sequence 1332, Appl 232
6.8 30.9 10 1 US-09-989-789-1333 Sequence 1333, Appl 233
6.8 30.9 10 1 US-09-989-789-1334 Sequence 1334, Appl 234
6.8 30.9 10 1 US-09-989-789-1335 Sequence 1335, Appl 235
6.8 30.9 10 1 US-09-337-304-56 Sequence 56, Appl 236
6.8 30.9 10 1 US-09-855-159A-7 Sequence 7, Appl 237
6.8 30.9 10 1 US-09-723-909-148 Sequence 148, Appl 238
6.8 30.9 10 1 US-08-466-639-7 Sequence 7, Appl 239
6.8 30.9 10 1 US-08-466-639-7 Sequence 7, Appl 240
6.8 30.9 10 1 PCT-US91-03680-75 Sequence 75, Appl 241
6.8 30.9 10 1 PCT-US93-08743-148 Sequence 148, Appl 242
6.4 29.1 8 1 US-07-739-642-14 Sequence 14, Appl 243
6.4 29.1 8 1 US-07-739-643-14 Sequence 14, Appl 244
6.4 29.1 8 1 US-07-739-142-14 Sequence 14, Appl 245
6.4 29.1 8 1 US-08-465-590-117 Sequence 117, Appl 246
6.4 29.1 8 1 US-08-859-954-38 Sequence 38, Appl 247
6.4 29.1 8 1 US-08-859-954-205 Sequence 205, Appl 248

253 6.4 29.1 8 1 US-08-859-954-375 Sequence 375, App
254 6.4 29.1 8 1 US-08-711-417C-117 Sequence 117, App
255 6.4 29.1 8 1 US-09-723-909-117 Sequence 117, App
256 6.4 29.1 8 1 PCT-US93-08743-117 Sequence 117, App
257 6.4 29.1 9 1 US-08-088-658-5 Sequence 5, Appl
258 6.4 29.1 9 1 US-08-410-779B-28 Sequence 28, Appl
259 6.4 29.1 9 1 US-08-465-590-126 Sequence 126, App
260 6.4 29.1 9 1 US-08-605-163-7 Sequence 7, Appl
261 6.4 29.1 9 1 US-08-605-163-18 Sequence 18, Appl
262 6.4 29.1 9 1 US-08-471-907A-5 Sequence 5, Appl
263 6.4 29.1 9 1 US-08-461-607-21 Sequence 21, Appl
264 6.4 29.1 9 1 US-08-711-417C-126 Sequence 126, App
265 6.4 29.1 9 1 US-09-363-600-21 Sequence 21, Appl
266 6.4 29.1 9 1 US-09-163-485-23 Sequence 23, Appl
267 6.4 29.1 9 1 US-09-327-138C-13 Sequence 13, Appl
268 6.4 29.1 9 1 US-09-989-789-530 Sequence 530, App
269 6.4 29.1 9 1 US-09-989-789-2021 Sequence 2021, Ap
270 6.4 29.1 9 1 US-09-989-789-2022 Sequence 2022, Ap
271 6.4 29.1 9 1 US-09-989-789-2401 Sequence 2401, Ap
272 6.4 29.1 9 1 US-09-989-789-2402 Sequence 2402, Ap
273 6.4 29.1 9 1 US-09-989-789-2403 Sequence 2403, Ap
274 6.4 29.1 9 1 US-09-723-909-126 Sequence 126, App
275 6.4 29.1 9 1 PCT-US93-08743-126 Sequence 126, App
276 6.4 29.1 9 1 PCT-US95-04477-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-106-038A-47/c
; Sequence 47, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106.038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-47

Query Match 77.3%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 732 GGAGAAACAGAACACCG 748
DB 18 GGAGAAACAGAACACCG 2
RESULT 2
US-08-485-942A-45/c
; Sequence 45, Application US/08485942A
; Patent No. 6048837
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE;
; TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
; TITLE OF INVENTION: AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,942A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6048837ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; DESCRIPTION: sequence tagged-site specific PCR primer sws2359
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-485-942A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 6.6; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

QY 730 CAGGAGAAACAGAACAC 746
DB 18 CAGGAGAAACAGAACAC 2

RESULT 3

US-08-488-214A-45/c

; Sequence 45, Application US/08488214A

; Patent No. 6124439

; GENERAL INFORMATION:

; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,

; APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE

; TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING

; TITLE OF INVENTION: (AS AMENDED)

; NUMBER OF SEQUENCES: 99

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,214A

; FILING DATE: JUNE 7, 1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/347,563

; FILING DATE: No. 6124439ember 30, 1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (primer)

; DESCRIPTION: sequence tagged-site specific PCR primer sWS2359

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Human

; US-08-488-214A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 6.6;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGACAC 746

| | | | | | | | | | | | | | | |

Db 18 CAGGAGAAACAGACAC 2

RESULT 4

US-08-488-208A-45/c

; Sequence 45, Application US/08488208A

; Patent No. 6124448

; GENERAL INFORMATION:

; APPLICANT: THE ROCKEFELLER UNIVERSITY

; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

; TITLE OF INVENTION: USES THEREOF

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,208A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/485,943

; FILING DATE: June 7, 1995

; APPLICATION NUMBER: 08/438,431

; FILING DATE: May 10, 1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/347,563

; FILING DATE: No. 6124448ember 30, 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (primer)

; DESCRIPTION: sequence tagged-site specific PCR primer sWS2359

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Human

; US-08-488-208A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 6.6;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGACAC 746

| | | | | | | | | | | | | | | |

Db 18 CAGGAGAAACAGACAC 2

RESULT 5

US-08-483-211A-45/c

; Sequence 45, Application US/08483211A

; Patent No. 6309853

; GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,211A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: August 17, 1994
CLASSIFICATION: 514
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
TELEFAX: 133521
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Human
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-08-483-211A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 6.6; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0

Qy 730 CAGGAGAAACAGAACAC 746
Db 18 CAGGAGAAACAGAACAC 2

RESULT 6
US-08-488-223A-45/c
Sequence 45, Application US/08488223A
Patent No. 6350730
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC

ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEI
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,223A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6350730ember 30, 1994
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Human
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-08-488-223A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 6.6;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGAACAC 746
Db 18 CAGGAGAAACAGAACAC 2

RESULT 7
US-08-438-431A-45/c
Sequence 45, Application US/08438431A
Patent No. 6429290
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAFFEI,
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438,431A
 FILING DATE: May 10, 1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/347,563
 FILING DATE: No. 6429290ember 30, 1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/292,345
 FILING DATE: August 17, 1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-087 CIP1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (primer)
 DESCRIPTION: sequence tagged-site specific PCR primer sWS2359
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Human
 US-08-438-431A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 6.6;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGACAC 746
 Db 18 CAGGAGAAACACACAC 2

RESULT 8
 US-08-488-225A-45/c
 ; Sequence 45, Application US/08488225A
 ; Patent No. 6471956
 ; GENERAL INFORMATION:
 ; APPLICANT: THE ROCKEFELLER UNIVERSITY
 ; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
 ; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USE
 ; NUMBER OF SEQUENCES: 98
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/488,225A
 ; FILING DATE: June 7, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/483,211
 FILING DATE: June 7, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/438,431
 FILING DATE: May 10, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/347,563
 FILING DATE: No. 6471956ember 30, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/292,345
 FILING DATE: August 17, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-087 CIP2J
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (primer)
 DESCRIPTION: sequence tagged-site specific PCR primer
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Human
 US-08-488-225A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 6.6;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGACAC 746
 Db 18 CAGGAGAAACACACAC 2

RESULT 9
 US-08-577-081A-67
 ; Sequence 67, Application US/08577081A
 ; Patent No. 6030775
 ; GENERAL INFORMATION:
 ; APPLICANT: Yang, Soo Young
 ; APPLICANT: Cereb, Nezh
 ; TITLE OF INVENTION: Methods and Reagents for Typing HLA
 ; TITLE OF INVENTION: Class I Genes
 ; NUMBER OF SEQUENCES: 84
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Oppedahl & Larson
 ; STREET: 1992 Commerce Street Suite 309
 ; CITY: Yorktown
 ; STATE: NY
 ; COUNTRY: US
 ; ZIP: 10598
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: Word Perfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/577,081A
 ; FILING DATE:
 ; CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: MSK-P-001-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: hybridization probe GE2-183 for typing of
; OTHER INFORMATION: HLA Class I genes
US-08-577-081A-67

Query Match 62.7%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGACACC 747
DB 2 AGGAGACACGGACACC 18

RESULT 10
US-08-465-095-6/c
; Sequence 6, Application US/08465095
; Patent No. 5849534
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Iida, Naoka
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,095
; FILING DATE: 07-JAN-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/001,177
; FILING DATE: 07-JAN-1993
; APPLICATION NUMBER: 07/472,377
; FILING DATE: 01-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GZI-003C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-179-656A-6

Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAGACACA 745
DB 16 GCAGAACAGACACA 3

RESULT 11
US-08-179-656A-6/G
; Sequence 6, Application US/08179656A
; Patent No. 6673893
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Iida, Naoka
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,656A
; FILING DATE: 07-JAN-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/001,177
; FILING DATE: 07-JAN-1993
; APPLICATION NUMBER: 07/472,377
; FILING DATE: 01-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GZI-003C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-179-656A-6

Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAGACACA 745
DB 16 GCAGAACAGACACA 3

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-465-095-6

Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAGACACA 745
DB 16 GCAGAACAGACACA 3
```

```
Db      16 GCAGAAACAGAAC 3

RESULT 12
PCT-US94-00300-6/c
; Sequence 6, Application PC/TUS9400300
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Iida, Naoka
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00300
; FILING DATE: 07-JAN-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/001,177
; FILING DATE: 07-JAN-1993
; APPLICATION NUMBER: 07/472,377
; FILING DATE: 01-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GZ1-003C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US94-00300-6

Query Match      56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      732 GCAGAAACAGAAC 745
Db      16 GCAGAAACAGAAC 3

RESULT 13
US-09-268-140-28/c
; Sequence 28, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28

Db      16 GCAGAAACAGAAC 3

Query Match      56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      732 GCAGAAACAGAAC 745
Db      16 GCAGAAACAGAAC 3

RESULT 14
US-09-422-978-4649/c
; Sequence 4649, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4649
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-16740 for SEQ 715,
US-09-422-978-4649

Query Match      55.5%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 25;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      731 AGGAGAAACAGAACACC 747
Db      17 AGGAGAAACAGAGGAAC 1

RESULT 15
US-08-912-129A-42
; Sequence 42, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANADRUZELA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARITEK, VINCENT A. JR.
; APPLICANT: NECKLAWS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEVARB, SUSHIL G.
; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
```

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912.129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dancakers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109 US.01
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-912-129A-42

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 29;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGAAC 744
Db 3 CAGCAGGAGACAGAAC 17

APPLICATION NUMBER: US 08/841,636
FILING DATE: 30-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,335
FILING DATE: 17-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,926
FILING DATE: 04-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,840
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/732,181
FILING DATE: 16-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI96/00550
FILING DATE: 17-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Shea Jr., Timothy
REGISTRATION NUMBER: 41,306
REFERENCE/DOCKET NUMBER: 1716.0510006/MAC/TJS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-329-350-40

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 32;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 735 GAAACAGACACCG 748
Db 4 GAAACAGACACCG 17

RESULT 16
US-09-329-350-40
Sequence 40, Application US/09329350
Patent No. 6184019
GENERAL INFORMATION:
APPLICANT: Miettinen-Oinonen, Arja
APPLICANT: Londenborough, John
APPLICANT: Vehmaanper, Jari
APPLICANT: Haakana, Heli
APPLICANT: M ntyl, Arja
APPLICANT: Lantto, Raija
APPLICANT: Elvoinio, Minna
APPLICANT: Joutsenoki, Vesa
APPLICANT: Falohelmo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,350
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:

RESULT 17
US-08-584-040-5499
Sequence 5499, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040

; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5499:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-5499

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAC 745
|||||
DB 2 GAGAAUAGAACA 14

RESULT 18
US-09-371-772B-2390
; Sequence 2390, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2390
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2390

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAC 745
|||||
DB 2 GAGAAUAGAACA 14

RESULT 19
US-08-584-040-6036/c
; Sequence 6036, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James

; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6036:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-6036

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGAA 743
|||||
DB 16 GCCAGGAGACGCTAA 1

RESULT 20
US-09-371-772B-2873/c
; Sequence 2873, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08


```
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2873
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2873

Query Match          50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAGAA 743
Db 16 GCCAGGAGACAGTAA 1

RESULT 21
5182195-60
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO; KAIISHO, YOSHIIKO; YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO: 60
; LENGTH: 15
5182195-60

Query Match          50.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAGAACAGA 742
Db 2 GGAGAGAACAGA 12

RESULT 22
US-08-291-932A-10/c
; Sequence 10, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2873
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2873

Query Match          49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAAC 744
Db 14 AGGGGAACAGATC 1

RESULT 23
US-08-242-664-12
; Sequence 12, Application US/08242664
; Patent No. 5571937
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,664
; FILING DATE: May 12, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-242-664-12

Query Match          47.3%; Score 10.4; DB 1; Length 12;
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Best Local Similarity 91.7%; Pred. No. 31;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 1 AGGAGAAAGAGA 12

RESULT 24
US-08-484-138-12
; Sequence 12, Application US/08484138
; Patent No. 5652350
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,138
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-484-138-12

Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 31;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 1 AGGAGAAAGAGA 12

RESULT 25
PCT-US95-06379-12
; Sequence 12, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York

Best Local Similarity 91.7%; Pred. No. 31;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 1 AGGAGAAAGAGA 12

RESULT 26
US-08-639-080-4
; Sequence 4, Application US/08639080
; Patent No. 5843661
; GENERAL INFORMATION:
; APPLICANT: Rothmund, Paul W.K.
; TITLE OF INVENTION: METHOD FOR CONSTRUCTING UNIVERSAL DNA
; TITLE OF INVENTION: BASED MOLECULAR TURING MACHINE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Ste 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,080
; FILING DATE: April 24, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Harris, Scott C.
; REGISTRATION NUMBER: 32,030
; REFERENCE/DOCKET NUMBER: 06618/123001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
```

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: oligonucleotide
US-08-639-080-4

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 735 GAAACAGAACAC 746
|||||
Db 2 GAAACAGTACAC 13

RESULT 27
US-08-535-249-125
; Sequence 125, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Retmar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-125

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
|||||
Db 14 AGCAGAAACAGA 3

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
|||||
Db 14 AGCAGAAACAGA 3

RESULT 29
US-08-291-932A-11/c
; Sequence 11, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Mcswiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994

Db 1 AGGAGAACAGA 12

RESULT 28
US-09-874-601-18/c
; Sequence 19, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 18
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-18

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
|||||
Db 14 AGCAGAAACAGA 3

RESULT 29
US-08-291-932A-11/c
; Sequence 11, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Mcswiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994

```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-291-932A-11

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGGAACACAGA 742
Db 13 AGGGGAACAGA 2

RESULT 30
US-08-363-240A-654/c
; Sequence 654, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600

```

```

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 654:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-654

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACACAGAA 743
Db 12 GGAGAACACAGAA 1

RESULT 31
US-09-081-646-132
; Sequence 132, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 132
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-132

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAGAA 738
Db 3 TGCCAGGAGAGAA 14

RESULT 32
US-09-081-646-867
; Sequence 867, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 867
; LENGTH: 15
; TYPE: DNA

```

; ORGANISM: Homo sapiens
US-09-081-646-867

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TGCAGGAGAAA 738
Db 3 TGCAGGAGGAA 14

RESULT 33

US-08-137-024-4
; Sequence 4, Application US/08137024
; Patent No. 6005167
; GENERAL INFORMATION:
; APPLICANT: VAN TUNEN, Adrianus, J.
; APPLICANT: VAN DER MEER, Ingrid M.
; APPLICANT: MOL, Josephus N.M.
; TITLE OF INVENTION: MALE-STERILE PLANTS, METHODS
; TITLE OF INVENTION: FOR OBTAINING MALE STERILE
; TITLE OF INVENTION: PLANTS AND RECOMBINANT DNA FOR
; TITLE OF INVENTION: USE THEREIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Pary
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50 inch, DS, DD 720
; MEDIUM TYPE: Kb/720Kb
; COMPUTER: IBM PC Compatible 286 SX 12 Mhz
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,024
; FILING DATE: 14-OCT-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL92/00075
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91200910
; FILING DATE: 16-APR-1991

ATTORNEY/AGENT INFORMATION:
; NAME: MASS, Clifford, J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-9373
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288

INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Petunia hybrida

US-08-137-024-4

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 4 AGGAGAAACAGA 15

RESULT 34

US-08-646-695-15
; Sequence 15, Application US/08646695
; Patent No. 6168943
; GENERAL INFORMATION:
; APPLICANT: Rose, John K.
; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
; TITLE OF INVENTION: USES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,695
; FILING DATE: On Even Date Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: RNA
US-08-646-695-15

Query Match 45.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739
Db 2 CAGGAGAAAC 11

RESULT 35

PCT-US96-06053-15
; Sequence 15, Application PC/TUS9606053
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
; TITLE OF INVENTION: USES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06053
; FILING DATE: 01-MAY-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-009-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9030
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: RNA
; PCT-US96-06053-15

```

```

Query Match 45.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 730 CAGGAGAAAC 739
Db 2 CAGGAGAAAC 11

```

```

RESULT 36
US-09-081-646-456
; Sequence 456, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081.646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 456
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-081-646-456

```

```

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 732 GGAGAAACAG 741
Db 5 GGAGAAACAG 14

```

```

RESULT 37
US-08-303-004-13
; Sequence 13, Application US/08303004
; Patent No. 5556955
; GENERAL INFORMATION:
; APPLICANT: Vergnaud, Gilles
; TITLE OF INVENTION: Process for Detection of New Polymor-

```

```

; TITLE OF INVENTION: phic Loci in an ADN Sequence, Nucleotide Sequences Forming
; TITLE OF INVENTION: Hybridisation Probes and Their Biological Applications
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ollif & Berridge
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,004
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/931,311B
; FILING DATE: 19920818
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; TELEX: 90-1799 PTO ALEX
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-303-004-13

```

```

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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QY 733 GAGAAACAGACA 745
Db 1 GAGAAACAGACA 13

```

```

RESULT 38
US-08-442-513A-11/c
; Sequence 11, Application US/08442513A
; Patent No. 5646031
; GENERAL INFORMATION:
; APPLICANT: DeYoung, Mary Beth
; APPLICANT: Siwkowski, Andrew M.
; APPLICANT: Hampel, Arnold E.
; TITLE OF INVENTION: METHOD FOR DERIVING RIBOZYMES FROM
; NUCLEOTIDE SEQUENCES AND RIBOZYMES DERIVED THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5646031thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,513A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,995
; REFERENCE/DOCKET NUMBER: 2384.00014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5055
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Ribozyme substrate"
US-08-442-513A-11

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACCG 748
Db 14 AACAGAACTCG 2

RESULT 39
US-08-442-513A-16/c
; Sequence 16, Application US/08442513A
; Patent No. 5646031
; GENERAL INFORMATION:
; APPLICANT: DeYoung, Mary Beth
; APPLICANT: Siwkowski, Andrew M.
; APPLICANT: Hampel, Arnold E.
; TITLE OF INVENTION: METHOD FOR DERIVING RIBOZYMES FROM
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND RIBOZYMES DERIVED THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 56460311thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/442,513A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,995
; REFERENCE/DOCKET NUMBER: 2384.00014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5055
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Ribozyme substrate"
US-08-442-513A-16

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACCG 748
Db 14 AACAGAACTCG 2

RESULT 40
US-08-173-489C-186/c
; Sequence 186, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from Hepatitis B
; DESCRIPTION: isolate adw2 sequence region in Seq ID No. 5861244185
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 186 :FROM 1 TO 14
US-08-173-489C-186

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACACAGAA 743
Db 13 AGGAGAACACAGAA 1

RESULT 41
US-08-173-489C-198/c
; Sequence 198, Application US/08173489C

Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESS: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244197
HYPOTHETICAL: yes
ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 198 :FROM 1 TO 14
US-08-173-489C-198
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAGAA 743
Db 13 AGGAGAGCAGGA 1
RESULT 42
US-08-535-249-126
Sequence 126, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESS: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.

CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-126
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 728 GCACGAGAAACA 740
Db 2 GCAGGAGAGCA 14
RESULT 43
US-09-049-190-11/C
Sequence 11, Application US/09049190
Patent No. 6190866
GENERAL INFORMATION:
APPLICANT: Nielsen et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having
TITLE OF INVENTION: Antibacterial Activity
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,190
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-2560
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone

FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-lysine-glycine
OTHER INFORMATION: backbone
US-09-049-190-11
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGAA 743
Db 15 AGGAGAAAGAGTA 3
RESULT 44
US-08-932-140C-11/c
Sequence 11, Application US/08932140C
Patent No. 6300319
GENERAL INFORMATION:
APPLICANT: Nielsen et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having
TITLE OF INVENTION: Antibacterial Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 6300319is LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,140C
FILING DATE: September 16, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-2560
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone

```
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-
OTHER INFORMATION: lysine-glycine backbone
US-08-932-140C-11
```

Query Match

44.5%; Score 9.8; DB 1; Length 15;

```
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db 15 AGGAGAAAGAGTA 3

RESULT 45
US-09-081-646-460/c
; Sequence 460, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; TITLE OF INVENTION: Cancer Cells
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 460
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-460
```

```
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 728 GCGAGAGAAACA 740
Db 15 GCGAGAGAAACA 3
```

```
RESULT 46
US-09-531-000-60
; Sequence 60, Application US/09531000
; Patent No. 6461810
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Marion D.
; APPLICANT: FRESCO, Jacques R.
; TITLE OF INVENTION: TRIPLEX IN-SITU HYBRIDIZATION
; FILE REFERENCE: 2448-103
; CURRENT APPLICATION NUMBER: US/09/531,000
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/23765
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/064,997
; PRIOR FILING DATE: 1997-11-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target
; OTHER INFORMATION: sequences
US-09-531-000-60
```

```
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 731 AGGAGAAACAGAA 743
Db 15 AGGAGAAAGAGTA 3
```

```
Db          2 AGGTGAAAAGAA 14

RESULT 47
US-08-560-313A-9/c
; Sequence 9, Application US/08560313A
; Patent No. 5763175
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: Simultaneous Sequencing of Tagged Polynucleotides
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: Power Macintosh
; OPERATING SYSTEM: Macintosh OS ver. 7.5.2
; SOFTWARE: Microsoft Word, vers. 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,313A
; FILING DATE: 17-NOV-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: estlus
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-560-313A-9

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          728 GCCAGGAGAA 738
Db          12 GCCAGGAGAG 2

RESULT 48
US-08-611-155B-13/c
; Sequence 13, Application US/08611155B
; Patent No. 5780231
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: DNA Extension and Analysis with Rolling Primers
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word, vers. 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,120A
; FILING DATE: 22-AUG-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/611,155
; FILING DATE: 05-VAR-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 811-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-916-120A-15

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          728 GCCAGGAGAA 738
Db          12 GCCAGGAGAG 2

RESULT 49
US-08-916-120A-15/c
; Sequence 15, Application US/08916120A
; Patent No. 5962228
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: DNA Extension and Analysis with Rolling Primers
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word, vers. 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,120A
; FILING DATE: 22-AUG-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/611,155
; FILING DATE: 05-VAR-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 811-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-916-120A-15
```

```

; TITLE OF INVENTION: sgment, Method of Assaying Microorganisms, Method of Analyzing Mic
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281.418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 162
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-281-418-162

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 2 AGGAGAAACGG 12

RESULT 52
US-09-513-783A-73
; Sequence 73, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-13
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase-9
; OTHER INFORMATION: substrate recognition sequence
; US-09-513-783A-73

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GCGAGAAACAGA 742
Db 1 GTAGAAACAGA 11

RESULT 53
US-08-809-513A-9/c
; Sequence 9, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising t
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York

; TITLE OF INVENTION: sgment, Method of Assaying Microorganisms, Method of Analyzing Mic
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281.418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 162
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-281-418-162

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
Db 12 GCCAGGAGAGA 2

RESULT 50
US-08-507-032-14
; Sequence 14, Application US/08507032
; Patent No. 5989810
; GENERAL INFORMATION:
; APPLICANT: Flanagan, William A.
; APPLICANT: Crabtree, Gerald R.
; TITLE OF INVENTION: Screening Methods for Immunosuppressive
; TITLE OF INVENTION: Agents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,032
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,944
; FILING DATE:
; APPLICATION NUMBER: US 07/749,385
; FILING DATE: 22-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 5490A-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-507-032-14

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACA 740
Db 1 CAGGAGAAAAA 11

RESULT 51
US-09-281-418-162
; Sequence 162, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
```

```
/ COUNTRY: USA
/ ZIP: 10591-5144
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
/ COMPUTER: Gateway Pentium II
/ OPERATING SYSTEM: Windows 98
/ SOFTWARE: Word 97
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/809,513A
/ FILING DATE: 24-MAR-1997
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/03663
/ FILING DATE: 18-SEP-1995
/ APPLICATION NUMBER: EP 94115505.3
/ FILING DATE: 30-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kurt G. Briscoe
/ REGISTRATION NUMBER: 33,141
/ REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
/ TELEPHONE: (914) 332-1700
/ TELEFAX: (914) 332-1844
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: RNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Influenza virus, vRNA 3' sequence
/ INDIVIDUAL ISOLATE: pHL1104 vRNA Promoter Element
/ US-08-809-513A-9

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAAACAG 2

RESULT 54
US-08-809-513A-4/c
/ Sequence 4, Application US/08809513A
/ Patent No. 6524588
/ GENERAL INFORMATION:
/ APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
/ TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
/ TITLE OF INVENTION: Method
/ TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
/ STREET: 660 White Plains Road
/ CITY: Tarrytown
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10591-5144
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
/ COMPUTER: Gateway Pentium II
/ OPERATING SYSTEM: Windows 98
/ SOFTWARE: Word 97
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/809,513A
/ FILING DATE: 24-MAR-1997
/ CLASSIFICATION: 424
```

```
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/03663
/ FILING DATE: 18-SEP-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94115505.3
/ FILING DATE: 30-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kurt G. Briscoe
/ REGISTRATION NUMBER: 33,141
/ REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
/ TELEPHONE: (914) 332-1700
/ TELEFAX: (914) 332-1844
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: RNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Influenza virus, vRNA 3' sequence
/ INDIVIDUAL ISOLATE: pHL1104 vRNA Promoter Element
/ US-08-809-513A-4

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 13 AGTAGAAACAG 3

RESULT 55
US-09-874-601-59/c
/ Sequence 59, Application US/09874601
/ Patent No. 6632057
/ GENERAL INFORMATION:
/ APPLICANT: LEWIN, ALFRED S.
/ APPLICANT: SHAW, LYNN C.
/ APPLICANT: GRANT, MARIA B.
/ TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS
/ TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
/ FILE REFERENCE: 4300.014100
/ CURRENT APPLICATION NUMBER: US/09/874,601
/ CURRENT FILING DATE: 2001-05-01
/ PRIOR APPLICATION NUMBER: 09/063,667
/ PRIOR FILING DATE: 1998-04-21
/ PRIOR APPLICATION NUMBER: 60/046,147
/ PRIOR FILING DATE: 1997-05-09
/ PRIOR APPLICATION NUMBER: 60/044,492
/ PRIOR FILING DATE: 1997-04-21
/ NUMBER OF SEQ ID NOS: 182
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 59
/ LENGTH: 13
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (..)
/ OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
/ US-09-874-601-59

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 13 AGTAGAAACAG 3
```

Db 11 AGCAGAAACAG 1

RESULT 56
US-08-535-249-35
; Sequence 35, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-35

Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 730 CAGCAGAAACAG 743
Db 1 CATGAGAGCAGGA 14

RESULT 57
US-09-508-753B-21/c
; Sequence 21, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yoko SHIBATA
; APPLICANT: Hiroko FUNAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-21

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 CAGGAGAA 738
Db 9 CAGGAGAAA 1

RESULT 58
US-09-508-753B-30
; Sequence 30, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yoko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-30

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 1 GAGAAACAG 9

RESULT 59
US-09-508-753B-64/c
; Sequence 64, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yoko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

```
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 64
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-64

Query Match      40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 10 GAGAAACAG 2

RESULT 60
US-09-513-783A-61
; Sequence 61, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-3
US-09-513-783A-61

Query Match      40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 61
US-09-513-783A-75
; Sequence 75, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-8
```

```
; OTHER INFORMATION: substrate recognition sequence
US-09-513-783A-75

Query Match      40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 62
US-09-513-783A-75
; Patent No. 5395927
; APPLICANT: BOCK, AUGUST;BINDER, FLORIAN;MULLER, FRANK
; TITLE OF INVENTION: DNA-FRAGMENT HAVING THE CYCLODEXTRIN
; GLYCOSYLTRANSFERASE GENE
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/450,126
; FILING DATE: 27-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 923,128
; FILING DATE: 24-OCT-1986
; SEQ ID NO:3;
; LENGTH: 13
;
5395927-3

Query Match      40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 3 GAAACAGAA 11

RESULT 63
US-09-332-319-5/c
; Sequence 5, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Hlston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-332-319-5

Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 745
Db 12 AAAGAGAGAAC 1

RESULT 64
US-09-332-319-6
; Sequence 6, Application US/09332319
; Patent No. 6171821
```

```
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-332-319-6

Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGAGAGACA 745
DB 1 AAAAAGAGACA 12

RESULT 65
US-09-332-319-10/c
; Sequence 10, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(1)
; OTHER INFORMATION: Wild-type polypyrimidine tract.
US-09-332-319-10

Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGAGAGACA 745
DB 1 AAAAAGAGACA 12

RESULT 66
US-09-580-923-28/c
; Sequence 28, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
; APPLICANT: Crouzet, Joel
; APPLICANT: Scherzman, Daniel
; APPLICANT: Wills, Pierre
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
```

```
; TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
; FILE REFERENCE: 03804.0138-01
; CURRENT APPLICATION NUMBER: US/09/580,923
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 08/860,038
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/FR95/01468
; PRIOR FILING DATE: 1995-11-08
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 28
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-580-923-28

Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
DB 12 AGGAAAAAAGA 1

RESULT 67
US-08-465-293A-8/c
; Sequence 8, Application US/08465293A
; Patent No. 5789651
; GENERAL INFORMATION:
; APPLICANT: Woychik, Richard P.
; TITLE OF INVENTION: Isolation and Characterization of
; TITLE OF INVENTION: Agouti A Diabetes/Obesity Related Gene.
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 555 13th Street, N.W., Suite #480 West
; CITY: Washington
; STATE: District of Columbia
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,293A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,385
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Edward A. Pennington
; REGISTRATION NUMBER: 32,588
; REFERENCE/POCKET NUMBER: 2240-7054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 857-7887
; TELEFAX: (202) 857-7929
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
```


STRAIN: Wild
TISSUE TYPE: Adult kidney and testis
IMMEDIATE SOURCE:
CLONE: Wild-type cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: transition point of exon 1 from exon 2 in
CHROMOSOME/SEGMENT: Agouti locus of mouse chromosome 2.
FEATURE:
NAME/KEY: Agouti locus
IDENTIFICATION METHOD: Experimental
OTHER INFORMATION: In addition to hair color in mice, the
OTHER INFORMATION: Agouti gene is responsible for embryonic lethality, obesity,
OTHER INFORMATION: and the development of tumor in a wide variety of tissues.
US-08-465-293A-8

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACA 745
Db 13 AGAAGCAGCACA 2

RESULT 68
US-08-463-387A-8/c
Sequence 8, Application US/08463387A
Patent No. 5843652
GENERAL INFORMATION:
APPLICANT: Woychik, Richard P.
TITLE OF INVENTION: Isolation and Characterization of
TITLE OF INVENTION: Agouti A Diabetes/Obesity Related Gene.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 555 13th Street, N.W., Suite #480 West
CITY: Washington
STATE: District of Columbia
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,387A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,385
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Edward A. Pennington
REGISTRATION NUMBER: 32,588
REFERENCE/DOCKET NUMBER: 2240-7054
TELEPHONE: (202) 857-7887
TELEFAX: (202) 857-7929
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: Wild
TISSUE TYPE: Adult kidney and testis
IMMEDIATE SOURCE:
CLONE: Wild-type cDNA clones

POSITION IN GENOME:
CHROMOSOME/SEGMENT: transition point of exon 1 from exon 2 in
CHROMOSOME/SEGMENT: Agouti locus of mouse chromosome 2.
FEATURE:
NAME/KEY: Agouti locus
IDENTIFICATION METHOD: Experimental
OTHER INFORMATION: In addition to hair color in mice, the
OTHER INFORMATION: Agouti gene is responsible for embryonic lethality, obesity,
OTHER INFORMATION: and the development of tumor in a wide variety of tissues.
US-08-463-387A-8

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACA 745
Db 13 AGAAGCAGCACA 2

RESULT 69
US-09-102-977-9/c
Sequence 9, Application US/09102977
Patent No. 6080550
GENERAL INFORMATION:
APPLICANT: Woychik, Richard P.
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF AGOUTI
TITLE OF INVENTION: A DIABETES/OBESITY RELATED GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,977
FILING DATE: 22-JUN-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/899,134
FILING DATE: 23-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,732
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ORNL:014--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
TELEFAX: (512)474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-102-977-9

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACA 745
Db 13 AGAAGCAGCACA 2

```
RESULT 70
US-09-102-977-14/c
; Sequence 14, Application US/09102977
; Patent No. 6808550
; GENERAL INFORMATION:
; APPLICANT: WOYCHIK, RICHARD P.
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF AGOUTI
; TITLE OF INVENTION: A DIABETES/OBESITY RELATED GENE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,977
; FILING DATE: 22-JUN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/899,134
; FILING DATE: 23-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,732
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ORNL:014--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512)418-3000
; TELEFAX: (512)474-7577
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-102-977-14
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACCA 745
Db 13 AGAAGCAGCACCA 2

RESULT 71
US-09-034-088A-23/c
; Sequence 23, Application US/09034088A
; Patent No. 6310034
; GENERAL INFORMATION:
; APPLICANT: WOYCHIK, RICHARD P.
; APPLICANT: BULTMAN, SCOTT J.
; APPLICANT: MICHAUD, EDWARD J.
; TITLE OF INVENTION: METHODS AND POLYPEPTIDES ENCODED BY AGOUTI GENE
; FILE REFERENCE: 4310.001600
; CURRENT APPLICATION NUMBER: US/09/034,088A
; CURRENT FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 08/064,385
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; MEDIUM TYPE: Floppy disk
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; SEQ ID NO 23
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-034-088A-23
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACCA 745
Db 13 AGAAGCAGCACCA 2

RESULT 72
US-09-781-811-23/c
; Sequence 23, Application US/09781811
; Patent No. 6514747
; GENERAL INFORMATION:
; APPLICANT: WOYCHIK, RICHARD P.
; APPLICANT: BULTMAN, SCOTT J.
; APPLICANT: MICHAUD, EDWARD J.
; TITLE OF INVENTION: AGOUTI POLYNUCLEOTIDE COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 4310.001682
; CURRENT APPLICATION NUMBER: US/09/781,811
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 09/034,088
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 08/064,385
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-781-811-23
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACCA 745
Db 13 AGAAGCAGCACCA 2

RESULT 73
US-08-808-474A-2
; Sequence 2, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; TITLE OF INVENTION: FOR ANTISENSE TARGETING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,474A
FILING DATE: 03-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTDAL:001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (214) 740-8000
TELEFAX: (214) 740-8800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-808-474A-2

Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCAGGAGA 736
DB 1 TGCCCGAGA 10

RESULT 74
US-08-388-353-478
Sequence 478, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 478:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-388-353-478
Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACACC 747
DB 1 AGAGAACACC 10

RESULT 75
US-08-488-551B-478
Sequence 478, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0239
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/488,551B
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 478:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-478

Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACACC 747
DB 1 AGAGAACACC 10

RESULT 76
US-09-508-753B-19

; Sequence 19, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:

; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yoko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiiji OHARA

; APPLICANT: Masanori WATAHIKI

; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

; FILE REFERENCE: 00162/HG

; CURRENT APPLICATION NUMBER: US/09/508,753B

; CURRENT FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: JP 9/270324

; PRIOR FILING DATE: 1997-09-18

; NUMBER OF SEQ ID NOS: 472

; SEQ ID NO 19

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-508-753B-19

Query Match 38.2%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 54;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739

Db 1 CTGGAGAAAC 10

RESULT 77

US-09-508-753B-41/c

; Sequence 41, Application US/09508753B

; Patent No. 6544736

; GENERAL INFORMATION:

; APPLICANT: Akira SHIMAMOTO

; APPLICANT: Yasuhiro FURUICHI

; APPLICANT: Yoko SHIBATA

; APPLICANT: Hiroko FUNAKI

; APPLICANT: Eiiji OHARA

; APPLICANT: Masanori WATAHIKI

; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

; FILE REFERENCE: 00162/HG

; CURRENT APPLICATION NUMBER: US/09/508,753B

; CURRENT FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: JP 9/270324

; PRIOR FILING DATE: 1997-09-18

; NUMBER OF SEQ ID NOS: 472

; SEQ ID NO 41

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-508-753B-41

Query Match 38.2%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 54;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739

Db 10 CTGGAGAAAC 1

RESULT 78

US-09-508-753B-127/c

; Sequence 127, Application US/09508753B

; Patent No. 6544736

; GENERAL INFORMATION:

; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yoko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 127
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-127

Query Match 38.2%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 54;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAGA 742

Db 10 GAGAACAGA 1

RESULT 79

US-09-769-482-47/c

; Sequence 47, Application US/09769482

; Patent No. 6566130

; GENERAL INFORMATION:

; APPLICANT: SRIVASTAVA, SHIV

; APPLICANT: MOUL, JUDD W.

; APPLICANT: XU, LINDA L.

; APPLICANT: SEGAWA, TAKEHIKO

; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

; FILE REFERENCE: POYNUCLEOTIDE ARRAY

; FILE REFERENCE: 04995.0057-00000

; CURRENT APPLICATION NUMBER: US/09/769,482

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/178,772

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/179,045

; PRIOR FILING DATE: 2000-01-31

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 47

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide

US-09-769-482-47

Query Match 38.2%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 54;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACA 740

Db 10 AGGATAAACA 1

RESULT 80

US-09-332-319-18/c

; Sequence 18, Application US/09332319

; Patent No. 6171821

; GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Holcik, Martin
APPLICANT: Liston, Peter
TITLE OF INVENTION: XIAP IRES AND USES THEREOF
FILE REFERENCE: 07891/021002
CURRENT APPLICATION NUMBER: US/09/332,319
CURRENT FILING DATE: 1999-06-14
EARLIER APPLICATION NUMBER: 09/121,979
EARLIER FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 12
TYPE: RNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (11) ..(12)
OTHER INFORMATION: Positions 11-12 are mutated.
US-09-332-319-18

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 745
Db 10 AAACAGAAC 1

RESULT 81
US-08-388-353-479
; Sequence 479, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 479:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-479

US-08-388-353-479
Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 AGAACACC 747
Db 2 AGAACACC 9

RESULT 82
US-08-388-353-480
; Sequence 480, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 480:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-480

US-08-388-353-479
Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 AGAACACC 747
Db 1 AGAACACC 8

RESULT 83
US-08-488-551B-479
; Sequence 479, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper

;; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
;; NUMBER OF SEQUENCES: 841
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
;; STREET: 400 GARDEN CITY PLAZA
;; CITY: GARDEN CITY
;; STATE: NEW YORK
;; COUNTRY: U.S.A.
;; ZIP: 11530-0299
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PM3864 (AU)
;; FILING DATE: 14-FEB-1994
;; APPLICATION NUMBER: PM4002 (AU)
;; FILING DATE: 21-FEB-1994
;; APPLICATION NUMBER: PN0284 (AU)
;; FILING DATE: 23-DEC-1994
;; APPLICATION NUMBER: US 08/388,353
;; FILING DATE: 14-FEB-1995
;; APPLICATION NUMBER: PN3021/95
;; FILING DATE: 17-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FRANK S. DIGIGLIO
;; REFERENCE/DOCKET NUMBER: 9606Z
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (516) 742-4343
;; TELEFAX: (516) 742-4366
;; INFORMATION FOR SEQ ID NO: 479:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-488-551B-479
Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 740 AGAACACC 747
Db 2 AGAACACC 9
RESULT 84
US-08-488-551B-480
; Sequence 480, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,551B
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PM3864 (AU)
;; FILING DATE: 14-FEB-1994
;; APPLICATION NUMBER: PM4002 (AU)
;; FILING DATE: 21-FEB-1994
;; APPLICATION NUMBER: PN0284 (AU)
;; FILING DATE: 23-DEC-1994
;; APPLICATION NUMBER: US 08/388,353
;; FILING DATE: 14-FEB-1995
;; APPLICATION NUMBER: PN3021/95
;; FILING DATE: 17-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FRANK S. DIGIGLIO
;; REFERENCE/DOCKET NUMBER: 9606Z
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (516) 742-4343
;; TELEFAX: (516) 742-4366
;; INFORMATION FOR SEQ ID NO: 480:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-488-551B-480
Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 740 AGAACACC 747
Db 1 AGAACACC 8
RESULT 85
US-09-229-151C-15/c
; Sequence 15, Application US/09229151C
; Patent No. 653784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: KappaB3 sequence
US-09-229-151C-15
Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 732 GGAGAAAC 739
Db 10 GGAGAAAC 3
RESULT 86

US-08-671-824-12/c
; Sequence 12, Application US/08671824
; Patent No. 6025167
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Zaug, Arthur J.
; APPLICANT: Been, Michael D.
; TITLE OF INVENTION: RNA RIBOZYME POLYMERASES,
; TITLE OF INVENTION: DIPHOSPHORYLASES, RESTRICTION
; TITLE OF INVENTION: ENDORIBONUCLEASES AND METHODS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671.824
; FILING DATE: June 5, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,624
; FILING DATE: July 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 220/166
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-671-824-12
Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 731 AGGAGAA 738
Db 11 AGGAGAA 4
RESULT 87
US-08-231-227-5
; Sequence 5, Application US/08231227
; Patent No. 5631148
; GENERAL INFORMATION:
; APPLICANT: URDEA, MICHAEL S.
; TITLE OF INVENTION: RIBOZYMES WITH PRODUCT EJECTION BY
; TITLE OF INVENTION: STRAND DISPLACEMENT
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,227
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Kenneth M.
; REFERENCE/DOCKET NUMBER: 0973.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; FEATURE:
; NAME/KEY: A
; LOCATION: 7
; OTHER INFORMATION: /label= variable
; OTHER INFORMATION: /note= an intervening sequence Nx of any length
; OTHER INFORMATION: may be inserted between nucleotides 7 and 8
US-08-231-227-5
Query Match 36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 731 AGGAGAAAC 739
Db 4 ANGAGAAC 12
RESULT 88
US-08-173-489C-10/c
; Sequence 10, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from c-myc
DESCRIPTION: sequence region in Seq ID No. 58612449
HYPOTHETICAL: Yes
ANTI-SENSE: No
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 10 :FROM 1 TO 12
US-08-173-489C-10

Query Match 36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 738
DB 8 AGGAGAA 1

RESULT 89
PCT-US95-04632-5
Sequence 5, Application PC/TUS9504632
GENERAL INFORMATION:
APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: RIBOZYMES WITH PRODUCT EJECTION BY STRAND DISPLACEMENT
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth M.
REFERENCE/DOCKET NUMBER: 0973.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
FEATURE:

NAME/KEY: A
LOCATION: 7
OTHER INFORMATION: /label= variable
OTHER INFORMATION: /note= an intervening sequence Nx of any length
OTHER INFORMATION: may be inserted between nucleotides 7 and 8
PCT-US95-04632-5

Query Match 36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 80;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAA 739
DB 4 ANGAGAA 12

RESULT 90
US-08-173-489C-89
Sequence 89, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: superoxide dismutase gene (accession # J02947) nucleotides 21 to 31
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 21
MAP POSITION: 21q22.1
PUBLICATION INFORMATION:
AUTHORS: Hjalmarsson, K, Marklund, S L,
AUTHORS: Engstrom, A, Edlund, T.
TITLE: Isolation and sequence of
TITLE: complementary dna encoding human extracellular-superoxide dismutase
JOURNAL: Proceedings of the National Academy of Sciences, USA
VOLUME: 84
PAGES: 6340-6344
DATE: 1987
RELEVANT RESIDUES IN SEQ ID NO: 89 :FROM 1 TO 11
US-08-173-489C-89

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
|||||
Db 1 AGGAGAAAG 11

RESULT 91
US-08-687-916-14/c
; Sequence 14, Application US/08687916
; Patent No. 5908972
; GENERAL INFORMATION:
; APPLICANT: HOUTZ, Robert L.
; TITLE OF INVENTION: ISOLATED SPINACH
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,916
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/391,000
; FILING DATE: 21-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Radio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 028750-138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-687-916-14

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
|||||
Db 11 GAGAAAAAAA 1

RESULT 92
US-09-072-435-8/c
; Sequence 8, Application US/09072435
; Patent No. 6215051
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; APPLICANT: Chan, Ming-Tsair

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 744
|||||
Db 11 AGAAACGCAAC 1

RESULT 93
US-09-138-614-14/c
; Sequence 14, Application US/09138614
; Patent No. 6245541
; GENERAL INFORMATION:
; APPLICANT: HOUTZ, Robert L.
; TITLE OF INVENTION: ISOLATED SPINACH
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/973,324
; FILING DATE: 04-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28123/34274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-072-435-8

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,614
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,916
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 028750-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-138-614-14

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
DB 11 GAGAAAAAAA 1

RESULT 94
US-08-083-945C-8
Sequence 8, Application US/08083945C
Patent No. 6274134
GENERAL INFORMATION:
APPLICANT: Beckner, Marie E.
APPLICANT: Liotta, Lance A.
APPLICANT: Krutzsch, Henry C.
TITLE OF INVENTION: AMP-1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,945C
FILING DATE: 25-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,043
FILING DATE: 29-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-156-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-083-945C-8

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 1 AGGAGGAAGAG 11

RESULT 95
US-09-072-917A-10/C
Sequence 10, Application US/09072917A
Patent No. 6288302
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-072-917A-10

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGAAC 744
DB 11 AGAAGCGCAAC 1

RESULT 96

<hr/>					
US-09-249-155A-73/c					
; Sequence 73, Application US/09249155A					
; Patent No. 6538173					
; GENERAL INFORMATION:					
; APPLICANT: Heber-Katz, Ellen					
; TITLE OF INVENTION: Compositions and Methods for Wound					
; TITLE OF INVENTION: Healing					
; FILE REFERENCE: 00486.78503					
; CURRENT APPLICATION NUMBER: US/09/249,155A					
; CURRENT FILING DATE: 1999-02-12					
; PRIOR APPLICATION NUMBER: US 60/074,737					
; PRIOR FILING DATE: 1998-02-13					
; PRIOR APPLICATION NUMBER: US 60/097,937					
; PRIOR FILING DATE: 1998-08-26					
; PRIOR APPLICATION NUMBER: US 60/102,051					
; PRIOR FILING DATE: 1998-09-28					
; NUMBER OF SEQ ID NOS: 346					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 73					
; LENGTH: 11					
; TYPE: DNA					
; ORGANISM: Mus musculus					
; US-09-249-155A-73					
Query Match 35.5%; Score 7.8; DB 1; Length 11;					
Best Local Similarity 81.8%; Pred. No. 78;					
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	732 GCAGAAACAGA 742				
DB	11 GCAGAAACCGA 1				
RESULT 97					
PCT-US94-07107A-8					
; Sequence 8, Application PC/TUS9407107A					
; GENERAL INFORMATION:					
; APPLICANT: The Government of the United States of					
; APPLICANT: America, as represented by the Secretary,					
; APPLICANT: Department of Health and Human Services					
; TITLE OF INVENTION: AAMP-1					
; NUMBER OF SEQUENCES: 15					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Townsend and Townsend Khourie and Crew					
; STREET: 379 Lytton Avenue					
; CITY: Palo Alto					
; STATE: California					
; COUNTRY: US					
; ZIP: 94301					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.25					
; CURRENT APPLICATION DATA:					
; FILING DATE: 25-JUN-1993					
; CLASSIFICATION:					
; PRIOR APPLICATION NUMBER: US 07/827,043					
; FILING DATE: 29-JAN-1992					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Dow, Karen B.					
; REGISTRATION NUMBER: 29,684					
; REFERENCE/DOCKET NUMBER: 15280-156-1					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (415) 326-2400					
; TELEFAX: (415) 326-2422					
; INFORMATION FOR SEQ ID NO: 8:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 11 base pairs					
; TYPE: nucleic acid					
; STRANDEDNESS: single					
US-09-249-155A-73/c					
; Sequence 73, Application US/09249155A					
; Patent No. 6538173					
; GENERAL INFORMATION:					
; APPLICANT: Heber-Katz, Ellen					
; TITLE OF INVENTION: Compositions and Methods for Wound					
; TITLE OF INVENTION: Healing					
; FILE REFERENCE: 00486.78503					
; CURRENT APPLICATION NUMBER: US/09/249,155A					
; CURRENT FILING DATE: 1999-02-12					
; PRIOR APPLICATION NUMBER: US 60/074,737					
; PRIOR FILING DATE: 1998-02-13					
; PRIOR APPLICATION NUMBER: US 60/097,937					
; PRIOR FILING DATE: 1998-08-26					
; PRIOR APPLICATION NUMBER: US 60/102,051					
; PRIOR FILING DATE: 1998-09-28					
; NUMBER OF SEQ ID NOS: 346					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 73					
; LENGTH: 11					
; TYPE: DNA					
; ORGANISM: Mus musculus					
; US-09-249-155A-73					
Query Match 35.5%; Score 7.8; DB 1; Length 11;					
Best Local Similarity 81.8%; Pred. No. 78;					
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	731 AGGAGAACAG 741				
DB	1 AGGAGGAAGAG 11				
RESULT 98					
US-08-441-887A-271/c					
; Sequence 271, Application US/08441887A					
; Patent No. 5837832					
; GENERAL INFORMATION:					
; APPLICANT: Chee, Mark					
; APPLICANT: Cronin, Maureen T.					
; APPLICANT: Fodor, Stephen P.A.					
; APPLICANT: Huang, Xiaohua X.					
; APPLICANT: Hubbell, Earl A.					
; APPLICANT: Lipschutz, Robert J.					
; APPLICANT: Lobban, Peter E.					
; APPLICANT: Morris, Macdonald S.					
; APPLICANT: Sheldon, Edward L.					
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on					
; TITLE OF INVENTION: Biological Chips					
; NUMBER OF SEQUENCES: 360					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Townsend and Townsend and Crew LLP					
; STREET: Two Embarcadero Center, 8th Floor					
; CITY: San Francisco					
; STATE: California					
; COUNTRY: USA					
; ZIP: 94111					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.25					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/441,887A					
; FILING DATE: 16-MAY-1995					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/143,312					
; FILING DATE: 26-OCT-1993					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/082,937					
; FILING DATE: 25-JUN-1993					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Liebeschuetz, Joseph O.					
; REGISTRATION NUMBER: 37,505					
; REFERENCE/DOCKET NUMBER: 018547-004160US					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: 650-326-2400					
; TELEFAX: 650-326-2422					
; INFORMATION FOR SEQ ID NO: 271:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 12 base pairs					
; TYPE: nucleic acid					
; STRANDEDNESS: single					
; TOPOLOGY: linear					
; MOLECULE TYPE: DNA (probe)					
; US-08-441-887A-271					
Query Match 35.5%; Score 7.8; DB 1; Length 12;					
Best Local Similarity 81.8%; Pred. No. 87;					
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					

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US-09-249-155A-73/c					
; Sequence 73, Application US/09249155A					
; Patent No. 6538173					
; GENERAL INFORMATION:					
; APPLICANT: Heber-Katz, Ellen					
; TITLE OF INVENTION: Compositions and Methods for Wound					
; TITLE OF INVENTION: Healing					
; FILE REFERENCE: 00486.78503					
; CURRENT APPLICATION NUMBER: US/09/249,155A					
; CURRENT FILING DATE: 1999-02-12					
; PRIOR APPLICATION NUMBER: US 60/074,737					
; PRIOR FILING DATE: 1998-02-13					
; PRIOR APPLICATION NUMBER: US 60/097,937					
; PRIOR FILING DATE: 1998-08-26					
; PRIOR APPLICATION NUMBER: US 60/102,051					
; PRIOR FILING DATE: 1998-09-28					
; NUMBER OF SEQ ID NOS: 346					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 73					
; LENGTH: 11					
; TYPE: DNA					
; ORGANISM: Mus musculus					
; US-09-249-155A-73					
Query Match 35.5%; Score 7.8; DB 1; Length 11;					
Best Local Similarity 81.8%; Pred. No. 78;					
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	732 GCAGAAACAGA 742				
DB	11 GCAGAAACCGA 1				
RESULT 97					
PCT-US94-07107A-8					
; Sequence 8, Application PC/TUS9407107A					
; GENERAL INFORMATION:					
; APPLICANT: The Government of the United States of					
; APPLICANT: America, as represented by the Secretary,					
; APPLICANT: Department of Health and Human Services					
; TITLE OF INVENTION: AAMP-1					
; NUMBER OF SEQUENCES: 15					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Townsend and Townsend Khourie and Crew					
; STREET: 379 Lytton Avenue					
; CITY: Palo Alto					
; STATE: California					
; COUNTRY: US					
; ZIP: 94301					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.25					
; CURRENT APPLICATION DATA:					
; FILING DATE: 25-JUN-1993					
; CLASSIFICATION:					
; PRIOR APPLICATION NUMBER: US 07/827,043					
; FILING DATE: 29-JAN-1992					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Dow, Karen B.					
; REGISTRATION NUMBER: 29,684					
; REFERENCE/DOCKET NUMBER: 15280-156-1					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (415) 326-2400					
; TELEFAX: (415) 326-2422					
; INFORMATION FOR SEQ ID NO: 8:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 11 base pairs					
; TYPE: nucleic acid					
; STRANDEDNESS: single					
US-09-249-155A-73/c					
; Sequence 73, Application US/09249155A					
; Patent No. 6538173					
; GENERAL INFORMATION:					
; APPLICANT: Heber-Katz, Ellen					
; TITLE OF INVENTION: Compositions and Methods for Wound					
; TITLE OF INVENTION: Healing					
; FILE REFERENCE: 00486.78503					
; CURRENT APPLICATION NUMBER: US/09/249,155A					
; CURRENT FILING DATE: 1999-02-12					
; PRIOR APPLICATION NUMBER: US 60/074,737					
; PRIOR FILING DATE: 1998-02-13					
; PRIOR APPLICATION NUMBER: US 60/097,937					
; PRIOR FILING DATE: 1998-08-26					
; PRIOR APPLICATION NUMBER: US 60/102,051					
; PRIOR FILING DATE: 1998-09-28					
; NUMBER OF SEQ ID NOS: 346					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 73					
; LENGTH: 11					
; TYPE: DNA					
; ORGANISM: Mus musculus					
; US-09-249-155A-73					
Query Match 35.5%; Score 7.8; DB 1; Length 11;					
Best Local Similarity 81.8%; Pred. No. 78;					
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	731 AGGAGAACAG 741				
DB	1 AGGAGGAAGAG 11				
RESULT 98					
US-08-441-887A-271/c					
; Sequence 271, Application US/08441887A					
; Patent No. 5837832					
; GENERAL INFORMATION:					
; APPLICANT: Chee, Mark					
; APPLICANT: Cronin, Maureen T.					
; APPLICANT: Fodor, Stephen P.A.					
; APPLICANT: Huang, Xiaohua X.					
; APPLICANT: Hubbell, Earl A.					
; APPLICANT: Lipschutz, Robert J.					
; APPLICANT: Lobban, Peter E.					
; APPLICANT: Morris, Macdonald S.					
; APPLICANT: Sheldon, Edward L.					
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on					
; TITLE OF INVENTION: Biological Chips					
; NUMBER OF SEQUENCES: 360					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Townsend and Townsend and Crew LLP					
; STREET: Two Embarcadero Center, 8th Floor					
; CITY: San Francisco					
; STATE: California					
; COUNTRY: USA					
; ZIP: 94111					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.25					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/441,887A					
; FILING DATE: 16-MAY-1995					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/143,312					
; FILING DATE: 26-OCT-1993					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/082,937					
; FILING DATE: 25-JUN-1993					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Liebeschuetz, Joseph O.					
; REGISTRATION NUMBER: 37,505					
; REFERENCE/DOCKET NUMBER: 018547-004160US					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: 650-326-2400					
; TELEFAX: 650-326-2422					
; INFORMATION FOR SEQ ID NO: 271:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 12 base pairs					
; TYPE: nucleic acid					
; STRANDEDNESS: single					
; TOPOLOGY: linear					
; MOLECULE TYPE: DNA (probe)					
; US-08-441-887A-271					
Query Match 35.5%; Score 7.8; DB 1; Length 12;					
Best Local Similarity 81.8%; Pred. No. 87;					
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					

QY 732 GGAGAAACAGA 742
 |||||
 Db 12 GGGGAACAGA 2

RESULT 99
 US-08-494-301A-3
 ; Sequence 3, Application US/08494301A
 ; Patent No. 5856461
 ; GENERAL INFORMATION:
 ; APPLICANT: Colote, Soudhir
 ; APPLICANT: Pirotsky, Eduardo
 ; TITLE OF INVENTION: Oligonucleotides to Inhibit the
 ; TITLE OF INVENTION: Expression of Isoprenyl Protein Transferases
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lucas & Just
 ; STREET: 205 E. 42nd Street
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10017
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch,
 ; MEDIUM TYPE: 1.44 MB storage
 ; COMPUTER: IBM 486 Compatible
 ; OPERATING SYSTEM: MS-DOS 5.0
 ; SOFTWARE: WordPerfect 5.0
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 23-JUNE-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9413035.8
 ; FILING DATE: 29-JUNE-1994
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 base pairs
 ; TYPE: nucleotide
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; ANTI-SENSE: Yes
 ; US-08-494-301A-3

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
 |||||
 Db 2 AGGAGTAGCAG 12

RESULT 100
 US-08-173-489C-215
 ; Sequence 215, Application US/08173489C
 ; Patent No. 5861244
 ; GENERAL INFORMATION:
 ; APPLICANT: WANG, C.-G.
 ; APPLICANT: HEPBURN, A. G.
 ; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
 ; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
 ; NUMBER OF SEQUENCES: 365
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
 ; STREET: 510 EAST 73RD STREET,
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10021
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44mb storage
 ; COMPUTER: IBM PC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2
 SOFTWARE: Wordperfect Version 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/173,489C
 FILING DATE: 22 DEC 1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/968,436
 FILING DATE: 29 OCT 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Handelman, Joseph H.
 REGISTRATION NUMBER: 26,179
 REFERENCE/DOCKET NUMBER: U9518-6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (attorney) (212) 708-1880
 TELEFAX: (attorney) (212) 246-8959
 INFORMATION FOR SEQ ID NO: 215:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 DESCRIPTION: 23s rRNA gene from Escherichia coli
 DESCRIPTION: (Accession # M25458) nucleotides 212 to 223
 HYPOTHETICAL: no
 ANTI-SENSE: no
 ORIGINAL SOURCE:
 ORGANISM: Escherichia coli
 STRAIN: MRE600
 PUBLICATION INFORMATION:
 AUTHORS: Branlant, C, Krol, A, Machatt, M, A,
 AUTHORS: Pouyet, J, Ebel, J P, Edwards, K, Roessel, H.
 TITLE: Primary and secondary
 TITLE: structures of Escherichia coli MRE 600 23S
 TITLE: ribosomal RNA Comparison with models of
 TITLE: secondary structure for maize chloroplast 23S
 TITLE: rRNA and for large portions of mouse and human
 TITLE: 16S mitochondrial rRNAs
 JOURNAL: Nucleic Acids Research
 VOLUME: 9
 PAGES: 4303-4324
 DATE: 1981
 RELEVANT RESIDUES IN SEQ ID NO: 215 :FROM 1 TO 12
 US-08-173-489C-215

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GGAGAACAGA 743
 |||||
 Db 1 GAGGAAGAGA 11

RESULT 101
 US-08-173-489C-229
 ; Sequence 229, Application US/08173489C
 ; Patent No. 5861244
 ; GENERAL INFORMATION:
 ; APPLICANT: WANG, C.-G.
 ; APPLICANT: HEPBURN, A. G.
 ; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
 ; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
 ; NUMBER OF SEQUENCES: 365
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
 ; STREET: 510 EAST 73RD STREET,
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10021.

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 229:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 23S rRNA gene from Halococcus morrhuae
; DESCRIPTION: (Accession # X05481) nucleotides 1628 to 1639
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Halococcus morrhuae
; PUBLICATION INFORMATION:
; AUTHORS: Leffers, H, Kjems, J, Ostergaard, L,
; AUTHORS: Larsen, N, Garrett, R A.
; TITLE: Evolutionary Relationship
; TITLE: Amongst Archaeobacteria: A Comparative Study of
; TITLE: 23 S Ribosomal RNAs of a Sulphur-dependent
; TITLE: Extreme Thermophile, an Extreme Halophile and a
; TITLE: Thermophilic Methanogen
; JOURNAL: Journal of Molecular Biology
; VOLUME: 195
; PAGES: 43-61
; DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 229 :FROM 1 TO 12
;
; US-08-173-489C-229
;
; Query Match 35.5%; Score 7.8; DB 1; Length 12;
; Best Local Similarity 81.8%; Pred. No. 87;
; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 733 GAGAACAGAA 743
; Db |||||
; 1 GAGATAGAGAA 11
;
; RESULT 102
; US-08-173-489C-351
; Sequence 351, Application US/08173489C
; Patent No. 5661244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 229:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 23S rRNA gene from Halococcus morrhuae
; DESCRIPTION: (Accession # X05481) nucleotides 1628 to 1639
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Halococcus morrhuae
; PUBLICATION INFORMATION:
; AUTHORS: Leffers, H, Kjems, J, Ostergaard, L,
; AUTHORS: Larsen, N, Garrett, R A.
; TITLE: Evolutionary Relationship
; TITLE: Amongst Archaeobacteria: A Comparative Study of
; TITLE: 23 S Ribosomal RNAs of a Sulphur-dependent
; TITLE: Extreme Thermophile, an Extreme Halophile and a
; TITLE: Thermophilic Methanogen
; JOURNAL: Journal of Molecular Biology
; VOLUME: 195
; PAGES: 43-61
; DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 229 :FROM 1 TO 12
;
; US-08-173-489C-229
;
; Query Match 35.5%; Score 7.8; DB 1; Length 12;
; Best Local Similarity 81.8%; Pred. No. 87;
; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 733 GAGAACAGAA 743
; Db |||||
; 1 GAGATAGAGAA 11
;
; RESULT 102
; US-08-173-489C-351
; Sequence 351, Application US/08173489C
; Patent No. 5661244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 351:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: p53 gene, nucleotides 1066-1077
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Harlow, E, Williamson, N M, Ralston, R,
; AUTHORS: Helfman, D M, Adams T E.
; TITLE: Molecular cloning and in
; TITLE: vitro expression of a cDNA for human cellular
; TITLE: tumor antigen p53
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; PAGES: 1601-1610
; DATE: 1985
; RELEVANT RESIDUES IN SEQ ID NO: 351 :FROM 1 TO 12
;
; US-08-173-489C-351
;
; Query Match 35.5%; Score 7.8; DB 1; Length 12;
; Best Local Similarity 81.8%; Pred. No. 87;
; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 733 GAGAACAGAA 743
; Db |||||
; 2 GAGGAGAGAA 12
;
; RESULT 103
; US-08-779-355-19
; Sequence 19, Application US/08779355
; Patent No. 6017701
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; APPLICANT: Mullinax, Rebecca L.
; TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING
; TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/779,355
 FILING DATE: 06-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/775,993
 FILING DATE: 03-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Kulik, David J.
 REGISTRATION NUMBER: 36,576
 REFERENCE/DOCKET NUMBER: 43092CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)628-8800
 TELEFAX: (202)628-8844
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-779-355-19

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
 |||||
 Db 2 TGCGAAGAGAA 12

RESULT 104
 US-08-938-835A-19
 Sequence 19, Application US/08938835A
 Patent No. 6060245
 GENERAL INFORMATION:
 APPLICANT: SORGE, Joseph A.
 APPLICANT: MULLINAX, Rebecca L.
 TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING
 TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ADDRESSEE: Dunner, L.L.P.
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/938,835A
 FILING DATE: 26-SEPT-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/775,993
 FILING DATE: 03-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/779,335
 FILING DATE: 06-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barker, M. Paul
 REGISTRATION NUMBER: 32,013
 REFERENCE/DOCKET NUMBER: 04121.0044-02000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-938-835A-19

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
 |||||
 Db 2 TGCGAAGAGAA 12

RESULT 105
 US-08-862-431-24
 Sequence 24, Application US/08862431
 Patent No. 6120994
 GENERAL INFORMATION:
 APPLICANT: TAM, SHUI-PANG
 TITLE OF INVENTION: ANTIOXIDANT RESPONSIVE ELEMENT
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: US
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/862,431
 FILING DATE: 23-MAY-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kim, Judith U.
 REGISTRATION NUMBER: 40,679
 REFERENCE/DOCKET NUMBER: 1669.0020000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-862-431-24

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGAC 744
 |||||
 Db 1 AGAACACAGC 11

RESULT 106
 US-09-043-149-33/C
 Sequence 33, Application US/09043149
 Patent No. 6355418
 GENERAL INFORMATION:
 APPLICANT: Schmidt, Gunter

; TITLE OF INVENTION: Chimeric Oligonucleotides and Uses Thereof in the
; TITLE OF INVENTION: Identification of Antisense Binding Sites
; FILE REFERENCE: 020600-272
; CURRENT APPLICATION NUMBER: US/09/043,149
; CURRENT FILING DATE: 1998-03-13
; PRIOR FILING DATE: 1996-09-13
; PRIOR FILING DATE: 1995-09-14
; PRIOR FILING DATE: 1995-09-14
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-043-149-33

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAGACGAC 744
Db 12 AGGAAGACGAC 2

RESULT 107
US-09-513-783A-65
; Sequence 65, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-11
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase-6
; OTHER INFORMATION: substrate recognition sequence
US-09-513-783A-65

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAACAGAC 742
Db 1 GTAGAACATAG 11

RESULT 108
US-09-475-947A-59
; Sequence 59, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS00667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 59
; LENGTH: 12
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-59

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGAGAACAC 740
Db 1 CAGCAGACAC 11

RESULT 109
US-09-475-947A-329/c
; Sequence 329, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS00667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 329
; LENGTH: 12
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-329

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAACAGAC 742
Db 12 GGAGAGAGAGA 2

RESULT 110
US-08-687-916-11/c
; Sequence 11, Application US/08687916
; Patent No. 5908972
; GENERAL INFORMATION:
; APPLICANT: HOUTZ, Robert L.
; TITLE OF INVENTION: ISOLATED SPINACH
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,916
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:

```
/ APPLICATION NUMBER: US 08/391,000
/ FILING DATE: 21-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dadio, Susan M.
/ REGISTRATION NUMBER: 40,373
/ REFERENCE/DOCKET NUMBER: 028750-138
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-687-916-11

Query Match 33.6%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 9 GAGAAAAG 1

RESULT 111
US-09-138-614-11/c
/ Sequence 11, Application US/09138614
/ Patent No. 6245541
/ GENERAL INFORMATION:
/ APPLICANT: HOUTZ, Robert L.
/ TITLE OF INVENTION: ISOLATED SPINACH
/ TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
/ TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
/ TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
/ TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
/ STREET: P.O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/138,614
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/687,916
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dadio, Susan M.
/ REGISTRATION NUMBER: 40,373
/ REFERENCE/DOCKET NUMBER: 028750-138
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-09-138-614-11

/ APPLICATION NUMBER: US 08/391,000
/ FILING DATE: 21-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dadio, Susan M.
/ REGISTRATION NUMBER: 40,373
/ REFERENCE/DOCKET NUMBER: 028750-138
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-687-916-11

Query Match 33.6%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 9 GAGAAAAG 1

RESULT 112
US-08-254-811D-5/c
/ Sequence 5, Application US/08254811D
/ Patent No. 5773213
/ GENERAL INFORMATION:
/ APPLICANT: Gullans, Steven R.
/ APPLICANT: Kojima, Ryoji
/ APPLICANT: Randall, Jeffrey
/ TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
/ TITLE OF INVENTION: Hybridization Steps
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Macwright, Robert S.
/ STREET: 1 Broadway
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 6.1 for Windows
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/254,811D
/ FILING DATE: 06-JUN-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Macwright, Robert S.
/ REGISTRATION NUMBER: 32,425
/ REFERENCE/DOCKET NUMBER: 1854/46101
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 425-7200
/ TELEFAX: (212) 425-5288
/ TELEX: 422141
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ HYPOTHETICAL: No
US-08-254-811D-5

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 10 AGAACAGA 2

RESULT 113
US-08-808-474A-3
/ Sequence 3, Application US/08808474A
/ Patent No. 5856103
/ GENERAL INFORMATION:
/ APPLICANT: Gray, Donald M.
/ APPLICANT: Clark, Chris L.
/ TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
/ TITLE OF INVENTION: FOR ANTISENSE TARGETING
/ NUMBER OF SEQUENCES: 37
```


;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Locke Purnell Rain Harrell
;; STREET: 2200 Ross Avenue, Suite 2200
;; CITY: Dallas
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 75201-6776
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/808,474A
;; FILING DATE: 03-MAR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mayfield, Denise L.
;; REGISTRATION NUMBER: 33,732
;; REFERENCE/DOCKET NUMBER: UTDA:001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (214) 740-8000
;; TELEFAX: (214) 740-8800
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-808-474A-3

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 1 GCCCGGAGA 9

RESULT 114
US-08-388-353-477
; Sequence 477, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Leamont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343

;; TELEFAX: (516) 742-4366
;; TELEX: 230 901 SANS UR
;; INFORMATION FOR SEQ ID NO: 477:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-388-353-477

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
Db 2 AGAGAACAC 10

RESULT 115
US-08-488-551B-477
; Sequence 477, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 477:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-477

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;

```
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGAACAC 746
Db 2 AGAGAACAC 10

RESULT 116
US-08-522-384-3/c
; Sequence 3, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-3

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 10 GCCAGGAGA 2

RESULT 117
US-08-522-384-35/c
; Sequence 35, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-35

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 10 GCCAGGAGA 2

RESULT 118
US-08-522-384-36/c
; Sequence 36, Application US/08522384
; Patent No. 6110667
```

```
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-36

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 10 GCCAGGAGA 2

RESULT 119
US-08-522-384-93/c
; Sequence 93, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-93

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 9 GCCAGGAGA 1

RESULT 120
US-08-849-567A-41/c
; Sequence 41, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMAIC DNA MOLECULES
; FILE REFERENCE: SCR1943S
; CURRENT APPLICATION NUMBER: US/08/849,567A
; CURRENT FILING DATE: 1997-08-25
; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
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; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: substrate
; OTHER INFORMATION: binding region
US-08-849-567A-41

Query Match          33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGCA 742
Db 10 AGAAATAGA 2

RESULT 121
US-09-475-947A-135
; Sequence 135, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-135

Query Match          33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACCA 745
Db 1 AACAGAATA 9

RESULT 122
US-09-508-753B-36/c
; Sequence 36, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHINAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence

; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; OTHER INFORMATION: 33.6%; Score 7.4; DB 1; Length 10;
US-09-508-753B-36

Query Match          33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 9 GAAGCAGAA 1

RESULT 123
PCT-US94-08023-32/c
; Sequence 32, Application PC/TUS9408023
; GENERAL INFORMATION:
; APPLICANT: de Kloet, Siwo R.
; TITLE OF INVENTION: Sex-Specific DNA Probe For Parrots,
; TITLE OF INVENTION: Methods And Kits
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08023
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,198
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: FL20979-34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-08023-32

Query Match          33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGGAACA 740
Db 10 GGAGAAAAA 2

RESULT 124
US-08-237-233-3/c
; Sequence 3, Application US/08237233
; Patent No. 5414077
; GENERAL INFORMATION:
; APPLICANT: LIN, KUEI-YING
; APPLICANT: MATTEUCCI, MARK
```

TITLE OF INVENTION: PSEUDONUCLEOSIDES AND
TITLE OF INVENTION: PSEUDONUCLEOTIDES AND THEIR POLYMERS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: IRELL & MANELLA
STREET: 545 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/237,233
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/594147
FILING DATE: 09-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29959
REFERENCE/DOCKET NUMBER: 4610-0006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-237-233-3
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 732 GGAGAAACA 740
Db 9 GGAGAAAAA 1
RESULT 125
US-08-435-350-92
Sequence 92, Application US/08435350
Patent No. 5599704
GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: TREATMENT OF BREAST CANCER
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,350
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936,531
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/245
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-350-92
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCCAGGAG 735
Db 1 UACCAGGAG 9
RESULT 126
US-08-254-811D-6/c
Sequence 6, Application US/08254811D
Patent No. 5773213
GENERAL INFORMATION:
APPLICANT: Gullans, Steven R.
APPLICANT: Kojima, Ryoji
APPLICANT: Randall, Jeffrey
TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
TITLE OF INVENTION: Hybridization Steps
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Macwright, Robert S.
STREET: 1 Broadway
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,811D
FILING DATE: 06-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Macwright, Robert S.
REGISTRATION NUMBER: 32,425
REFERENCE/DOCKET NUMBER: 1854/46101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: 422141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: No
US-08-254-811D-6
Query Match 33.6%; Score 7.4; DB 1; Length 11;

Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 734 AGAACAGCA 742
|||||
Db 11 AGAACAGCA 3

RESULT 127

US-08-764-522A-8
; Sequence 8, Application US/08764522A
; Patent No. 6090544
; GENERAL INFORMATION:
; APPLICANT: HARADA, SHUN-ICHI
; APPLICANT: SAMPATH, T. K.
; APPLICANT: RODAN, GIDSON A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,522A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: VITO, CHRISTINE C.
; REGISTRATION NUMBER: 39,061
; REFERENCE/DOCKET NUMBER: CRP-126
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..11
; OTHER INFORMATION: /product= "MEP-2 MUTANT CONSENSUS"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 744
|||||
Db 3 AAACATAAC 11

RESULT 128
US-08-764-522A-8
; Sequence 8, Application US/08764528
; Patent No. 6103491
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, K. T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,522A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: VITO, CHRISTINE C.
; REGISTRATION NUMBER: 39,061
; REFERENCE/DOCKET NUMBER: CRP-126
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..11
; OTHER INFORMATION: /product= "MEP-2 MUTANT CONSENSUS"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 744
|||||
Db 3 AAACATAAC 11

RESULT 128

US-08-764-528-8
; Sequence 8, Application US/08764528
; Patent No. 6103491
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, K. T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,528
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: VITO, CHRISTINE C.
; REGISTRATION NUMBER: 39,061
; REFERENCE/DOCKET NUMBER: CRP-127
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..11
; OTHER INFORMATION: /product= "MEF-2 MUTANT CONSENSUS"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 CCAGGAGAA 737
|||||

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,528
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: VITO, CHRISTINE C.
REGISTRATION NUMBER: 39,061
REFERENCE/DOCKET NUMBER: CRP-127
TELEPHONE: (617)-248-7000
TELEFAX: (617)-248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..11
OTHER INFORMATION: /product= "MEF-2 MUTANT CONSENSUS"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 744
|||||
Db 3 AAACATAAC 11

RESULT 129
US-09-196-523-23
; Sequence 23, Application US/09196523A
; Patent No. 6248525
; GENERAL INFORMATION:
; APPLICANT: Nilsen, Timothy W.
; TITLE OF INVENTION: Method for Identifying and Inactivating Essential or
; TITLE OF INVENTION: Functional Genes
; FILE REFERENCE: ILI 130
; CURRENT APPLICATION NUMBER: US/09/196,523A
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/079,851
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-196-523-23

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 CCAGGAGAA 737
|||||

Db 2 CCTGGAGAA 10

US-08-930-828A-25
; Sequence 25, Application US/08930828A
; Patent No. 6261768
; GENERAL INFORMATION:
; APPLICANT: TODD, Alison
; TITLE OF INVENTION: METHOD FOR AMPLIFYING SPECIFIC NUCLEIC
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,828A
; FILING DATE: 16-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KORNEAU, Anne M.
; REGISTRATION NUMBER: 25,864
; REFERENCE/DOCKET NUMBER: TODD-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-930-828A-25

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAA 737
Db 1 CCAGGAGAA 9

RESULT 131
US-08-722-015A-4
; Sequence 4, Application US/08722015A
; Patent No. 6379881
; GENERAL INFORMATION:
; APPLICANT: Fouchier, Ronaldus A.M.
; APPLICANT: Schuitemaker, Johanna
; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCYTII
; TITLE OF INVENTION: INDUCING AND NON SYNCYTII INDUCING VARIANTS OF THE HUMAN IMMUN
; FILE REFERENCE: 9250.25
; CURRENT APPLICATION NUMBER: US/08/722,015A
; CURRENT FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide.

US-08-722-015A-4

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAACAACA 742
Db 3 AGAACAACA 11

RESULT 132
US-09-249-155A-86
; Sequence 86, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-86

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
Db 1 ACAGAACAC 9

RESULT 133
US-09-249-155A-124
; Sequence 124, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-124

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 738 ACAGAACAC 746
|| |||||
Db 3 ACCGACAC 11

RESULT 134
5214136-10/c
; APPLICANT: LIN, KUI-YING; MATTEUCCI, MARK
; TITLE OF INVENTION: ANTHRAQUINONE-DERIVATIVES
; OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,941
; FILING DATE: 20-FEB-1990
; SEQ ID NO: 10:
; LENGTH: 11
5214136-10

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 GGAGAACAC 740
|| |||||
Db 9 GGAGAACAC 1

RESULT 135
US-08-376-362A-3/c
; Sequence 3, Application US/08376362A
; Patent No. 5693756
; GENERAL INFORMATION:
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Blackshaw, Seth
; APPLICANT: Snyder, Solomon H.
; TITLE OF INVENTION: AMILORIDE-SENSITIVE SODIUM CHANNEL AND
; TITLE OF INVENTION: METHOD OF IDENTIFYING SUBSTANCES WHICH STIMULATE OR BLOCK
; TITLE OF INVENTION: SALTY TASTE PERCEPTION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, LTD
; STREET: 1001 G Street, N.W., Eleventh Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/376,362A
; FILING DATE: 23-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan A., Sarah
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-376-362A-3

Query Match 31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 729 CCAGGAG 735
|| |||||
Db 7 CCAGGAG 1

RESULT 136
US-08-859-954-30/c
; Sequence 30, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-30

Query Match 31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 738 ACAGAAC 744
|| |||||
Db 8 ACAGAAC 2

RESULT 137
US-08-859-954-541/c
; Sequence 541, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.

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; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 541:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-541

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Query Match 31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 730 CAGGAGA 736
Db 7 CAGGAGA 1

```

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RESULT 138
US-09-985-799-19
; Sequence 19, Application US/09985799
; Patent No. RE38392
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1239 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/985,799
; FILING DATE: 06-NOV-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-985-799-19

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 TGCCAGG 733
Db 4 TGCCAGG 10

RESULT 139
US-07-739-642-13
; Sequence 13, Application US/07739642
; Patent No. 5173427
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: Vectors And Hosts With Increased
; TITLE OF INVENTION: Expression Of Hbcag
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/739,642
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

```



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;
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-739-642-13

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 AACAGAA 743
Db 1 AACAGAA 7

RESULT 140
US-07-739-643-13
; Sequence 13, Application US/07739643
; Patent No. 5175094
; GENERAL INFORMATION:
; APPLICANT: Mallonee,, Richard L.
; TITLE OF INVENTION: Increased Expression of HbcAg
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt,, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-739-142-13

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 AACAGAA 743
Db 1 AACAGAA 7

RESULT 142
US-08-548-199-14/c
; Sequence 14, Application US/08548199
; Patent No. 5652106
; GENERAL INFORMATION:
; APPLICANT: Plikeytis, Bonnie B.
; APPLICANT: Shinnick, Thomas M.
; APPLICANT: Crawford, Jack T.
; TITLE OF INVENTION: RAPID AMPLIFICATION-BASED SUBTYPING OF
; MYCOBACTERIUM TUBERCULOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 1200, The Candler Building
; STREET: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 25-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/072,450
; FILING DATE: 04 JUNE 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414,062
```

```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..10
; OTHER INFORMATION: /number=10
; OTHER INFORMATION: /note="Consensus sequence of 10 bp tandem repeat
; OTHER INFORMATION: of MPTR (Hermans et al. 1992)"
US-08-548-199-14

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 742 AACACCG 748
Db 9 AACACCG 3

RESULT 143
US-08-440-787A-66/c
; Sequence 66, Application US/08440787A
; Patent No. 5770434
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; NUMBER OF SEQUENCES: 174
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440.787A
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-440-787A-70

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGAGAA 737
Db 9 AGAGAA 3

RESULT 145
US-08-594-031-19
; Sequence 19, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
```

```
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20004-2400
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/594,031
/ FILING DATE: 30-JAN-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/006,838
/ FILING DATE: 16-NOV-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Remenick, James
/ REGISTRATION NUMBER: 36,902
/ REFERENCE/DOCKET NUMBER: 0A146-0110
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-639-7700
/ TELEFAX: 202-639-7890
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ US-08-594-031-19

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 TGCCAGG 733
Db 4 TGCCAGG 10

RESULT 146
US-08-388-353-481
; Sequence 481, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424

US-08-488-551B-481
; Sequence 481, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 481:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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TOPOLOGY:	linear	Score 7:	DB 1;	Length 10;	Indels	Mismatches	Gaps
MOLECULE TYPE:	DNA						
US-08-488-551B-481							
Query Match	31.8%;	Score 7;	DB 1;	Length 10;			
Best Local Similarity	100.0%;	Pred. No. 95;					
Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;
Query	741 GAACACC 747						
Db	1 GAACACC 7						
RESULT 148							
US-08-522-384-13/c							
Sequence 13,	Application US/08522384						
Patent No. 6110667							
GENERAL INFORMATION:							
APPLICANT:	LOPEZ-NIETO, CARLOS E						
APPLICANT:	NIGAM, SANJAY KUMAR						
TITLE OF INVENTION:	PROCESSES, APPARATUS AND COMPOSITIONS FOR						
TITLE OF INVENTION:	CHARACTERIZING NUCLEOTIDE SEQUENCES						
FILE REFERENCE:	2458-4029						
CURRENT APPLICATION NUMBER:	US/08/522,384						
CURRENT FILING DATE:	1996-11-15						
NUMBER OF SEQ ID NOS:	122						
SOFTWARE:	Patentin Ver. 2.1						
SEQ ID NO 13							
LENGTH:	10						
TYPE:	DNA						
ORGANISM:	Unknown Organism						
FEATURE:							
OTHER INFORMATION:	Description of Unknown Organism: Primer						
US-08-522-384-13							
Query Match	31.8%;	Score 7;	DB 1;	Length 10;			
Best Local Similarity	100.0%;	Pred. No. 95;					
Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;
Query	728 GCCAGGA 734						
Db	9 GCCAGGA 3						
RESULT 149							
US-09-054-832-3							
Sequence 3,	Application US/09054832						
Patent No. 6312894							
GENERAL INFORMATION:							
APPLICANT:	Meyer, Rich						
TITLE OF INVENTION:	IMPROVED HYBRIDIZATION AND						
TITLE OF INVENTION:	MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES						
TITLE OF INVENTION:	CONJUGATED TO MINOR GROOVE BINDERS						
NUMBER OF SEQUENCES:	40						
CORRESPONDENCE ADDRESS:							
ADDRESSEE:	MORRISON & FOERSTER						
STREET:	755 PAGE MILL ROAD						
CITY:	PALO ALTO						
STATE:	CA						
COUNTRY:	USA						
ZIP:	94304-1018						
COMPUTER READABLE FORM:							
MEDIUM TYPE:	Diskette						
COMPUTER:	IBM Compatible						
OPERATING SYSTEM:	Windows						
SOFTWARE:	FastSeq for Windows Version 2.0b						
CURRENT APPLICATION DATA:							
APPLICATION NUMBER:	US/09/054,832						
FILING DATE:							
CLASSIFICATION:							
PRIOR APPLICATION DATA:							
APPLICATION NUMBER:	08/415,370						
FILING DATE:	03-APR-1995						

```
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 736 AAACAGA 742
Db 4 AAACAGA 10
|||||

RESULT 151
US-09-867-915-21
; Sequence 21, Application US/09867915
; Patent No. 6521747
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Finkel, Kevin
; APPLICANT: Koshi, Beena
; APPLICANT: Lee, Helen H.
; TITLE OF INVENTION: HAPLOTYPES OF THE AGTR1 GENE
; FILE REFERENCE: ACTR1-1136test
; CURRENT APPLICATION NUMBER: US/09/867,915
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/228,542
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-915-21

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAAACAG 741
Db 3 GAAACAG 9
|||||

RESULT 152
US-09-508-753B-135/c
; Sequence 135, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 135
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-135

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 GGAGAAA 738
Db 3 GGAGAAA 9
|||||

RESULT 153
US-09-508-753B-319/c
; Sequence 319, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 319
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-319

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAAACAG 741
Db 8 GAAACAG 2
|||||

RESULT 154
US-09-769-482-22/c
; Sequence 22, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-22

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 737
Db 7 AGGAGAA 9
|||||
```

```
Db          9 AGGAGAA 3

RESULT 155
US-09-769-482-29
; Sequence 29, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-29

Query Match          31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          739 CAGAAC 745
Db          2 CAGAAC 8

RESULT 156
US-09-083-235A-52/c
; Sequence 52, Application US/09083235A
; Patent No. 6632919
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Peter E
; APPLICANT: Haaima, Gerald
; APPLICANT: Eldrup, Anne B
; TITLE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers
; FILE REFERENCE: ISIS3044
; CURRENT APPLICATION NUMBER: US/09/083,235A
; CURRENT FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 08/862,629
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence
US-09-083-235A-52

Query Match          31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          740 AGAACAC 746
Db          8 AGAACAC 2

RESULT 157
US-09-083-235A-56/c
; Sequence 56, Application US/09083235A
; Patent No. 6632919
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Peter E
; APPLICANT: Haaima, Gerald
; APPLICANT: Eldrup, Anne B
; TITLE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers
; FILE REFERENCE: ISIS3044
; CURRENT APPLICATION NUMBER: US/09/083,235A
; CURRENT FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 08/862,629
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence
US-09-083-235A-56

Query Match          31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          740 AGAACAC 746
Db          8 AGAACAC 2

RESULT 158
US-07-681-703B-55
; Sequence 55, Application US/07681703B
; Patent No. 5443965
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Moockli, Randolph
; TITLE OF INVENTION: Hepatitis C Virus Epitopes
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/681,703B
; FILING DATE: 05-APR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,611
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 594,854
; FILING DATE: 09-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-076.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; INFORMATION FOR SEQ ID NO: 55:
```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Codon Change, Example 20
; US-07-681-703B-55

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      734 AGAAGAGAA 743
Db      1 AGAAGAGAA 10

RESULT 159
US-08-049-283A-32/c
; Sequence 32, Application US/08049283A
; Patent No. 5502176
; GENERAL INFORMATION:
; APPLICANT: Tenen, Daniel G.
; APPLICANT: Pahl, Heike L.
; APPLICANT: Burn, Timothy C.
; TITLE OF INVENTION: Cell Specific Promoter and Uses Thereof
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatenIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,283A
; FILING DATE: 14-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/020,465
; FILING DATE: 19-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/837,776
; FILING DATE: 13-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BIH91-03'A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-049-283A-32

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-08-049-283A-32
```

```

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      732 GGAGAAACAG 741
Db      10 GGAGAAGTAG 1

RESULT 160
US-07-949-541A-13
; Sequence 13, Application US/07949541A
; Patent No. 5552270
; GENERAL INFORMATION:
; APPLICANT: Khrapko, Konstantin R.
; APPLICANT: Khorlin, Alexandr A.
; APPLICANT: Ivanov, Igor B.
; APPLICANT: Ershov, Gennady M.
; APPLICANT: Lysov, Yuri P.
; APPLICANT: Florentiev, Vladimir L.
; APPLICANT: Mirzabekov, Andrei D.
; TITLE OF INVENTION: Method for Determining a DNA Nucleotide
; TITLE OF INVENTION: Sequence and a Device for Carrying Out Same
; Patent No. 5552270
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladass & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/949,541A
; FILING DATE: 09-No. 5552270-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/RU92/00052
; FILING DATE: 18-Mar-1992
; APPLICATION NUMBER: Russian Federation 4919321
; FILING DATE: 18-Mar-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janet I. Cord
; REGISTRATION NUMBER: 33,778
; REFERENCE/DOCKET NUMBER: U-8999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: chemically synthesized
; MOLECULE TYPE: desoxyribonucleotide.
; FEATURE: oligonucleotide was synthesized by phosphoramidite
; FEATURE: method.
; OTHER INFORMATION: The sequence is listed from 3' to 5'
; OTHER INFORMATION: left to right and this is a part of SEQ ID NO:4.
; US-07-949-541A-13

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      728 GCCAGAGAA 737
Db      1 GCCAGAGAA 10
```

RESULT 161
 US-08-396-479B-16
 ; Sequence 16, Application US/08396479B
 ; Patent No. 5612455
 ; GENERAL INFORMATION:
 ; APPLICANT: HOEY, Timothy
 ; TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/396.479B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: A-59450-1/RAO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 494-8700
 ; TELEFAX: (415) 494-8771
 ; TELEX: 210 277299
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; US-08-396-479B-16

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
 DB 1 GGAAAAAAGT 10

RESULT 162
 US-08-088-658-4
 ; Sequence 4, Application US/08088658
 ; Patent No. 5641625
 ; GENERAL INFORMATION:
 ; APPLICANT: Ecker, David J.
 ; APPLICANT: Buchardt, Ole
 ; APPLICANT: Egholm, Michael
 ; APPLICANT: Nielsen, Peter E.
 ; APPLICANT: Berg, Rolf H.
 ; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/088.658
 ; FILING DATE: 19930702
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/054,363
 ; FILING DATE: 26-APRIL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lucci, Joseph
 ; REGISTRATION NUMBER: 33,307
 ; REFERENCE/DOCKET NUMBER: ISIS-1052
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-568-3100
 ; TELEFAX: 215-568-3439
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; US-08-088-658-4

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAAACA 745
 DB 1 AAAAAGAAAA 10

RESULT 163
 US-08-818-823-16
 ; Sequence 16, Application US/08818823
 ; Patent No. 5708158
 ; GENERAL INFORMATION:
 ; APPLICANT: HOEY, Timothy
 ; TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/818.823
 ; FILING DATE: 14-MAR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/396.479
 ; FILING DATE: 02-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: A-59450-1/RAO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 494-8700
 ; TELEFAX: (415) 494-8771
 ; TELEX: 210 277299
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-818-823-16

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAG 741
||| |||||
Db 1 GGAAAACTG 10

RESULT 164

US-08-686-116A-49
; Sequence 49, Application US/08686116A
; Patent No. 5714331
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Binding Affinity, Sequence Specificity
; Patent No. 5714331
; TITLE OF INVENTION: ans Solubility
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5714331 Iris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,116A
; FILING DATE: July 24, 1996
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2271

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-686-116A-49

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGACA 745
||| |||||
Db 1 AAAAAGAAA 10

RESULT 165

US-08-685-484-49
; Sequence 49, Application US/08685484
; Patent No. 5719262

GENERAL INFORMATION:

; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
; TITLE OF INVENTION: Side Chains
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5719262 Iris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/685,484
; FILING DATE: 24-JUL-1996

CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/108,591

; FILING DATE: 22-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Michael P. Straher

; REGISTRATION NUMBER: 38,325

; REFERENCE/DOCKET NUMBER: ISIS-2270

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear
US-08-685-484-49

Query Match 30.9%; Score 6.8; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 1e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGACA 745

||| |||||

Db 1 AAAAAGAAA 10

RESULT 166

US-08-847-108-49

; Sequence 49, Application US/08847108

; Patent No. 5736336

; GENERAL INFORMATION:

; APPLICANT: Buchardt et al.

; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced

; TITLE OF INVENTION: Binding Affinity, Sequence Specificity

; Patent No. 5736336

; TITLE OF INVENTION: and Solubility

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736336 Iris LLP

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/847,108

```

; FILING DATE: 01-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,116
; FILING DATE: July 24, 1996
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-847-108-49
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAAC 745
DB 1 AAAAAGAAA 10

RESULT 167
US-08-686-113A-56
; Sequence 56, Application US/08686113A
; Patent No. 5766855
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Affinity And Sequence Specificity
; Patent No. 5766855
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5766855ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,113A
; FILING DATE: July 24, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-847-108-49
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAAC 745
DB 1 AAAAAGAAA 10

RESULT 169
US-08-465-590-148
; Sequence 148, Application US/08465590
; Patent No. 5824770
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
;
US-08-847-095A-49
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAAC 745
DB 1 AAAAAGAAA 10

RESULT 169
US-08-847-095A-49
; Sequence 49, Application US/08847095A
; Patent No. 5786461
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
; TITLE OF INVENTION: Side Chains
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5786461ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,095A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,484
; FILING DATE: 24-JUL-1996
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-847-095A-49
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAAC 745
DB 1 AAAAAGAAA 10

RESULT 169
US-08-465-590-148
; Sequence 148, Application US/08465590
; Patent No. 5824770
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
;
```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465.590
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MFG-006C2DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-465-590-148

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
|||
Db 1 AGGAGGAAAA 10

RESULT 170
US-08-808-474A-4
; Sequence 4, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,474A

; FILING DATE: 03-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTDAL-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 740-8000
; TELEFAX: (214) 740-8800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-808-474A-4

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAAA 738
|||
Db 1 CCGGAGAGA 10

RESULT 171
US-08-173-489C-67
; Sequence 67, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; DESCRIPTION: esterase D gene (Accession # M13450)
; DESCRIPTION: nucleotides 34 to 43
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:

ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 13
MAP POSITION: 13q14.1-q14.2
PUBLICATION INFORMATION:
AUTHORS: Lee, E Y H P, Lee, W H.
TITLE: Molecular cloning of the
TITLE: human esterase D gene, a genetic marker of
JOURNAL: Proceedings of the National Academy of
JOURNAL: Sciences, USA
VOLUME: 83
PAGES: 6337-6341
DATE: 1986
RELEVANT RESIDUES IN SEQ ID NO: 67 :FROM 1 TO 10
US-08-173-489C-67

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
||| |||
DB 1 AGGAAAGAA 10

RESULT 172
US-08-173-489C-72/c
; Sequence 72, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
FILING DATE: 22 DEC 1993
APPLICATION NUMBER: US/08/173,489C
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from esterase D
HYPOTHETICAL: Yes
ANTI-SENSE: No

; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 72 :FROM 1 TO 10
US-08-173-489C-72
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAA 743
||| |||
DB 10 AGAAAGGAA 1
RESULT 173
US-08-173-489C-151/c
; Sequence 151, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: hepatitis B virus ayw isolate,
DESCRIPTION: nucleotides 807 to 816
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: ayw
PUBLICATION INFORMATION:
AUTHORS: Galibert, F, Mandart, E, Pitoussi, F,
AUTHORS: Tiollais, P, Charnay, P.
TITLE: Nucleotide sequence of the
TITLE: Hepatitis B virus genome (subtype ayw) cloned
TITLE: in E coli
JOURNAL: Nature
VOLUME: 281
PAGES: 646-650
DATE: 1979

RELEVANT RESIDUES IN SEQ ID NO: 151 :FROM 1 TO 10
US-08-173-489C-151

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred.No.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGAA 743
|||||
Db 10 AGAAGACAGAA 1

RESULT 174

US-08-173-489C-175
; Sequence 175, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: hepatitis B virus adw2 isolate,
; DESCRIPTION: nucleotides 563 to 572
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis B virus
; INDIVIDUAL ISOLATE: adw2
; PUBLICATION INFORMATION:
; AUTHORS: Valenzuela, P, Quiroga, M, Zaldivar, J,
; AUTHORS: Gray, P, Ruter, W J.
; TITLE: The nucleotide sequence of
; TITLE: the Hepatitis B viral genome and the
; TITLE: identification of the major viral genes
; JOURNAL: In "Animal Virus Genetics", Fields, B N,
; JOURNAL: Jaenisch, R, Fox C F eds
; VOLUME: 57-70
; PAGES: 1980
; DATE: 1980

RELEVANT RESIDUES IN SEQ ID NO: 175 :FROM 1 TO 10
US-08-173-489C-175

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred.No.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGAA 743
|||||
Db 1 AGAAGACAGAA 10

RESULT 175

US-08-173-489C-205
; Sequence 205, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: hepatitis B virus adr isolate,
; DESCRIPTION: nucleotides 2241 to 2250
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis B virus
; INDIVIDUAL ISOLATE: adr
; PUBLICATION INFORMATION:
; AUTHORS: Fujiyama, A, Miyanochara, A, No. 5861244aki, C,
; AUTHORS: Toneyama, T, Ohromo, N, Matsubara, K.
; TITLE: Cloning and structural
; TITLE: analysis of Hepatitis B virus DNAs subtype adr
; JOURNAL: Nucleic Acids Research
; VOLUME: 11
; PAGES: 4601-4610
; DATE: 1983
; RELEVANT RESIDUES IN SEQ ID NO: 205 :FROM 1 TO 10
US-08-173-489C-205

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Mon Oct 18 14:40:09 2004

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; LOCATION: 1..10
US-08-286-819A-48
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAGACGAA 743
|||||
Db 1 AGAAGACGAA 10

RESULT 176
US-08-286-819A-48
; Sequence 48, Application US/08286819A
; Patent No. 5971910
; GENERAL INFORMATION:
; APPLICANT: ARTHUR, MICHEL
; APPLICANT: DUKTA-WALEN, SYLVIE
; APPLICANT: MOLINAS, CATHERINE
; APPLICANT: COURVALIN, PATRICE
; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPROTEIDS, IN PARTICULAR
; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.819A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/174,682
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/917,146
; FILING DATE: 10-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR/91/00855
; FILING DATE: 29-OCT-1991
; APPLICATION NUMBER: FR 9013579
; FILING DATE: 31-OCT-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5871910man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: RBS

; Query Match 30.9%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 1e+02;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 739 CAGAACACCG 748
|||||
Db 1 CCGAACACCG 10

RESULT 177
US-08-545-253A-5
; Sequence 5, Application US/08545253A
; Patent No. 5908978
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; APPLICANT: Henry V. Amerson
; APPLICANT: Phillip Wilcox
; APPLICANT: E. George Kuhlman
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
; TITLE OF INVENTION: SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5908978th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,253A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-545-253A-5

; Query Match 30.9%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 1e+02;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 739 CAGAACACCG 748
|||||
Db 1 CCGAACACCG 10

RESULT 178
US-08-471-907A-4
; Sequence 4, Application US/08471907A
; Patent No. 5986053

```

GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Nielsen, Peter E.
APPLICANT: Berg, Rolf H.
APPLICANT: M Ilegard, Niels E.
TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,907A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/088,658
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-471-907A-4

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 745
Db 1 AAAAAGAAA 10

RESULT 179
US-08-388-353-73
Sequence 73, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-73

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGAGAA 737
Db 1 GCCAGAGCA 10

RESULT 180
US-08-388-353-175
Sequence 175, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-388-353-175

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 734 AGAAGACAA 743
 Db 1 AGAAGACAA 10

RESULT 181

US-08-388-353-186
 ; Sequence 186, Application US/08388353
 ; Patent No. 6010895

GENERAL INFORMATION:

APPLICANT: Deacon, Nicholas J.
 APPLICANT: Learmont, Jennifer C.
 APPLICANT: McPhee, Dale A.
 APPLICANT: Crowe, Suzanne
 APPLICANT: Cooper, David
 TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 NUMBER OF SEQUENCES: 800
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Preseer
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,353

FILING DATE: 14-FEB-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 9606

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 186:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-388-353-186

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAACAA 740
 Db 1 AGGAGAACAA 10

RESULT 182

US-08-388-353-187
 ; Sequence 187, Application US/08388353
 ; Patent No. 6010895

GENERAL INFORMATION:
 APPLICANT: Deacon, Nicholas J.
 APPLICANT: Learmont, Jennifer C.
 APPLICANT: McPhee, Dale A.
 APPLICANT: Crowe, Suzanne
 APPLICANT: Cooper, David
 TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 NUMBER OF SEQUENCES: 800
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Preseer
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,353

FILING DATE: 14-FEB-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 9606

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 187:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-388-353-187

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 GGAGAACAG 741
 Db 1 GGAGAACAG 10

RESULT 183
 US-08-980-357-48
 ; Sequence 48, Application US/08980357
 ; Patent No. 6013508

GENERAL INFORMATION:

APPLICANT: ARTHUR, MICHEL

APPLICANT: DUKTA-MALEN, SYLVIE

APPLICANT: MOLINAS, CATHERINE

APPLICANT: COURVALIN, PATRICE

TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE

EXPRESSION OF RESISTANCE TO GLYCOPROTEINS, IN PARTICULAR

IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR

THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/980,357
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,819
 FILING DATE: 05-AUG-1994
 APPLICATION NUMBER: US 08/174,682
 FILING DATE: 28-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/917,146
 FILING DATE: 10-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR/91/00855
 FILING DATE: 29-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 9013579
 FILING DATE: 31-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 6013508man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 660-060-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: RBS
 LOCATION: 1..10
 US-08-980-357-48

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGA 736
 |||||
 Db 1 TGAAGGAGA 10

RESULT 184
 US-08-488-551B-73
 ; Sequence 73, Application US/08488551B
 ; Patent No. 6015661
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas J. Deacon
 ; APPLICANT: Dale A. McPhee
 ; APPLICANT: David Cooper
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 ; NUMBER OF SEQUENCES: 841
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 GARDEN CITY PLAZA
 ; CITY: GARDEN CITY
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 11530-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/980,357
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PM3864 (AU)
 ; FILING DATE: 14-FEB-1994
 ; APPLICATION NUMBER: PM4002 (AU)
 ; FILING DATE: 21-FEB-1994
 ; APPLICATION NUMBER: PM0284 (AU)
 ; FILING DATE: 23-DEC-1994
 ; APPLICATION NUMBER: US 08/388,353
 ; FILING DATE: 14-FEB-1995
 ; APPLICATION NUMBER: PM3021/95
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,551B
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PM3864 (AU)
 FILING DATE: 14-FEB-1994
 APPLICATION NUMBER: PM4002 (AU)
 FILING DATE: 21-FEB-1994
 APPLICATION NUMBER: PM0284 (AU)
 FILING DATE: 23-DEC-1994
 APPLICATION NUMBER: US 08/388,353
 FILING DATE: 14-FEB-1995
 APPLICATION NUMBER: PM3021/95
 FILING DATE: 17-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: FRANK S. DIGILIO
 REFERENCE/DOCKET NUMBER: 96062
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-488-551B-73

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAA 737
 |||||
 Db 1 GCCAGGAGCA 10

RESULT 185
 US-08-488-551B-175
 ; Sequence 175, Application US/08488551B
 ; Patent No. 6015661
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas J. Deacon
 ; APPLICANT: Dale A. McPhee
 ; APPLICANT: David Cooper
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 ; NUMBER OF SEQUENCES: 841
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 GARDEN CITY PLAZA
 ; CITY: GARDEN CITY
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 11530-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/488,551B
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PM3864 (AU)
 ; FILING DATE: 14-FEB-1994
 ; APPLICATION NUMBER: PM4002 (AU)
 ; FILING DATE: 21-FEB-1994
 ; APPLICATION NUMBER: PM0284 (AU)
 ; FILING DATE: 23-DEC-1994
 ; APPLICATION NUMBER: US 08/388,353
 ; FILING DATE: 14-FEB-1995
 ; APPLICATION NUMBER: PM3021/95
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-175

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAA 743
|||||
DB 1 AGAAGACAA 10

RESULT 186
US-08-488-551B-186
Sequence 186, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA
US-08-488-551B-186
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGAGGAACA 740
|||||
DB 1 AGAGGAACA 10

RESULT 187
US-08-488-551B-187
Sequence 187, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-187

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGGAACAG 741
|||||
DB 1 GGAGGAACAG 10

RESULT 188

US-08-993-303-2
; Sequence 2, Application US/08993303
; Patent No. 6020132
; GENERAL INFORMATION:
; APPLICANT: ORUM, Henrik
; APPLICANT: KOCH, Troels
; APPLICANT: BORRE, Martin
; APPLICANT: HANSEN, Henrik Frydenlund
; TITLE OF INVENTION: METHOD OF ANALYSIS USING SIGNAL
; TITLE OF INVENTION: AMPLIFICATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street, N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993.303
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berman, Richard B.
; REGISTRATION NUMBER: 39,107
; REFERENCE/DOCKET NUMBER: P1614-7082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4910
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OLIGODEOXYRIBONUCLEOTIDE"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "AT THE TERMINUS IS AN AMINOHEXYL
; OTHER INFORMATION: ALKYLATED GROUP"
US-08-993-303-2
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACA 740
Db 1 AAGAGAAAAA 10
RESULT 189
US-08-719-337-5
; Sequence 5, Application US/08719337
; Patent No. 6054634
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Darlo
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte

STATE: No. 6054634th Carolina
COUNTRY: U.S.A.
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719.337
FILING DATE: 25-SEP-1996
CLASSIFICATION: 047
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,567
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-719-337-5
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 739 CAGACACCG 748
Db 1 CCGACACCG 10
RESULT 190
US-08-724-466B-26
; Sequence 26, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.;
; APPLICANT: Beckett, Barbara R.; Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724.466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344

```
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-724-466B-26

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGGA 736
DB 1 TCCAGGAGGA 10

RESULT 191
US-08-522-384-121/c
; Sequence 121, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-121

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
DB 10 GCCAGGAGAA 1

RESULT 192
US-08-711-417C-148
; Sequence 148, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 148:
US-08-711-417C-148

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAGACA 740
DB 1 AGGAGAGAAA 10

RESULT 193
US-08-088-661F-20
; Sequence 20, Application US/08088661F
; Patent No. 6228982
; GENERAL INFORMATION:
; APPLICANT: No. 6228982den, Benget
; APPLICANT: Wittung, Pernilla
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf
; TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
; FILE REFERENCE: IS11108
; CURRENT APPLICATION NUMBER: US/08/088,661F
; CURRENT FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/054,363
; PRIOR FILING DATE: 1993-04-26
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6228982e1 Sequence
US-08-088-661F-20

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAGACA 745
DB 1 AAACAGAGAAA 10

RESULT 194
US-08-088-661F-30
```

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; Sequence 30, Application US/08088661F
; Patent No. 6228982
; GENERAL INFORMATION:
; APPLICANT: No. 6228982den, Bengel
; APPLICANT: Wittung, Perrilla
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf
; TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
; FILE REFERENCE: IS181108
; CURRENT APPLICATION NUMBER: US/08/088,661F
; CURRENT FILING DATE: 1993-07-02
; PRIOR FILING DATE: 1993-04-26
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence
US-08-088-661P-30

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      734 AGAACACGAA 743
Db      1 AAAACACAAA 10

RESULT 195
US-09-245-041-129
; Sequence 129, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 129
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-245-041-129

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      732 GGACACACAG 741
Db      1 GGACACACAG 10

RESULT 196
US-08-882-164D-26

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; Sequence 26, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-26

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      727 TGCCAGGAGA 736
Db      1 TGCCAGTGGA 10

RESULT 197
US-08-150-156A-5
; Sequence 5, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150,156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91

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; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-5

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACAA 745
Db 1 AAAAAGAAAA 10

RESULT 198
US-08-150-156A-6
; Sequence 6, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150.156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-6

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
Db 1 AAAAAGAAAA 10

RESULT 198
US-08-150-156A-6
; Sequence 6, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150.156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-6

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
Db 1 AAAAAGAAAA 10

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Db 1 AAAACAAAA 10

RESULT 199
US-08-150-156A-14/c
; Sequence 14, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150.156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-14

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACAA 745
Db 10 AAAAAGAAAA 1

RESULT 200
US-08-150-156A-17/c
; Sequence 17, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150.156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
; US-08-150-156A-17

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACA 740
Db 10 AGAAGAAAAA 1

RESULT 201
US-08-618-834C-33
; Sequence 33, Application US/08618834C
; Patent No. 6361937
; GENERAL INFORMATION:
; APPLICANT: Stryer, Lubert
; TITLE OF INVENTION: Computer-Aided Nucleic Acid
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: CA
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,834C
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFYP002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-618-834C-45

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 739 CAGAACACCG 748
Db 1 CACATCACCG 10

RESULT 203
US-08-108-591B-8
; Sequence 8, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Sgholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
```

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-8

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACAA 745
DB      10 AAAAAAGAAAA 1

RESULT 204
US-08-108-591B-9
; Sequence 9, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-9

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACAA 745
DB      10 AAAAAAGAAAA 10

RESULT 205
US-08-108-591B-12/c
; Sequence 12, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-12

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACAA 745
DB      10 AAAAAAGAAAA 10

RESULT 206
US-08-108-591B-15/c
; Sequence 15, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-15

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGAACAA 740
DB      10 AGAGAGAAAA 1

RESULT 207
US-08-108-591B-28
; Sequence 28, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-28

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAACAGAA 743
DB      1 AAAAAAGAAAA 10
```



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RESULT 208
US-08-686-114B-56
; Sequence 56, Application US/08686114B
; Patent No. 6414112
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleob
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6414112ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,114B
; FILING DATE: July 24, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Homo sapiens
;
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACCA 745
Db 1 AAAAGAGAAA 10

RESULT 209
US-09-154-750A-14/c
; Sequence 14, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACCA 745
Db 1 AAAAGAGAAA 10

RESULT 210
US-09-154-750A-54
; Sequence 54, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACACGA 742
Db 1 GGAAGACGAGA 10

RESULT 211
US-09-394-457C-7/c
; Sequence 7, Application US/09394457C
; Patent No. 6440705
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides
; FILE REFERENCE: 246/020
; CURRENT APPLICATION NUMBER: US/09/394,457C
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence to demonstrate application.
;
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAGAACCA 740
Db 10 AGGAGAGAACCA 1
```

RESULT 212
US-08-275-951-61/c
; Sequence 61, Application US/08275951
; Patent No. 6451968
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Kiely, John
; APPLICANT: Griffin, Michael
; APPLICANT: Coull, James M.
; APPLICANT: Neilson, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: IS181577
; CURRENT APPLICATION NUMBER: US/08/275,951
; CURRENT FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 08/088,658
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/088,661
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-22
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1991-04-15
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence
US-08-275-951-61

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGAA 743
| | | | |
Db 10 AGAGAGAGAA 1

RESULT 213
US-09-709-596A-7/c
; Sequence 7, Application US/09709596A
; Patent No. 6458945
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides
; FILE REFERENCE: 258/239
; CURRENT APPLICATION NUMBER: US/09/709,596A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence to demonstrate application.
US-09-709-596A-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
| | | | |
Db 10 AGGAGGAATA 1

RESULT 214
US-09-486-853-8/c
; Sequence 8, Application US/09486853
; Patent No. 6461871
; GENERAL INFORMATION:
; APPLICANT: KUBISTA, MIKHAEL
; APPLICANT: SVANVIK, NICKIE
; APPLICANT: WESTMAN, GUNNAR
; TITLE OF INVENTION: METHOD FOR THE PREPARATION OF A PROBE FOR NUCLEIC ACID HYBRIDIZATION
; FILE REFERENCE: GOTEPO29US
; CURRENT APPLICATION NUMBER: US/09/486,853
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/SE98/01580
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: SE 9703251-0
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-486-853-8

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
| | | | |
Db 10 GGAGAGAGGAG 1

RESULT 215
US-09-475-947A-106/c
; Sequence 106, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-106

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGAA 743
| | | | |
Db 10 AGAAGAGAAA 1

RESULT 216
US-09-475-947A-122/c
; Sequence 122, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:

; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-122

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAACAGAA 743
Db 10 AGAAAAAAA 1

RESULT 217

US-09-914-259-101/c
; Sequence 101, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
US-09-914-259-101

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 733 GAGAAACAGA 742
Db 10 GAGAGAGAGA 1

RESULT 218

US-09-916-228-7
; Sequence 7, Application US/09916228
; Patent No. 6498013
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Sparks, Andrew
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Serial analysis of transcript expression
; FILE REFERENCE: 001107.00172
; CURRENT APPLICATION NUMBER: US/09/916,228
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,556
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/233,431

; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: tag or tag concatenamer
US-09-916-228-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGACAA 745
Db 1 AAACAATCA 10

RESULT 219

US-09-655-104A-7/c
; Sequence 7, Application US/09655104A
; Patent No. 6500650
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Identifying Polymorphisms
; FILE REFERENCE: 257/078
; CURRENT APPLICATION NUMBER: US/09/655,104A
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence to demonstrate application.
US-09-655-104A-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACA 740
Db 10 AGGAGGAATA 1

RESULT 220

US-08-301-037-7/c
; Sequence 7, Application US/08301037
; Patent No. 6528313
; GENERAL INFORMATION:
; APPLICANT: Le Mouellic, Herve
; Brulet, Philippe
; TITLE OF INVENTION: Procedure for Specific Replacement of a Copy of a
; Gene Present in the Recipient Genome by the Integration of
; That Where the Integration is Made
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/301,037
;; FILING DATE: 06-SEP-1994
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/301,037
;; FILING DATE: 06-SEP-1994
;; APPLICATION NUMBER: US 07/867,744
;; FILING DATE: 13-APR-1992
;; APPLICATION NUMBER: US 07/598,679
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: WO PCT/FR90/00185
;; FILING DATE: 19-MAR-1990
;; APPLICATION NUMBER: FR 8903630
;; FILING DATE: 19-MAR-1990
;; APPLICATION NUMBER: FR 8903630
;; FILING DATE: 20-MAR-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Potter, Jane E.
;; REGISTRATION NUMBER: 33,332
;; REFERENCE/DOCKET NUMBER: 02356-0053-06000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4400
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-301-037-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAAC 739
DB 10 CATCGGAAAC 1

RESULT 221
US-08-466-539-7/C
;; Sequence 7, Application US/08466539
;; Patent No. 6528314
;; GENERAL INFORMATION:
;; APPLICANT: Le Mouellic, Herve
;; APPLICANT: Brulet, Philippe
;; TITLE OF INVENTION: Procedure for Specific Replacement
;; TITLE OF INVENTION: of a Copy of a Gene Present in the Recipient Genome by the
;; TITLE OF INVENTION: Integration of a Gene Different From That Where the Integrat
;; TITLE OF INVENTION: is Made
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/466,539
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/301,037
;; FILING DATE: 06-SEP-1994

;;
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/867,744
;; FILING DATE: 13-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/598,679
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: WO PCT/FR90/00185
;; FILING DATE: 19-MAR-1990
;; APPLICATION NUMBER: FR 8903630
;; FILING DATE: 20-MAR-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Potter, Jane E.
;; REGISTRATION NUMBER: 33,332
;; REFERENCE/DOCKET NUMBER: 02356-0053-05000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4400
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-466-539-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAAC 739
DB 10 CATCGGAAAC 1

RESULT 222
US-09-394-455-53
;; Sequence 53, Application US/09394455
;; Patent No. 6531305
;; GENERAL INFORMATION:
;; APPLICANT: Witman, George F.
;; APPLICANT: San Agustín, Jovenal
;; APPLICANT: Leszyk, John D.
;; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
;; FILE REFERENCE: 07917/078001
;; CURRENT APPLICATION NUMBER: US/09/394,455
;; CURRENT FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: US 60/099,771
;; PRIOR FILING DATE: 1998-09-10
;; NUMBER OF SEQ ID NOS: 56
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 53
;; LENGTH: 10
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-09-394-455-53

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCCAGGAA 737
DB 1 GCCCAGGAA 10

RESULT 223
US-09-508-753B-37
;; Sequence 37, Application US/09508753B

; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 37
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-37

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAG 741
Db 1 GGAAAGCAG 10

RESULT 224
US-09-508-753B-51
; Sequence 51, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 51
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-51

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739
Db 1 CACCAGAAAC 10

RESULT 225
US-09-508-753B-76/c
; Sequence 76, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO

; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 76
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-76

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAG 741
Db 10 GGAAAGCAG 1

RESULT 226
US-09-508-753B-79/c
; Sequence 79, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 79
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-79

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739
Db 10 CACCAGAAAC 1

RESULT 227
US-09-508-753B-82
; Sequence 82, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI

APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
PRIOR FILING DATE: 2000-06-16
CURRENT FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
PRIOR FILING DATE: 1997-09-18
SEQ ID NO 82
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-82

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 744
||| ||| |||
DB 1 GAGACACAAC 10

RESULT 228
US-09-508-753B-126
Sequence 126, Application US/09508753B
Patent No. 6544736
GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 126
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-126

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 744
||| ||| |||
DB 1 GAAACTGAGC 10

RESULT 229
US-09-508-753B-131/c
Sequence 131, Application US/09508753B
Patent No. 6544736
GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 131
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-131

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 744
||| ||| |||
DB 10 GAAACTGAGC 1

RESULT 230
US-09-508-753B-133/c
Sequence 133, Application US/09508753B
Patent No. 6544736
GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 133
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-133

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCGAGAGAAA 738
||| ||| |||
DB 10 CCGAGAGAAA 1

RESULT 231
US-09-508-753B-157/c
Sequence 157, Application US/09508753B
Patent No. 6544736
GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 157
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Description of Artificial Sequence: Primer
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-157

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 735 GAAACAGAAC 744
||| ||| |||
Db 10 GAGACACAC 1

RESULT 232

US-09-508-753B-160
; Sequence 160, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiichi OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 160
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Description of Artificial Sequence: Primer
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-160

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 738 ACAGAACACC 747
||| ||| |||
Db 1 ACTGAACACC 10

RESULT 233

US-10-042-111-42
; Sequence 42, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 42
; LENGTH: 10
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-42

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 738 ACAGAACACC 747
||| ||| |||
Db 1 ACTGAACACC 10

RESULT 234

US-10-042-111-43/c
; Sequence 43, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-43

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 738 ACAGAACACC 747
||| ||| |||
Db 10 ACGAGACACC 1

RESULT 235

US-09-394-467-7/c
; Sequence 7, Application US/09394467
; Patent No. 6566059
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides
; FILE REFERENCE: 245/287
; CURRENT APPLICATION NUMBER: US/09/394,467
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Used to demonstrate how indicated aspect of invention works.
US-09-394-467-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAACCA 740


```
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1335

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      737 AACAGAACAC 746
DB      10 ACCAGCACAC 1

RESULT 241
US-09-337-304-56
; Sequence 56, Application US/09337304
; Patent No. 6613873
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases
; FILE REFERENCE: ISIS-3809
; CURRENT APPLICATION NUMBER: US/09/337,304
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 08/847,110
; PRIOR FILING DATE: 1997-05-01
; PRIOR APPLICATION NUMBER: 08/685,114
; PRIOR FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1992-04-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-337-304-56

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AACAGAACAC 745
DB      1 AAAAAAGAAA 10

RESULT 242
US-09-855-159A-7/c
; Sequence 7, Application US/09855159A
; Patent No. 6620595
; GENERAL INFORMATION:
; APPLICANT: Cannon, Paula
; APPLICANT: Barcova, Maria
; TITLE OF INVENTION: Retroviral Vectors Comprising An Enhanced 3' Transcription Termin
; FILE REFERENCE: 4-31439A/USC
; CURRENT APPLICATION NUMBER: US/09/855,159A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/203,884
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Adenovirus type 2
US-09-855-159A-7

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAACAGAA 743
DB      10 ACAAAGAA 1

RESULT 243
US-09-723-909-148
; Sequence 148, Application US/09723909
; Patent No. 6630141
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/723,909
; FILING DATE: 28-NOV-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417
; FILING DATE: 05-SEP-1996
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 148:
US-09-723-909-148

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGAAACA 740
DB      1 AGGAGAGAAA 10
```

RESULT 244
 US-08-466-699-7/c
 ; Sequence 7, Application US/08466699
 ; Patent No. 6638768
 ; GENERAL INFORMATION:
 ; APPLICANT: Le Mouellic, Herve
 ; APPLICANT: Brulet, Philippe
 ; TITLE OF INVENTION: Procedure for Specific Replacement of a Copy
 ; of a Gene Present in the Recipient Genome by the Integration of
 ; TITLE OF INVENTION: Different From That Where the Integration is Made
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Durner
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,699
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/301,037
 ; FILING DATE: 06-SEP-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/867,744
 ; FILING DATE: 13-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/598,679
 ; FILING DATE: 19-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/FR90/00185
 ; FILING DATE: 19-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 8903630
 ; FILING DATE: 20-MAR-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Potter, Jane E.
 ; REGISTRATION NUMBER: 33,332
 ; REFERENCE/DOCKET NUMBER: 02356-0053-06000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-466-699-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGGAAC 739
 DB 10 CATCGAAC 1

RESULT 245
 PCT-US91-03680-75/c
 ; Sequence 75, Application PC/TUS9103680

; GENERAL INFORMATION:
 ; APPLICANT: Matteucci, Mark D.
 ; APPLICANT: Krawczyk, Steven
 ; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
 ; CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
 ; TITLE OF INVENTION: DUPLEX DNA
 ; NUMBER OF SEQUENCES: 158
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 545 Middlefield Road, Suite 200
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/03680
 ; FILING DATE: 19910524
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 4610-0011.40
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-327-7250
 ; TELEFAX: 415-327-2951
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 75:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: 2
 ; OTHER INFORMATION: /mod_base= OTHER
 ; OTHER INFORMATION: /note= "5-methylcytosine"
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: 5
 ; OTHER INFORMATION: /mod_base= OTHER
 ; OTHER INFORMATION: /note= "5-methylcytosine"
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: 8
 ; OTHER INFORMATION: /mod_base= OTHER
 ; OTHER INFORMATION: /note= "5-methylcytosine"
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: 10
 ; OTHER INFORMATION: /mod_base= OTHER
 ; OTHER INFORMATION: /note= "T-T, linking group o-xyloso (nucleotides
 ; that have xylose sugar linked via the o-xylo
 ; OTHER INFORMATION: ring)"
 ; PCT-US91-03680-75

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGA 742
 DB 10 GAGAGAGA 1

RESULT 246
 PCT-US93-08743-148
 ; Sequence 148, Application PC/TUS9308743

GENERAL INFORMATION:
APPLICANT: IKAROS: A T CELL PATHWAY REGULATORY GENE
TITLE OF INVENTION: 152
NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-08743-148

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
Db 1 AGGAGGAAAA 10

RESULT 247
US-07-739-642-14
Sequence 14, Application US/07739642
Patent No. 5173427
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: Vectors And Hosts With Increased
TITLE OF INVENTION: Expression Of Hbcag
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,642
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear

US-07-739-642-14

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; 1; Indels 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAAC 744
Db 1 AACAGACC 8

RESULT 248
US-07-739-643-14
Sequence 14, Application US/07739643
Patent No. 5175094
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: Increased Expression Of Hbcag
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,643
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-739-643-14

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; 1; Indels 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAAC 744
Db 1 AACAGACC 8

RESULT 249
US-07-739-142-14
Sequence 14, Application US/07739142
Patent No. 5175272
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: DNA Sequences With Increased Expression
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey

COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,142
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-739-142-14

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0

QY 737 AACAGAAC 744
|||||
Db 1 AACAGACC 8

RESULT 250
US-08-465-590-117
Sequence 117, Application US/08465590
Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-465-590-117
Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0
QY 731 AGGAGAAA 738
|||||
Db 1 AGGGGAAA 8

RESULT 251
US-08-859-954-38/c
Sequence 38, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-38

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0

QY 740 AGAACACC 747

Db ||| |||
 8 AGATCACC 1

RESULT 252
US-08-859-954-205
; Sequence 205, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-205

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGA 742
 ||| |||
Db 1 GAGACAGA 8

RESULT 253
US-08-859-954-375
; Sequence 375, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-375

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGA 736
 |||||
Db 1 CCAGGAGA 8

RESULT 254
US-08-711-417C-117
; Sequence 117, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994

```
;
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-08-711-417C-117

Query Match      29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAA 738
Db      1 AGGGGAAA 8

RESULT 255
PCT-US93-08743-117
; Sequence 117, Application PC/TUS9308743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08743
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 946,233
; FILING DATE: 14-SEP-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US93-08743-117

Query Match      29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAA 738
Db      1 AGGGGAAA 8

RESULT 257
US-08-088-658-5
; Sequence 5, Application US/08088658
; Patent No. 5641625
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M. Illegard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
```

STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
FILING DATE: 19930702
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,363
FILING DATE: 26-APRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-088-658-5

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAA 738
Db 1 AAGAGAA 8

RESULT 258
US-08-410-779B-28/c
Sequence 28, Application US/08410779B
Patent No. 5814517
GENERAL INFORMATION:
APPLICANT: SEIDEL, H. MARTI
APPLICANT: LAMB, I. PETER
TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
STREET: 9393 TOWNE CENTRE DRIVE
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,779B
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/228,935
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: JURGENSEN, THOMAS E
REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 016-0013A.US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 550-7675
TELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
SYNTHETIC DNA"
US-08-410-779B-28
Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGA 734
Db 9 TTCCAGGA 2

RESULT 259
US-08-465-590-126
Sequence 126, Application US/08465590
Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-465-590-126

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 CGAGAAC 739
|||||
Db 1 CGAGAAC 8

RESULT 260
US-08-605-163-7/c
; Sequence 7, Application US/08605163
; Patent No. 5879886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-605-163-18

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACAC 746
|||||
Db 8 CAGAGCAC 1

RESULT 262
US-08-471-907A-5
; Sequence 5, Application US/08471907A
; Patent No. 5986053
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M. Ilegard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,907A


```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/088,658
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lucci, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-471-907A-5

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAA 738
Db 1 AAGAGAAA 8

RESULT 263
US-08-461-607-21/c
; Sequence 21, Application US/08461607
; Patent No. 6054633
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Stanbrook, Peter J.
; TITLE OF INVENTION: Live Animal Mutagenesis Systems for
; TITLE OF INVENTION: Testing Mutagenic Agents in Vivo
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,607
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,105
; FILING DATE:
; APPLICATION NUMBER: US 07/874,974
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-711-417C-126

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 GGAGGAAAC 739
Db 1 GGAGGAAAC 8

RESULT 264
US-08-711-417C-126
; Sequence 126, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-08-711-417C-126

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCAGGAG 735
Db 8 GCAGGAG 1
```

```
RESULT 265
US-09-363-600-21/c
; Sequence 21, Application US/09363600
; Patent No. 6232524
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: Live Animal Mutagenesis Systems for
; TITLE OF INVENTION: Testing Mutagenic Agents in Vivo
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/363.600
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,607
; FILING DATE:
; APPLICATION NUMBER: US 07/874,974
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..9
; OTHER INFORMATION: /note= "This sequence represents
; OTHER INFORMATION: mutation of base 2486 of Seq id No. 62325243"
US-09-363-600-21

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAG 735
Db 8 GCCAGCAG 1

RESULT 266
US-09-163-485-23
; Sequence 23, Application US/09163485
; Patent No. 6277571
; GENERAL INFORMATION:
; APPLICANT: FILMORE, HELEN
; TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
; TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
```

```
; TITLE OF INVENTION: KNOWN AND NOVEL MEMBERS OF GENE FAMILIES
; FILE REFERENCE: VCUIP4B
; CURRENT APPLICATION NUMBER: US/09/163,485
; CURRENT FILING DATE: 1998-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide, consensus sequence from human
; OTHER INFORMATION: matrix metalloproteinases
US-09-163-485-23

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAA 738
Db 1 AGGAGGAA 8

RESULT 267
US-09-327-138C-13
; Sequence 13, Application US/09327138C
; Patent No. 6541244
; GENERAL INFORMATION:
; APPLICANT: AUERNHAMMER, CHRISTOPH J.
; APPLICANT: MELMED, SHLOMO
; TITLE OF INVENTION: SUPPRESSOR OF CYTOKINE SIGNALING
; TITLE OF INVENTION: (SOCS)-3 PROMOTER AND METHODS FOR ITS USE IN GENETIC THERAPY
; FILE REFERENCE: P07 42591 (18810-803)
; CURRENT APPLICATION NUMBER: US/09/327,138C
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Mus musculus
; NAME/KEY: promoter
; FEATURE:
; LOCATION: (-74)...(-66)
; OTHER INFORMATION: STAT-BINDING SITE AT -74 TO -66
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (0)...(0)
; OTHER INFORMATION: STAT-BINDING SITE AT -74 TO -66
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (0)...(0)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (0)...(0)
; OTHER INFORMATION: STAT-BINDING SITE AT -74 TO 66
US-09-327-138C-13

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGA 734
Db 1 TTCCAGGA 8

RESULT 268
US-09-989-789-530/c
; Sequence 530, Application US/09989789
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; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 530
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-530

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 CCAGCAGA 736
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Db 8 CCAGCAGA 1

RESULT 269
US-09-989-789-2021
; Sequence 2021, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2021
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2021

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAA 737
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Db 1 CAGGAGAA 8

RESULT 270
US-09-989-789-2022
; Sequence 2022, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2022

; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2022

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAA 737
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Db 1 CAGGAGAA 8

RESULT 271
US-09-989-789-2401
; Sequence 2401, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2401
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2401

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAA 738
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Db 2 AGGAGAAA 9

RESULT 272
US-09-989-789-2402
; Sequence 2402, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2402
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2402

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 731 AGGAGAAA 738
DB 2 AGGAGAAA 9

RESULT 273
US-09-989-789-2403
; Sequence 2403, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2403
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2403

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAA 738
DB 2 AGGAGAAA 9

RESULT 274
US-09-723-909-126
; Sequence 126, Application US/09723909
; Patent No. 6630141
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/723,909
; FILING DATE: 28-Nov. 6630141-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417
; FILING DATE: 05-Sep-1996
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-09-723-909-126

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGGAAC 739
DB 1 GGAGGAAC 8

RESULT 275
PCT-US93-08743-126
; Sequence 126, Application PC/TUS9308743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08743
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 946,233
; FILING DATE: 14-SEP-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
PCT-US93-08743-126

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGGAAC 739
DB 1 GGAGGAAC 8

RESULT 276
PCT-US95-0477-28/c
; Sequence 28, Application PC/TUS950477
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
; TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 165
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
PCT-US95-04477-28

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Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 727 TGCCAGGA 734
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Db 9 TTCCAGGA 2

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Search completed: October 18, 2004, 14:09:44
Job time : 1 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 14:11:18 ; Search time 0.001 Seconds
(without alignments)
165.484 Million cell updates/sec

Title: US-09-695-451-1

Perfect score: 22

Sequence: 1 tgcagaggaacacagacacg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 286 seqs, 3761 residues

Total number of hits satisfying chosen parameters: 572

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 286 summaries

Database : rnpb1-727.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	90.9	22	1	US-10-409-107A-1	Sequence 1, Appli
2	16.4	74.5	22	1	US-10-321-039-633	Sequence 633, App
3	15.4	70.0	18	1	US-09-736-084-45	Sequence 45, Appl
4	15	68.2	18	1	US-10-453-792-274	Sequence 274, App
5	14.6	66.4	22	1	US-10-270-258-7	Sequence 7, Appli
6	14.6	66.4	22	1	US-10-270-258-11	Sequence 11, Appl
7	14.6	66.4	22	1	US-10-270-258-17	Sequence 17, Appl
8	14.2	64.5	21	1	US-09-904-368A-29	Sequence 29, Appl
9	14	63.6	18	1	US-10-453-792-276	Sequence 276, App
10	13.4	60.9	18	1	US-10-453-792-270	Sequence 270, App
11	13.4	60.9	18	1	US-10-453-792-272	Sequence 272, App
12	13.4	60.9	18	1	US-10-453-792-273	Sequence 273, App
13	12.8	58.2	17	1	US-10-060-756A-1254	Sequence 1254, App
14	12.8	58.2	17	1	US-10-060-756A-1255	Sequence 1255, App
15	12.4	56.4	17	1	US-10-060-756A-1256	Sequence 1256, App
16	12.4	56.4	17	1	US-10-060-756A-1257	Sequence 1257, App
17	12.4	56.4	17	1	US-10-453-792-275	Sequence 275, App
18	12.4	56.4	18	1	US-10-453-792-278	Sequence 278, App
19	12.4	56.4	19	1	US-09-998-533-28	Sequence 28, Appl
20	12.2	55.5	18	1	US-10-349-143-4649	Sequence 4649, App
21	12	54.5	17	1	US-10-676-154-188	Sequence 188, App
22	11.8	53.6	17	1	US-09-877-478-169	Sequence 169, App
23	11.8	53.6	17	1	US-09-877-478-170	Sequence 170, App
24	11.8	53.6	17	1	US-09-877-478-178	Sequence 178, App
25	11.8	53.6	17	1	US-10-342-902-169	Sequence 169, App
26	11.8	53.6	17	1	US-10-342-902-170	Sequence 170, App
27	11.8	53.6	17	1	US-10-342-902-878	Sequence 878, App
28	11.8	53.6	17	1	US-10-060-756A-1253	Sequence 1253, App
29	11.8	53.6	17	1	US-10-156-306-4512	Sequence 4512, App
30	11.8	53.6	17	1	US-10-156-306-5193	Sequence 5193, App
31	11.8	53.6	17	1	US-10-156-306-5194	Sequence 5194, App
32	11.8	53.6	17	1	US-10-339-793-241	Sequence 241, App
33	11.8	53.6	17	1	US-10-138-674-9242	Sequence 9242, App

Sequence 9242, App	17	53.6	11.8	1	US-10-287-949A-9242
Sequence 169, App	17	53.6	11.8	1	US-10-669-841-169
Sequence 170, App	17	53.6	11.8	1	US-10-669-841-170
Sequence 878, App	17	53.6	11.8	1	US-10-669-841-878
Sequence 42, Appl	18	53.6	11.8	1	US-08-911-824-42
Sequence 269, App	18	53.6	11.8	1	US-10-453-792-269
Sequence 271, App	18	53.6	11.8	1	US-10-453-792-271
Sequence 40, Appl	17	51.8	11.4	1	US-08-841-636A-40
Sequence 1258, App	17	51.8	11.4	1	US-10-060-756A-1258
Sequence 2390, App	17	51.8	11.4	1	US-10-138-674-2390
Sequence 2390, App	17	51.8	11.4	1	US-10-287-949A-2390
Sequence 40, Appl	17	51.8	11.4	1	US-10-782-002-40
Sequence 40, Appl	17	51.8	11.4	1	US-10-825-378-40
Sequence 983, App	17	50.9	11.2	1	US-09-776-474-983
Sequence 133, App	17	50.9	11.2	1	US-10-238-700-133
Sequence 788, App	17	50.9	11.2	1	US-10-230-006-788
Sequence 1196, App	17	50.9	11.2	1	US-10-297-068-1196
Sequence 2873, App	17	50.9	11.2	1	US-10-138-674-2873
Sequence 2873, App	17	50.9	11.2	1	US-10-138-674-2873
Sequence 653, App	15	49.1	10.8	1	US-09-504-231A-653
Sequence 653, App	15	49.1	10.8	1	US-09-274-553D-653
Sequence 10, Appl	15	49.1	10.8	1	US-10-056-414-10
Sequence 11, Appl	15	49.1	10.8	1	US-10-116-993-11
Sequence 11, Appl	15	49.1	10.8	1	US-10-743-163-11
Sequence 558, App	16	48.1	10.8	1	US-10-339-674-558
Sequence 1160, App	16	48.1	10.8	1	US-10-339-674-1160
Sequence 78, Appl	12	47.3	10.4	1	US-10-171-897-78
Sequence 125, App	14	47.3	10.4	1	US-10-146-058-125
Sequence 6035, App	15	47.3	10.4	1	US-09-877-478-6035
Sequence 6035, App	15	47.3	10.4	1	US-10-342-902-6035
Sequence 1179, App	15	47.3	10.4	1	US-10-339-674-1179
Sequence 3197, App	15	47.3	10.4	1	US-10-339-674-3197
Sequence 11, Appl	15	47.3	10.4	1	US-10-056-414-11
Sequence 2438, App	15	47.3	10.4	1	US-10-669-841-2438
Sequence 2, Appli	16	47.3	10.4	1	US-09-997-326-2
Sequence 715, App	15	46.4	10.2	1	US-09-504-231A-715
Sequence 715, App	15	46.4	10.2	1	US-09-504-231A-716
Sequence 715, App	15	46.4	10.2	1	US-09-274-553D-715
Sequence 715, App	15	46.4	10.2	1	US-09-274-553D-716
Sequence 19, Appl	15	46.4	10.2	1	US-09-835-694-19
Sequence 420, App	15	46.4	10.2	1	US-10-339-674-420
Sequence 421, App	15	46.4	10.2	1	US-10-339-674-421
Sequence 717, App	15	45.5	10	1	US-09-504-231A-717
Sequence 717, App	15	45.5	10	1	US-09-274-553D-717
Sequence 1341, App	14	44.5	9.8	1	US-09-504-231A-1341
Sequence 1341, App	14	44.5	9.8	1	US-09-274-553D-1341
Sequence 126, App	14	44.5	9.8	1	US-10-146-058-126
Sequence 21, Appl	14	44.5	9.8	1	US-10-104-025-9
Sequence 654, App	15	44.5	9.8	1	US-10-324-409B-21
Sequence 654, App	15	44.5	9.8	1	US-09-504-231A-654
Sequence 654, App	15	44.5	9.8	1	US-09-274-553D-654
Sequence 95, Appl	15	44.5	9.8	1	US-10-347-510A-95
Sequence 95, Appl	15	44.5	9.8	1	US-09-544-934B-95
Sequence 1871, App	15	44.5	9.8	1	US-10-339-674-1871
Sequence 1219, App	11	42.7	9.4	1	US-10-450-797-1219
Sequence 73, Appl	12	42.7	9.4	1	US-10-100-957A-73
Sequence 5, Appl	12	42.7	9.4	1	US-10-073-377-5
Sequence 6, Appl	12	42.7	9.4	1	US-10-073-377-6
Sequence 32, Appl	14	42.7	9.4	1	US-10-076-587-32
Sequence 19, Appl	14	42.7	9.4	1	US-10-073-377-19
Sequence 1, Appl	14	42.7	9.4	1	US-10-151-997-1
Sequence 35, Appl	14	42.7	9.4	1	US-10-146-058-35
Sequence 1787, App	10	40.9	9	1	US-10-033-145-1787
Sequence 1921, App	10	40.9	9	1	US-10-033-145-1921
Sequence 167, App	11	40.9	9	1	US-10-450-797-167
Sequence 843, App	12	40.9	9	1	US-09-283-959-843
Sequence 61, Appl	12	40.9	9	1	US-10-100-957A-61
Sequence 75, Appl	12	40.9	9	1	US-1A-100-957A-75
Sequence 47, Appl	12	40.0	8.8	1	US-09-981-803-47
Sequence 28, Appl	12	40.0	8.8	1	US-10-275-071-28
Sequence 393, App	12	40.0	8.8	1	US-10-091-281-393
Sequence 34, Appl	12	40.0	8.8	1	US-10-684-830-34
Sequence 37, Appl	12	40.0	8.8	1	US-10-684-830-37

107	8.8	40.0	13	1	US-09-152-059-3	Sequence 3, Appl	C 180	8.4	38.2	10	1	US-10-330-627-1363	Sequence 1363, Appl
108	8.8	40.0	13	1	US-09-152-059-4	Sequence 4, Appl	C 181	8.4	38.2	10	1	US-10-434-479-47	Sequence 47, Appl
109	8.8	40.0	13	1	US-09-152-059-5	Sequence 5, Appl	C 182	8.4	38.2	10	1	US-10-450-797-47	Sequence 47, Appl
110	8.8	40.0	13	1	US-03-152-059-6	Sequence 6, Appl	C 183	8.4	38.2	11	1	US-10-450-797-532	Sequence 532, Appl
111	8.8	40.0	13	1	US-09-152-059-7	Sequence 7, Appl	C 184	8.4	38.2	11	1	US-10-450-797-537	Sequence 537, Appl
112	8.8	40.0	13	1	US-09-152-059-8	Sequence 8, Appl	C 185	8.4	38.2	11	1	US-10-450-797-613	Sequence 613, Appl
113	8.8	40.0	13	1	US-09-152-059-9	Sequence 9, Appl	C 186	8.4	38.2	11	1	US-10-450-797-741	Sequence 741, Appl
114	8.8	40.0	13	1	US-09-152-059-28	Sequence 28, Appl	C 187	8.4	38.2	12	1	US-09-179-536B-81	Sequence 81, Appl
115	8.8	40.0	13	1	US-09-152-059-29	Sequence 29, Appl	C 188	8.4	38.2	12	1	US-09-179-536B-86	Sequence 86, Appl
116	8.8	40.0	13	1	US-09-152-059-30	Sequence 30, Appl	C 189	8.4	38.2	12	1	US-09-263-959-477	Sequence 477, Appl
117	8.8	40.0	13	1	US-09-152-059-31	Sequence 31, Appl	C 190	8.4	38.2	12	1	US-09-263-959-492	Sequence 492, Appl
118	8.8	40.0	13	1	US-09-152-059-32	Sequence 32, Appl	C 191	8.4	38.2	12	1	US-09-263-959-755	Sequence 755, Appl
119	8.8	40.0	13	1	US-09-152-059-43	Sequence 43, Appl	C 192	8.4	38.2	12	1	US-09-263-959-850	Sequence 850, Appl
120	8.8	40.0	13	1	US-09-152-059-46	Sequence 46, Appl	C 193	8.4	38.2	12	1	US-09-845-938A-7	Sequence 7, Appl
121	8.8	40.0	13	1	US-09-152-059-46	Sequence 46, Appl	C 194	8.4	38.2	12	1	US-09-845-938A-7	Sequence 7, Appl
122	8.8	40.0	13	1	US-09-152-059-46	Sequence 46, Appl	C 195	8.4	38.2	12	1	US-09-297-576A-81	Sequence 81, Appl
123	8.8	40.0	13	1	US-09-152-059-48	Sequence 48, Appl	C 196	8.4	38.2	12	1	US-09-297-576A-86	Sequence 86, Appl
124	8.8	40.0	13	1	US-09-152-059-71	Sequence 71, Appl	C 197	8.4	38.2	12	1	US-10-164-875C-3	Sequence 3, Appl
125	8.8	40.0	13	1	US-09-152-059-74	Sequence 74, Appl	C 198	8.4	38.2	12	1	US-10-164-875C-3	Sequence 3, Appl
126	8.8	40.0	13	1	US-09-152-059-77	Sequence 77, Appl	C 199	8.4	38.2	12	1	US-10-164-875C-5	Sequence 5, Appl
127	8.8	40.0	13	1	US-09-781-811-13	Sequence 23, Appl	C 200	8.4	38.2	12	1	US-10-661-165-433	Sequence 433, Appl
128	8.8	40.0	13	1	US-10-027-632-177279	Sequence 177279, Appl	C 201	8	36.4	9	1	US-10-667-81-32	Sequence 222, Appl
129	8.8	40.0	13	1	US-10-027-632-177279	Sequence 177279, Appl	C 202	8	36.4	10	1	US-10-091-281-222	Sequence 222, Appl
130	8.8	40.0	13	1	US-10-008-029-3	Sequence 3, Appl	C 203	8	36.4	10	1	US-10-293-222-96	Sequence 96, Appl
131	8.8	40.0	13	1	US-10-008-029-4	Sequence 4, Appl	C 204	8	36.4	10	1	US-10-033-145-537	Sequence 537, Appl
132	8.8	40.0	13	1	US-10-008-029-5	Sequence 5, Appl	C 205	8	36.4	10	1	US-10-329-465-139	Sequence 139, Appl
133	8.8	40.0	13	1	US-10-008-029-6	Sequence 6, Appl	C 206	8	36.4	10	1	US-10-355-820-2	Sequence 2, Appl
134	8.8	40.0	13	1	US-10-008-029-7	Sequence 7, Appl	C 207	8	36.4	10	1	US-10-330-627-26	Sequence 26, Appl
135	8.8	40.0	13	1	US-10-008-029-8	Sequence 8, Appl	C 208	8	36				

C 253	7.4	33.6	10	1	US-10-033-145-1342	Sequence 1342, App
C 254	7.4	33.6	10	1	US-10-033-145-1346	Sequence 1396, App
C 255	7.4	33.6	10	1	US-10-033-145-1419	Sequence 1419, App
C 256	7.4	33.6	10	1	US-10-033-145-1496	Sequence 1496, App
C 257	7.4	33.6	10	1	US-10-033-145-1773	Sequence 1773, App
C 258	7.4	33.6	10	1	US-10-033-145-1999	Sequence 1999, App
C 259	7.4	33.6	10	1	US-10-010-802-261	Sequence 261, App
C 260	7.4	33.6	10	1	US-10-010-802-287	Sequence 287, App
C 261	7.4	33.6	10	1	US-10-176-464-59	Sequence 59, Appl
C 262	7.4	33.6	10	1	US-10-329-465-95	Sequence 95, Appl
C 263	7.4	33.6	10	1	US-10-330-627-238	Sequence 238, App
C 264	7.4	33.6	10	1	US-10-330-627-399	Sequence 399, App
C 265	7.4	33.6	10	1	US-10-193-507-79	Sequence 79, Appl
C 266	7.4	33.6	11	1	US-09-735-363A-82	Sequence 82, Appl
C 267	7.4	33.6	11	1	US-08-249-155-86	Sequence 86, Appl
C 268	7.4	33.6	11	1	US-09-249-155-124	Sequence 124, Appl
C 269	7.4	33.6	11	1	US-09-918-715-66	Sequence 66, Appl
C 270	7.4	33.6	11	1	US-10-191-302-8	Sequence 8, Appl
C 271	7.4	33.6	11	1	US-10-314-322-86	Sequence 86, Appl
C 272	7.4	33.6	11	1	US-10-314-322-124	Sequence 124, App
C 273	7.4	33.6	11	1	US-10-612-224-78	Sequence 78, Appl
C 274	7.4	33.6	11	1	US-10-450-797-51	Sequence 51, Appl
C 275	7.4	33.6	11	1	US-10-450-797-110	Sequence 110, App
C 276	7.4	33.6	11	1	US-10-450-797-284	Sequence 284, App
C 277	7.4	33.6	11	1	US-10-450-797-285	Sequence 285, App
C 278	7.4	33.6	11	1	US-10-450-797-335	Sequence 335, App
C 279	7.4	33.6	11	1	US-10-450-797-538	Sequence 538, App
C 280	7.4	33.6	11	1	US-10-450-797-626	Sequence 626, App
C 281	7.4	33.6	11	1	US-10-450-797-662	Sequence 662, App
C 282	7.4	33.6	11	1	US-10-450-797-681	Sequence 681, App
C 283	7.4	33.6	11	1	US-10-450-797-1118	Sequence 1118, App
C 284	7.4	33.6	11	1	US-10-450-797-1250	Sequence 1280, App
C 285	7.4	33.6	11	1	US-10-450-797-1286	Sequence 1286, App
C 286	7.4	33.6	11	1	US-10-450-797-1320	Sequence 1320, App

ALIGNMENTS

```

RESULT 1
US-10-409-107A-1
; Sequence 1, Application US/10409107A
; Publication No. US20040053288A1
; GENERAL INFORMATION:
; APPLICANT: YANAI, Yoshiaki
; APPLICANT: YAMAMOTO, Shigeto
; APPLICANT: YAMAMOTO, Kozo
; APPLICANT: IKEGAMI, Hakuo
; TITLE OF INVENTION: Method for estimating therapeutic efficacy of tumor necrosis
; TITLE OF INVENTION: factor
; FILE REFERENCE: YANAI-3
; CURRENT APPLICATION NUMBER: US/10/409,107A
; CURRENT FILING DATE: 2003-04-19
; PRIOR APPLICATION NUMBER: JP 107126/2002
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used as primer for PCR detection of TNF-R55 mRNA
US-10-409-107A-1

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```

RESULT 2
US-10-321-039-633
; Sequence 633, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kutensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 633
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-321-039-633

Query Match          74.5%; Score 16.4; DB 1; Length 2
Best Local Similarity 94.4%; Pred.No. 8.8;
Matches 17; Conservative 0; Mismatches 1; Indels

QY      727 TCCAGGAGGAAACAGAAC 744
Db       5 TCCAGGAGACACAGAAC 22

RESULT 3
US-09-736-084-45/c
; Sequence 45, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 98
; ADDRESSSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/736,084
; FILING DATE: 13-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. US20020107211A1,ember 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

```

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-736-084-45
Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 730 CAGGAGAAACAGACAC 746
DB 18 CAGGAGAAACAGACAC 2
RESULT 4
US-10-453-792-274/c
; Sequence 274, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 274:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 274:
US-10-453-792-274

Query Match 68.2%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
DB 18 GCCAGGAGAAACAGA 4

RESULT 5
US-10-270-258-7/c
; Sequence 7, Application US/10270258
; Publication No. US20030148951A1
; GENERAL INFORMATION:
; APPLICANT: Hsi-Hsien, Lin
; APPLICANT: Gordon, Siamon
; APPLICANT: McKnight, Andrew J.
; APPLICANT: Stacey, Martin
; APPLICANT: Isis Innovation Limited
TITLE OF INVENTION: Human EMR2, A G-Protein Coupled Receptor from the EGF-TM7 Family
FILE REFERENCE: 1365.061US1
CURRENT APPLICATION NUMBER: US/10/270,258
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: PCT/GB01/01729
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: GB 0009181.9
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In version 3.0
SEQ ID NO 7
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
US-10-270-258-7

Query Match 66.4%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 727 TCCACGAGAACAGACACC 747
DB 22 TCCACGAGAACAGACACC 2

RESULT 6
US-10-270-258-11/c
; Sequence 11, Application US/10270258
; Publication No. US20030148951A1
; GENERAL INFORMATION:
; APPLICANT: Hsi-Hsien, Lin
; APPLICANT: Gordon, Siamon
; APPLICANT: McKnight, Andrew J.
; APPLICANT: Stacey, Martin
; APPLICANT: Isis Innovation Limited
TITLE OF INVENTION: Human EMR2, A G-Protein Coupled Receptor from the EGF-TM7 Family
FILE REFERENCE: 1365.061US1
CURRENT APPLICATION NUMBER: US/10/270,258
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: PCT/GB01/01729
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: GB 0009181.9
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In version 3.0


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RESULT 10
US-10-453-792-270/c
; Sequence 270, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 270:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 270:
US-10-453-792-270
Query Match 60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGA 742
Db 18 GCCAAGAGAAACAGA 4

RESULT 11
US-10-453-792-272/c
; Sequence 272, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-10-453-792-272
Query Match 60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGA 742
Db 18 GCCATGAGAAACAGA 4

RESULT 12
US-10-453-792-273/c
; Sequence 273, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-10-453-792-273

Query Match 60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACACA 742
Db 18 GCCAGGAGAAACGGA 4

RESULT 13
US-10-060-756A-1254/c
; Sequence 1254, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1254
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1254

Query Match 58.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 727 TGCCAGGAGAAACACA 742
Db 17 TGCCAGGAGAAACACA 2

RESULT 14
US-10-060-756A-1255/c
; Sequence 1255, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1255
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1255

Query Match 58.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 727 TGCCAGGAGAAACACA 742
Db 16 TGCCAGGAGAAACACA 1

RESULT 15
US-10-060-756A-1256/c
; Sequence 1256, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/327,898
 ; PRIOR FILING DATE: 2001-10-09
 ; NUMBER OF SEQ ID NOS: 4804
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1256
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-060-756A-1256

Query Match 56.4%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 32;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAACA 740
 Db 15 TGCCAGGTGAACA 2

RESULT 16

US-10-060-756A-1257/c
 ; Sequence 1257, Application US/10060756A
 ; Publication No. US20030046717A1
 ; GENERAL INFORMATION:

; APPLICANT: Zhang, Jian
 ; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
 ; FILE REFERENCE: PB0177
 ; CURRENT APPLICATION NUMBER: US/10/060,756A
 ; CURRENT FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/327,898
 ; PRIOR FILING DATE: 2001-10-09
 ; NUMBER OF SEQ ID NOS: 4804
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1257
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-10-060-756A-1257

Query Match 56.4%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 32;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAACA 740
 Db 14 TGCCAGGTGAACA 1

RESULT 17

US-10-453-792-275/c
 ; Sequence 275, Application US/10453792
 ; Publication No. US20040029110A1
 ; GENERAL INFORMATION:

; APPLICANT: STUYVER, LIEVEN
 ; ROSSAU, RUDI
 ; MAERTENS, GEERT

TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

; NUMBER OF SEQUENCES: 313
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHVE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION NUMBER: US/10/453,792
 ; FILING DATE: 04-Jun-2003
 ; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/155,885A
 ; FILING DATE: 08-Oct-1998
 ; APPLICATION NUMBER: PCT/EP97/02002
 ; FILING DATE: 21-APR-1997
 ; APPLICATION NUMBER: EP 96870053.4
 ; FILING DATE: 19-APR-1996

ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B.J.
 ; REGISTRATION NUMBER: 36,663
 ; REFERENCE/POCKET NUMBER: 2551-5

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000
 ; TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 275:

SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHEITICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 275:

US-10-453-792-275

Query Match 56.4%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 33;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
 Db 18 GCCAGGAGAAACGG 5

RESULT 18

US-10-453-792-278/c
 ; Sequence 278, Application US/10453792
 ; Publication No. US20040029110A1

GENERAL INFORMATION:

; APPLICANT: STUYVER, LIEVEN
 ; ROSSAU, RUDI
 ; MAERTENS, GEERT

TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

NUMBER OF SEQUENCES: 313

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHVE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 278:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 278:
US-10-453-792-278

Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 33;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAG 741
Db 18 GCCATGAGAAACAG 5

RESULT 19

US-09-898-533-28/c
Sequence 28, Application US/09898533
Patent No. US20020106656A1
GENERAL INFORMATION:
APPLICANT: Gemmill, Robert M.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR,
FILE REFERENCE: 93445-00004
CURRENT APPLICATION NUMBER: US/09/898,533
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US/09/268,140
PRIOR FILING DATE: 2000-03-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-09-898-533-28

Query Match 56.4%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 34;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAAACA 740
Db 16 TGCCAGGAGAAACA 3

RESULT 20

US-10-349-143-4649/c

Sequence 4649, Application US/10349143
Publication No. US20040005584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 4649
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-16740 for SEQ 715,
US-10-349-143-4649

Query Match 55.5%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 36;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGAACACC 747
Db 17 AGGAGAAACAGAGGAAC 1

RESULT 21

US-10-676-154-188/c
Sequence 188, Application US/10676154
Publication No. US20040081996A1
GENERAL INFORMATION:
APPLICANT: John Landers
APPLICANT: David Houseman
APPLICANT: Barbara Jordan
APPLICANT: Alain Charest
TITLE OF INVENTION: Methods and Products Related to
FILE REFERENCE: M0656/7045(HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/676,154
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US 60/101,757
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22283
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 691
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 188
LENGTH: 17
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-676-154-188

Query Match 54.5%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
Db 13 AAACAGAACACC 2

```
RESULT 22
US-09-877-478-169/c
; Sequence 169, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 169
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-169

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
    |||||
Db 17 GCCAAGAGAAACGGA 3

RESULT 23
US-09-877-478-170/c
; Sequence 170, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
```

```
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 170
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-170

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
    |||||
Db 16 GCCAAGAGAAACGGA 2

RESULT 24
US-09-877-478-878/c
; Sequence 878, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 878
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-878

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
    |||||
Db 15 GCCAAGAGAAACGGA 1

RESULT 25
US-10-342-902-169/c
; Sequence 169, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
```


APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO 169
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-342-902-169

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGA 742
DB 17 GCCAAGAGAAACGGA 3

RESULT 26
US-10-342-902-170/c
Sequence 170, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO 170
LENGTH: 17
TYPE: RNA

ORGANISM: Hepatitis B virus
US-10-342-902-170
Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGA 742
DB 16 GCCAAGAGAAACGGA 2

RESULT 27
US-10-342-902-878/c
Sequence 878, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO 878
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-342-902-878
Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGA 742
DB 15 GCCAAGAGAAACGGA 1

RESULT 28
US-10-060-756A-1253/c
Sequence 1253, Application US/10060756A
Publication No. US20030046717A1
GENERAL INFORMATION:
APPLICANT: Zhang, Jian
TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: PB0177
CURRENT APPLICATION NUMBER: US/10/060,756A
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 1253
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1253

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACACA 742
| | | | | | | | | | | | | | | | | | | | |
DB 17 GCCAGGTGAACACA 3

RESULT 29

US-10-156-306-4512/c
; Sequence 4512, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4512
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-4512

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACAG 741
| | | | | | | | | | | | | | | | | | | | |
DB 17 TCCAGGGGAGACG 3

RESULT 30

US-10-156-306-5193/c
; Sequence 5193, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5193
; LENGTH: 17
; TYPE: RNA

; ORGANISM: Homo sapiens
US-10-156-306-5193

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACAG 741
| | | | | | | | | | | | | | | | | | | | |
DB 16 TCCAGGGGAGACG 2

RESULT 31

US-10-156-306-5194/c
; Sequence 5194, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5194
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5194

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACAG 741
| | | | | | | | | | | | | | | | | | | | |
DB 15 TCCAGGGGAGACG 1

RESULT 32

US-10-339-793-241
; Sequence 241, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
; FILE REFERENCE: 37-000310US
; CURRENT APPLICATION NUMBER: US/10/339,793
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 443
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-793-241

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACAG 741
| | | | | | | | | | | | | | | | | | | | |
DB 3 TCCAGGGGAGATCAG 17

RESULT 33

US-10-138-674-9242/c
; Sequence 9242, Application US/10138674

```
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9242
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-9242

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAACAGACACCG 748
Db 17 AGAAACAGACACCG 3

RESULT 34
US-10-287-949A-9242/c
; Sequence 9242, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9242
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-9242

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAACAGACACCG 748
Db 17 AGAAACAGACACCG 3

RESULT 35
US-10-669-841-169/c
; Sequence 169, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
```

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; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; FILE REFERENCE: 400/042US (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 169
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-169

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGAGAAACAGA 742
Db 17 GCCAAGAGAAACGGA 3

RESULT 36
US-10-669-841-170/c
; Sequence 170, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; FILE REFERENCE: 400/042US (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
```

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; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 170
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-170

Query Match      53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
DB 16 GCCAGGAGAAACAGA 2

RESULT 37
US-10-669-841-878/c
; Sequence 878, Application US/10669841
; Publication No. US2004012746A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCI/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 878
; LENGTH: 17

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; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-878

Query Match      53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
DB 15 GCCAGGAGAAACAGA 1

RESULT 38
US-08-911-824-42
; Sequence 42, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: PCR Primer 41sy-3
US-08-911-824-42

Query Match      53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAAC 744
DB 3 CAGGAGAAACAGAAC 17

RESULT 39
US-10-453-792-269/c
; Sequence 269, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792

```

;; FILING DATE: 04-Jun-2003
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/155,885A
;; FILING DATE: 08-Oct-1998
;; APPLICATION NUMBER: PCT/EP97/02002
;; FILING DATE: 21-APR-1997
;; APPLICATION NUMBER: EP 96870053.4
;; FILING DATE: 19-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SADOFF, B.J.
;; REGISTRATION NUMBER: 36,663
;; REFERENCE/DOCKET NUMBER: 2551-5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 269:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; SEQUENCE DESCRIPTION: SEQ ID NO: 269:
US-10-453-792-269

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAAGAGAAACGGA 4

RESULT 40
US-10-453-792-271/c
;; Sequence 271, Application US/10453792
;; Publication No. US20040029110A1
;; GENERAL INFORMATION:
;; APPLICANT: STUYVEN, RUDY
;; MAERTENS, GEERT
;; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
;; NUMBER OF SEQUENCES: 313
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHYE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/453,792
;; FILING DATE: 04-Jun-2003
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/155,885A
;; FILING DATE: 08-Oct-1998
;; APPLICATION NUMBER: PCT/EP97/02002
;; FILING DATE: 21-APR-1997
;; APPLICATION NUMBER: EP 96870053.4
;; FILING DATE: 19-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SADOFF, B.J.
;; REGISTRATION NUMBER: 36,663

;; REFERENCE/DOCKET NUMBER: 2551-5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 271:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; SEQUENCE DESCRIPTION: SEQ ID NO: 271:
US-10-453-792-271

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCATGAGAAACGGA 4

RESULT 41
US-08-841-636A-40
;; Sequence 40, Application US/08841636A
;; Publication No. US20020168751A1
;; GENERAL INFORMATION:
;; APPLICANT: Miettinen-Oinonen, Arja
;; APPLICANT: Lonsborough, John
;; APPLICANT: Vehmaanper, Jari
;; APPLICANT: Haakana, Heli
;; APPLICANT: M ntyl, Arja
;; APPLICANT: Lantto, Raija
;; APPLICANT: Elovainio, Minna
;; APPLICANT: Joutsenjo, Vesa
;; APPLICANT: Paloheimo, Marja
;; APPLICANT: Suominen, Pirkko
;; TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
;; STREET: 1100 New York Avenue, N.W., Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/841,636A
;; FILING DATE: 30-APR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/005,335
;; FILING DATE: 17-OCT-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/007,926
;; FILING DATE: 04-DEC-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/020,840
;; FILING DATE: 28-JUN-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/732,181
;; FILING DATE: 16-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FI96/00550

```

; FILING DATE: 17-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Timothy J. Shea, Jr.
; REGISTRATION NUMBER: 41,306
; REFERENCE/DOCKET NUMBER: 1716.0510005/WAC/TJS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-841-636A-40

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 46;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGACACCG 748
Db ||||| ||||| |||||

RESULT 42
US-10-060-756A-1258/c
; Sequence 1258, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1258
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-060-756A-1258

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 46;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGGAAC 739
Db ||||| ||||| |||||

RESULT 43
US-10-138-674-2390
; Sequence 2390, Application US/10138674
; Publication No. US20040077565A1

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; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2390
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
; US-10-138-674-2390

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 46;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAACA 745
Db ||||| ||||| |||||

RESULT 44
US-10-287-949A-2390
; Sequence 2390, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2390
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
; US-10-287-949A-2390

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 46;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAACA 745
Db ||||| ||||| |||||

RESULT 45
US-10-782-002-40
; Sequence 40, Application US/10782002
; Publication No. US2004014244A1
; GENERAL INFORMATION:
; APPLICANT: Miettinen-Oinonen, Arja
; APPLICANT: Londenborough, John
; APPLICANT: Vehmaanpera, Jari
; APPLICANT: Haakana, Heli
; APPLICANT: Mantyla, Arja
; APPLICANT: Lantto, Raija
; APPLICANT: Elovainio, Minna
; APPLICANT: Joutsjoki, Vesa

```

APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Novel Cellulases, The Genes Encoding Them and Uses Thereof
FILE REFERENCE: 1716.051000A
CURRENT APPLICATION NUMBER: US/10/782,002
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US 08/841,636
PRIOR FILING DATE: 1997-04-30
PRIOR APPLICATION NUMBER: PCT/FI96/00550
PRIOR FILING DATE: 1996-10-17
PRIOR APPLICATION NUMBER: US 08/732,181
PRIOR FILING DATE: 1996-10-16
PRIOR APPLICATION NUMBER: US 60/020,840
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: US 60/007,926
PRIOR FILING DATE: 1995-12-04
PRIOR APPLICATION NUMBER: US 60/005,335
PRIOR FILING DATE: 1995-10-17
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
LENGTH: 17
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PCR Primer
NAME/KEY: misc_feature
LOCATION: (9)..(9)
OTHER INFORMATION: n is a, c, g, or t
US-10-782-002-40

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 46;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 735 GAAACAGAACACCG 748
Db 4 GARACNGARCAVMG 17
||:||||:|

RESULT 46
US-10-825-378-40
Sequence 40, Application US/10825378
Publication No. US20040185498A1
GENERAL INFORMATION:
APPLICANT: Miettinen-Oinonen, Arja
APPLICANT: Londeborough, John
APPLICANT: Vehmaanpera, Jari
APPLICANT: Haakana, Heli
APPLICANT: Mantyla, Arja
APPLICANT: Lauto, Raija
APPLICANT: Elovalnio, Minna
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Novel Cellulases, The Genes Encoding Them and Uses Thereof
FILE REFERENCE: 1716.0510009
CURRENT APPLICATION NUMBER: US/10/825,378
CURRENT FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 08/841,636
PRIOR FILING DATE: 1997-04-30
PRIOR APPLICATION NUMBER: PCT/FI96/00550
PRIOR FILING DATE: 1996-10-17
PRIOR APPLICATION NUMBER: US 08/732,181
PRIOR FILING DATE: 1996-10-16
PRIOR APPLICATION NUMBER: US 60/020,840
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: US 60/007,926
PRIOR FILING DATE: 1995-12-04
PRIOR APPLICATION NUMBER: US 60/005,335
PRIOR FILING DATE: 1995-10-17
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2

SEQ ID NO 40
LENGTH: 17
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PCR Primer
NAME/KEY: misc_feature
LOCATION: (9)..(9)
OTHER INFORMATION: n is a, c, g, or t
US-10-825-378-40
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 46;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 735 GAAACAGAACACCG 748
Db 4 GARACNGARCAVMG 17
||:||||:|

RESULT 47
US-09-776-474-983
Sequence 983, Application US/09776474
Publication No. US20030087847A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: Bocher, Robert
APPLICANT: Holman, Patricia
APPLICANT: Fattaey, Ali
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK-1)
FILE REFERENCE: MEH00-955-A (400/008)
CURRENT APPLICATION NUMBER: US/09/776,474
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,983
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 2992
SOFTWARE: PatentIn version 3.0
SEQ ID NO 983
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-983
Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 731 AGGAGAACAGACAC 746
Db 2 AGGAGAACACAAUAAAC 17
|||||||

RESULT 48
US-10-238-700-133
Sequence 133, Application US/10238700
Publication No. US2003015321A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level 1
FILE REFERENCE: 400/057 (WBH01-1158-A)
CURRENT APPLICATION NUMBER: US/10/238,700
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/318,471
PRIOR FILING DATE: 2001-09-10

; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-133

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 730 CAGGAGAACAGAAC 745
DB 1 CAGUAGACACAAACA 16

RESULT 49
US-10-230-006-788
; Sequence 788, Application US/10230006
; Publication No. US2003019107A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC COND
; FILE REFERENCE: 400/056 (MBH01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 788
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-788

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 732 GGAGAACAGAACACC 747
DB 1 GAAGAAGCAGAAGACC 16

RESULT 50
US-10-237-068-1196
; Sequence 1196, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1196
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: capture

US-10-297-068-1196

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAACAGAAC 744
DB 1 CCGGAGATACAGATC 16

RESULT 51
US-10-138-674-2873/c
; Sequence 2873, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2873
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-2873

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAGAA 743
DB 16 GCCAGGAGACACGTAA 1

RESULT 52
US-10-287-949A-2873/c
; Sequence 2873, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2873
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-2873

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAGAA 743
DB 16 GCCAGGAGACACGTAA 1

RESULT 53
US-09-504-231A-653/c
; Sequence 653, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1999-02-24
; PRIOR FILING DATE: 1999-02-24
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 653
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-653

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACCG 748
Db 15 GAAACAGTACTG 2

RESULT 54
US-09-274-553D-653/c
; Sequence 653, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1999-02-24
; PRIOR FILING DATE: 1999-02-24
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 653
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-653

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAAC 744
Db 14 AGGGAGAACAGATC 1

US-09-274-553D-653

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACCG 748
Db 15 GAAACAGTACTG 2

RESULT 55
US-10-056-414-10/c
; Sequence 10, Application US/10056414
; Publication No. US20030003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; RELATED TO LEVELS OF
; NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,414
; FILING DATE: 23-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-056-414-10

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAAC 744
Db 14 AGGGAGAACAGATC 1

```

; LENGTH: 16
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (616577)...(616592)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 743
US-10-339-674-558

Query Match 49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
Db 16 GAAACAAACACCG 3

RESULT 59
US-10-339-674-1160/c
; Sequence 1160, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1160
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (1302700)...(1302715)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1513
US-10-339-674-1160

Query Match 49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
Db 16 GAAACAAACACCG 3

RESULT 60
US-10-717-897-78
; Sequence 78, Application US/10717897
; Publication No. US20040163146A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: PUTHIGAE, SATHISH
; APPLICANT: YAO, JIALONG
; APPLICANT: FLINN, BARRY
; APPLICANT: FORSTER, RICHARD S.
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTERS
; FILE REFERENCE: 044463-0264
; CURRENT APPLICATION NUMBER: US/10/717,897
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/428,287
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 78
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide motif sequence

```

US-10-717-897-78

Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAGAA 743
Db 1 GGAGAACAGAA 12
|||||
|

RESULT 61
US-10-146-058-125
; Sequence 125, Application US/10146058
; Publication No. US2003004099A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-125

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 57;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAA 742
Db 1 AGGAGAACAGAA 12
|||||
|

US-10-146-058-125

RESULT 62
US-09-877-478-6035/c
; Sequence 6035, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6035
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-6035

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGAGAAAC 739
Db 12 GCCAGAGAAAC 1
|||||
|

RESULT 63
US-10-342-902-6035/c
; Sequence 6035, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07

;; PRIOR APPLICATION NUMBER: US 07/882,712
;; PRIOR FILING DATE: 1992-05-14
;; PRIOR APPLICATION NUMBER: US 09/436,430
;; PRIOR FILING DATE: 1999-11-08
;; NUMBER OF SEQ ID NOS: 6592
;; SOFTWARE: Patent version 3.2
;; SEQ ID NO 6035
;; LENGTH: 15
;; TYPE: RNA
;; ORGANISM: Hepatitis B virus
US-10-342-902-6035

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAC 739
DB 12 GCCAGGAGAAC 1

RESULT 64
US-10-339-674-1179/c
;; Sequence 1179, Application US/10339674
;; Publication No. US20030204318A1
;; GENERAL INFORMATION:
;; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
;; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;; CURRENT APPLICATION NUMBER: US/10/339,674
;; CURRENT FILING DATE: 2003-06-06
;; NUMBER OF SEQ ID NOS: 3537
;; SOFTWARE: Proprietary
;; SEQ ID NO 1179
;; LENGTH: 15
;; TYPE: DNA
;; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
;; FEATURE:
;; LOCATION: (1357006) ... (1357020)
;; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1542
US-10-339-674-1179

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
DB 13 AACAGAACACC 2

RESULT 65
US-10-339-674-3197/c
;; Sequence 3197, Application US/10339674
;; Publication No. US20030204318A1
;; GENERAL INFORMATION:
;; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
;; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;; CURRENT APPLICATION NUMBER: US/10/339,674
;; CURRENT FILING DATE: 2003-06-06
;; NUMBER OF SEQ ID NOS: 3537
;; SOFTWARE: Proprietary
;; SEQ ID NO 3197
;; LENGTH: 15
;; TYPE: DNA
;; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
;; FEATURE:
;; LOCATION: (4276408) ... (4276422)
;; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 4240
US-10-339-674-3197

Query Match 47.3%; Score 10.4; DB 1; Length 15;

Best Local Similarity 91.7%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
DB 13 AACAGAACACC 2

RESULT 66
US-10-056-414-11/c
;; Sequence 11, Application US/10056414
;; Publication No. US20030003469A1
;; GENERAL INFORMATION:
;; APPLICANT: Stinchcomb, Dan T.
;; Draper, Kenneth G.
;; McSwiggen, James
;; TITLE OF INVENTION: RIBOZYME TREATMENT OF
;; DISEASES OR CONDITIONS
;; RELATED TO LEVELS OF
;; NF-KB
;; NUMBER OF SEQUENCES: 830
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/056,414
;; FILING DATE: 23-Jan-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/291,932A
;; FILING DATE: August 15, 1994
;; APPLICATION NUMBER: 08/245,466
;; FILING DATE: May 18, 1994
;; APPLICATION NUMBER: 07/987,132
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 208/157
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-056-414-11

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGGAACACAGA 742
DB 13 AGGGAACACAGA 2

RESULT 67

```

; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-997-326-2

Query Match          47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. NO. 62;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      732 GGAGAAACAGAA 743
      |||||
Db       16 GGGAAACAGAA 5

RESULT 69
US-09-504-231A-715/c
; Sequence 715, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 715
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-715

Query Match          46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. NO. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      729 CCAGGAGAACAGAA 743
      |||||
Db       15 CCAGGAGAGGAAA 1

RESULT 70
US-09-504-231A-716/c
; Sequence 716, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15

```

```
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 716
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-716

Query Match          46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAGAA 742
DB 15 GCCAGGAGAGAGAAA 1

RESULT 71
US-09-274-553D-715/c
; Sequence 715, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 715
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-715

Query Match          46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAACAGAA 743
DB 15 CCAGGAGAGAGAAA 1

RESULT 72
US-09-274-553D-716/c
; Sequence 716, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
```

```
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 716
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-716

Query Match          46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAGAA 742
DB 15 GCCAGGAGAGAGAAA 1

RESULT 73
US-09-835-694-19
; Sequence 19, Application US/09835694
; Publication No. US20040087521A1
; GENERAL INFORMATION:
; APPLICANT: DONNELLY, JOHN J.
; APPLICANT: DWARKI, VARAVANI J.
; APPLICANT: LIU, MARGARET A.
; APPLICANT: MONTGOMERY, DONNA L.
; APPLICANT: PARKER, SUEZANNE E.
; APPLICANT: SHIVER, JOHN W.
; APPLICANT: ULMER, JEFFREY B.
; TITLE OF INVENTION: NUCLEIC ACID PHARMACEUTICALS - INFLUENZA MATRIX
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/835,694
; FILING DATE: 16-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,268
; FILING DATE: 05-June-1995
; APPLICATION NUMBER: PCT/US94/02751
; FILING DATE: 14-March-1994
; APPLICATION NUMBER: 08/089,985
; FILING DATE: 08-July-1993
; APPLICATION NUMBER: 08/032,383
; FILING DATE: 18-March-1993
```

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18972PCA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-835-694-19

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGCA 745
Db 1 AGCAGAGCAGACGA 15

RESULT 74
US-10-339-674-420
; Sequence 420, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 420
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (435971)...(435985)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 553
US-10-339-674-420

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 727 TCCAGGAGAAACAG 741
Db 1 TGCCAGGGCAAAAAG 15

RESULT 75
US-10-339-674-421
; Sequence 421, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 421
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (435971)...(435985)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 552
US-10-339-674-421

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAAACAG 741
Db 1 TGCCAGGGCAAAAAG 15

RESULT 76
US-09-504-231A-717/c
; Sequence 717, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 717
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-717

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAA 737
Db 13 GCCAGGAGAA 4

RESULT 77
US-09-274-553D-717/c
; Sequence 717, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
US-09-274-553D-717/c
```

; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 717
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-717

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAA 737
||| ||||| |||
Db 13 GCCAGGAGAA 4

RESULT 78
US-09-504-231A-1341/c
; Sequence 1341, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1341
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1341

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAGAAC 744
||| ||||| |||
Db 13 GGTGAACAGTAC 1

RESULT 79
US-09-274-553D-1341/c
; Sequence 1341, Application US/09274553D
; Patent No. US2002008225A1

; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1341
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1341

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAGAAC 744
||| ||||| |||
Db 13 GGTGAACAGTAC 1

RESULT 80
US-10-146-058-126
; Sequence 126, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta ()
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993


```

; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/PS8418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202)393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-10-146-058-126

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAGCA 740
Db 2 GCAAGGAGAGCA 14

RESULT 81
US-10-104-025-9
; Sequence 9, Application US/10104025
; Publication No. US20030165876A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMA SA
; APPLICANT: CAMERON, Francis
; APPLICANT: BEATRICE
; TITLE OF INVENTION: PROCESSES FOR PURIFYING AND FOR DETECTING TARGET DOUBLE-STRANDED
; TITLE OF INVENTION: SEQUENCES BY TRIPLE HELIX INTERACTION
; FILE REFERENCE: 03806.0546
; CURRENT APPLICATION NUMBER: US/10/104,025
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 60/285,272
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: FR 0103953
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-104-025-9
```

```

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAACAGAA 743
Db 2 AGGAGAACAGAA 14

RESULT 82
US-10-324-409B-21
; Sequence 21, Application US/10324409B
; Publication No. US2004008680A1
; GENERAL INFORMATION:
; APPLICANT: Sampson, et al.
; TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced
; TITLE OF INVENTION: Secondary Structure
; FILE REFERENCE: 2003309-0028
; CURRENT APPLICATION NUMBER: US/10/324,409B
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 33
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Predicted
; US-10-324-409B-21

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAGACAGAAC 746
Db 2 AGAGACTGAAC 14

RESULT 83
US-09-504-231A-654/C
; Sequence 654, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 654
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
; US-09-504-231A-654
```

```

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAACAGAAC 744
Db 13 GGTGAACAGTAC 1

RESULT 84
US-09-274-553D-654/C
; Sequence 654, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
```

FILE REFERENCE: ipi 247/282
CURRENT APPLICATION NUMBER: US/09/274,553D
CURRENT FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: PatentIn version 3.0
SEQ ID NO 654
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-654

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 732 GGAGAACGAC 744
DB 13 GGTGAACAGTAC 1

RESULT 85
US-10-347-510A-95/c
Sequence 95, Application US/10347510A
Publication No. US20040063110A1
GENERAL INFORMATION:
APPLICANT: Henrik Stender
Kaare Lund
Tina Anderson Hollerup
TITLE OF INVENTION: No. US20040063110A1el Process For The Detection of Mycobact
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER
STREET: 1300 I ST. NW
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ASCXI
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/347,510A
FILING DATE: 21-Jan-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,392
FILING DATE: 15-Oct-96
APPLICATION NUMBER: 60/029,595
FILING DATE: 23-Oct-96
APPLICATION NUMBER: 60/045,962
FILING DATE: 08-May-97
APPLICATION NUMBER: 08/943,777
FILING DATE: 3-Oct-97
ATTORNEY/AGENT INFORMATION:
NAME: Anthony C. Tridico
REGISTRATION NUMBER: 45,958
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4173
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 basepairs
TYPE: nucleic acid basepairs
STRANDEDNESS: single

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-10-347-510A-95
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 730 CAGGAGAACAGCA 742
DB 14 CAGGACGACAGCA 2
RESULT 86
US-09-544-934B-95/c
Sequence 95, Application US/09544934B
Publication No. US20020137035A1
GENERAL INFORMATION:
APPLICANT: Henrik Stender
Kaare Lund
Tina Anderson Hollerup
TITLE OF INVENTION: Novel Process For The Detection of Mycobacteria
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER
STREET: 1300 I ST. NW
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ASCXI
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/544,934B
FILING DATE: 07-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,392
FILING DATE: 15-Oct-96
APPLICATION NUMBER: 60/029,595
FILING DATE: 23-Oct-96
APPLICATION NUMBER: 60/045,962
FILING DATE: 08-May-97
APPLICATION NUMBER: 08/943,777
FILING DATE: 3-Oct-97
ATTORNEY/AGENT INFORMATION:
NAME: Anthony C. Tridico
REGISTRATION NUMBER: 45,958
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4173
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 basepairs
TYPE: nucleic acid basepairs
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-544-934B-95
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 730 CAGGAGAACAGCA 742
DB 14 CAGGACGACAGCA 2
RESULT 87
US-10-339-674-1871/c

```
; Sequence 1871, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1871
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (2551260)...(2551274)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 2480
US-10-339-674-1871

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      729 CCAGGAGAAACAG 741
Db      13 CCAGGTTAAACAG 1

RESULT 88
US-10-450-797-1219/c
; Sequence 1219, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1219
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1219

Query Match      42.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 69;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      734 AGAAACAGAAC 744
Db      11 AGAAACAGATC 1

RESULT 89
US-10-100-957A-73
; Sequence 73, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-LIA
; CURRENT APPLICATION NUMBER: US/10/100,957A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180

; Sequence 1871, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1871
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (2551260)...(2551274)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 2480
US-10-339-674-1871

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 73;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      732 GGAGAAACAGA 742
Db      1 GTAGAAACAGA 11

RESULT 90
US-10-073-377-5/c
; Sequence 5, Application US/10073377
; Publication No. US2003009670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and
; TITLE OF INVENTION: Replicative Capacities
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified
; OTHER INFORMATION: Influenza A 3'-sequence
US-10-073-377-5

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 73;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
Db      12 AGTAGAAACAG 2

RESULT 91
US-10-073-377-6/c
; Sequence 6, Application US/10073377
; Publication No. US2003009670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and
; TITLE OF INVENTION: Replicative Capacities
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified
; OTHER INFORMATION: Influenza A 3'-sequence
US-10-073-377-6
```


APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-35

Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 87;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 730 CAGGAGAACAGAA 743
DB 1 CATGAGAGCAGGA 14

RESULT 96
US-10-033-145-1787
Sequence 1787, Application US/10033145
Publication No. US2002015151A1
GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18.
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1787
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-145-1787

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAACAGCA 742
DB 2 AGAACAGCA 10

RESULT 97
US-10-033-145-1921/c
Sequence 1921, Application US/10033145
Publication No. US2002015151A1
GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800

PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1921
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-145-1921

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
DB 9 ACAGAACAC 1

RESULT 98
US-10-450-797-167
Sequence 167, Application US/10450797
Publication No. US20040142335A1
GENERAL INFORMATION:
APPLICANT: Petersohn, Dirk
APPLICANT: Conradt, Marcus
APPLICANT: Hofmann, Kay
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
FILE REFERENCE: HENK-0041
CURRENT APPLICATION NUMBER: US/10/450,797
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: PCT/EP01/15178
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: DE 101 00 121.5
PRIOR FILING DATE: 2001-01-03
NUMBER OF SEQ ID NOS: 1435
SOFTWARE: PatentIn version 3.2
SEQ ID NO 167
LENGTH: 11
TYPE: DNA
ORGANISM: Homo sapiens
US-10-450-797-167

Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 CCAGGAGAA 737
DB 3 CCAGGAGAA 11

RESULT 99
US-09-263-959-843/c
Sequence 843, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/263,959
;; FILING DATE: 05-MAR-1999
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mcmasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 920010.426C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 843:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-263-959-843

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 AACAGACACA 745
DB 11 AACAGACACA 3

RESULT 100

US-10-100-957A-61
;; Sequence 61, Application US/10100957A
;; Publication No. US20030096322A1
;; GENERAL INFORMATION:
;; APPLICANT: Giuliano, Kenneth A.
;; APPLICANT: Kapur, Ravi
;; TITLE OF INVENTION: A System for Cell Based Screening
;; FILE REFERENCE: 97-022-LIA
;; CURRENT APPLICATION NUMBER: US/10/100,957A
;; CURRENT FILING DATE: 2002-03-19
;; NUMBER OF SEQ ID NOS: 180
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 61
;; LENGTH: 12
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-3
US-10-100-957A-61

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACACAGA 742
DB 3 AGAAACACAGA 11

RESULT 101

US-10-100-957A-75
;; Sequence 75, Application US/10100957A
;; Publication No. US20030096322A1
;; GENERAL INFORMATION:
;; APPLICANT: Giuliano, Kenneth A.
;; APPLICANT: Kapur, Ravi
;; TITLE OF INVENTION: A System for Cell Based Screening
;; FILE REFERENCE: 97-022-LIA
;; CURRENT APPLICATION NUMBER: US/10/100,957A
;; CURRENT FILING DATE: 2002-03-19
;; NUMBER OF SEQ ID NOS: 180
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 75

;; LENGTH: 12
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-8
;; OTHER INFORMATION: substrate recognition sequence
US-10-100-957A-75

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACACAGA 742
DB 3 AGAAACACAGA 11

RESULT 102

US-09-981-803-47/c
;; Sequence 47, Application US/09981803
;; Publication No. US20030032092A1
;; GENERAL INFORMATION:
;; APPLICANT: Joel CROUZET-
;; APPLICANT: Daniel SCHERMAN
;; APPLICANT: Beatrice CAMERON
;; APPLICANT: Pierre WILS
;; APPLICANT: Anne-Marie DARQUET
;; TITLE OF INVENTION: DNA MOLECULES, PREPARATION AND USE IN GENE THERAPY
;; FILE REFERENCE: MINICIRCLE
;; CURRENT APPLICATION NUMBER: US/09/981,803
;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 47
;; LENGTH: 12
;; TYPE: DNA
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Description of the artificial sequence:
;; OTHER INFORMATION: oligonucleotide
US-09-981-803-47

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
DB 12 AGGAAAAAAGA 1

RESULT 103

US-10-273-071-28/c
;; Sequence 28, Application US/10275071
;; Publication No. US20030186268A1
;; GENERAL INFORMATION:
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Scherman, Daniel
;; APPLICANT: Wils, Pierre
;; APPLICANT: Cameron, Beatrice
;; APPLICANT: Blanche, Francis
;; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
;; FILE REFERENCE: 08888.0138-02
;; CURRENT APPLICATION NUMBER: US/10/275,071
;; CURRENT FILING DATE: 2003-04-07
;; PRIOR APPLICATION NUMBER: 09/580,923
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 08/860,038
;; PRIOR FILING DATE: 1997-06-09
;; PRIOR APPLICATION NUMBER: PCT/FR95/01468
;; PRIOR FILING DATE: 1995-11-08
;; NUMBER OF SEQ ID NOS: 36

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-10-275-071-28

Query Match          40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 12 AGGAAAAAAGA 1

RESULT 104
US-10-091-281-393
; Sequence 393, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091.281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 393
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative SORY/SRY.01 motif
US-10-091-281-393

Query Match          40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAACAGAAACA 745
Db 1 AAAAAACAAACA 12

RESULT 105
US-10-684-830-34/c
; Sequence 34, Application US/10684830
; Publication No. US20040142452A1
; GENERAL INFORMATION:
; APPLICANT: Gencell S.A.; Aventis Pharmaceuticals, Inc.
; APPLICANT: Soubrier, Fabienne
; TITLE OF INVENTION: Circular DNA Molecule with Conditional Origin of Replication, Met
; TITLE OF INVENTION: Preparing Same, and Use Thereof in Gene Therapy
; FILE REFERENCE: 8888.0132-02
; CURRENT APPLICATION NUMBER: US/10/684.830
; CURRENT FILING DATE: 2003-10-15
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 09/043,193
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: PCT/FR96/01414
; PRIOR FILING DATE: 1996-09-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 12
; TYPE: DNA
```

```
; ORGANISM: Escherichia coli
US-10-684-830-34

Query Match          40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 12 AGGAAAAAAGA 1

RESULT 106
US-10-684-830-37/c
; Sequence 37, Application US/10684830
; Publication No. US20040142452A1
; GENERAL INFORMATION:
; APPLICANT: Gencell S.A.; Aventis Pharmaceuticals, Inc.
; APPLICANT: Soubrier, Fabienne
; TITLE OF INVENTION: Circular DNA Molecule with Conditional Origin of Replication, Met
; TITLE OF INVENTION: Preparing Same, and Use Thereof in Gene Therapy
; FILE REFERENCE: 8888.0132-02
; CURRENT APPLICATION NUMBER: US/10/684.830
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 10/268,948
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 09/043,193
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: PCT/FR96/01414
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-684-830-37

Query Match          40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 12 AGGAAAAAAGA 1

RESULT 107
US-09-152-059-3/c
; Sequence 3, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
```

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-3
```

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Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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QY 736 AAACAGACACC 747
Db 12 AAACAAACACC 1
```

```
RESULT 108
US-09-152-059-4/c
; Sequence 4, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
```

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; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-4
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 736 AAACAGACACC 747
Db 12 AAACAAACACC 1
```

```
RESULT 109
US-09-152-059-5/c
; Sequence 5, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
```

```
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-5
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 736 AAACAGACACC 747
Db 12 AAACAAACACC 1
```

```
RESULT 110
US-09-152-059-6/c
; Sequence 6, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
```

```
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-6

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
| | | | | | | | | |
Db 12 AAACAAACCACC 1

RESULT 111

US-09-152-059-7/c
; Sequence 7, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152.059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
| | | | | | | | | |
Db 12 AAACAAACCACC 1

RESULT 112
US-09-152-059-8/c
; Sequence 8, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152.059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
| | | | | | | | | |
Db 12 AAACAAACCACC 1

RESULT 112

US-09-152-059-8/c
; Sequence 8, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152.059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
US-09-152-059-8

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
| | | | | | | | | |
Db 12 AAACAAACCACC 1

RESULT 113

US-09-152-059-9/c
; Sequence 9, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152.059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
US-09-152-059-9

; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-7

```

US-09-152-059-9
Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
   ||||| |||||
Db 12 AAACAGAACACC 1

RESULT 114
US-09-152-059-28/c
; Sequence 28, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-29
Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
   ||||| |||||
Db 12 AAACAGAACACC 1

RESULT 116
US-09-152-059-30/c
; Sequence 30, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,309
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-30
Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
   ||||| |||||
Db 12 AAACAGAACACC 1

RESULT 115
US-09-152-059-29/c
; Sequence 29, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591

```

```
Db      12 AACACAAACCACC 1

RESULT 117
US-09-152-059-31/c
; Sequence 31, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION: Description of Artificial Sequence: Probe
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-31

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AACACAGAACACC 747
      ||||| |||||
Db      12 AACACAAACCACC 1

RESULT 118
US-09-152-059-43/c
; Sequence 43, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
US-09-152-059-43

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AACACAGAACACC 747
      ||||| |||||
Db      12 AACACAAACCACC 1

RESULT 120
US-09-152-059-44/c
; Sequence 44, Application US/09152059
; Patent No. US20020068708A1
```

```
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-152-059-44

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
      ||||| |||||
Db      12 AAACAAACCACC 1

RESULT 121
US-09-152-059-46/c
; Sequence 46, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
```

```
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-09-152-059-46

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
      ||||| |||||
Db      12 AAACAAACCACC 1

RESULT 122
US-09-152-059-47/c
; Sequence 47, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-152-059-47

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
      ||||| |||||
Db      12 AAACAAACCACC 1

RESULT 123
US-09-152-059-48/c
; Sequence 48, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
```

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; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-152-059-48
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Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 736 AACAGAACACC 747
Db 12 AACAAACCACC 1
```

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RESULT 124
US-09-152-059-71/c
; Sequence 71, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-71
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 736 AACAGAACACC 747
```

```
Db 12 AACAAACCACC 1
RESULT 125
US-09-152-059-74/c
; Sequence 74, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
US-09-152-059-74
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 736 AACAGAACACC 747
Db 12 AACAAACCACC 1
```

```
RESULT 126
US-09-152-059-77/c
; Sequence 77, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
```

; PRIOR APPLICATION NUMBER: 60/088,309
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/094,355
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 146
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 77
 ; LENGTH: 13
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: (1)..(12)
 ; OTHER INFORMATION: LNA monomer
 ; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
 ; OTHER INFORMATION: oligonucleotide
 US-09-152-059-77

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
 Db 12 AACAAACCACC 1

RESULT 127

US-09-781-811-23/c
 ; Sequence 23, Application US/09781811
 ; Patent No. US20020151463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WOYCHIK, RICHARD P.
 ; APPLICANT: BULTMAN, SCOTT J.
 ; APPLICANT: MICHAUD, EDWARD J.
 ; TITLE OF INVENTION: AGOUTI POLYNUCLEOTIDE COMPOSITIONS AND METHODS OF USE
 ; FILE REFERENCE: 4310.001682
 ; CURRENT APPLICATION NUMBER: US/09/781,811
 ; CURRENT FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 09/034,088
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: 08/064,385
 ; PRIOR FILING DATE: 1993-05-21
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 13
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
 ; OTHER INFORMATION: OLIGONUCLEOTIDE
 US-09-781-811-23

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAGACCA 745
 Db 13 AGAACAGACCA 2

RESULT 128

US-10-027-632-177279/c
 ; Sequence 177279, Application US/10027632
 ; Publication No. US2002019837A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 177279
 ; LENGTH: 13
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-177279

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCACAGAGAAA 738
 Db 12 TTCTGGAGAAA 1

RESULT 129

US-10-027-632-177279/c
 ; Sequence 177279, Application US/10027632
 ; Publication No. US20030204075A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 177279
 ; LENGTH: 13
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-177279

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCACAGAGAAA 738
 Db 12 TTCTGGAGAAA 1

RESULT 130
US-10-008-029-3/c
; Sequence 3, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/088,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-3

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
|||||
Db 12 AAACAAACCACC 1

RESULT 131
US-10-008-029-4/c
; Sequence 4, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/088,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-4

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
|||||
Db 12 AAACAAACCACC 1

RESULT 132
US-10-008-029-5/c
; Sequence 5, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-5

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
|||||
Db 12 AAACAAACCACC 1


```

Db      12 AACAAACACC 1

RESULT 136
US-10-008-029-9/c
; Sequence 9, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-9

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      736 AACAGAACACC 747
Db      12 AACAAACACC 1

RESULT 137
US-10-008-029-28/c
; Sequence 28, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-28

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      736 AACAGAACACC 747
Db      12 AACAAACACC 1

RESULT 138
US-10-008-029-29/c
; Sequence 29, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-29

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      736 AACAGAACACC 747
Db      12 AACAAACACC 1

RESULT 139
US-10-008-029-29/c
; Sequence 29, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-29

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      736 AACAGAACACC 747
Db      12 AACAAACACC 1

```

RESULT 139
US-10-008-029-30/c
; Sequence 30, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-30

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACAGAACACC 747
Db 12 AACACACACC 1

RESULT 140
US-10-008-029-31/c
; Sequence 31, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-008-029-31

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACAGAACACC 747
Db 12 AACACACACC 1

RESULT 141
US-10-008-029-32/c
; Sequence 32, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-32

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACAGAACACC 747
Db 12 AACACACACC 1

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACAGAACACC 747
Db 12 AACACACACC 1

RESULT 140
US-10-008-029-31/c
; Sequence 31, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACAGAACACC 747
Db 12 AACACACACC 1

```
RESULT 142
US-10-008-029-43/c
; Sequence 43, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, JOEL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 43
; LENGTH: 13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-43
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

RESULT 143
US-10-008-029-44/c
; Sequence 44, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, JOEL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 44
; LENGTH: 13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-44
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

RESULT 144
US-10-008-029-45/c
; Sequence 45, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, JOEL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 45
; LENGTH: 13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-45
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

RESULT 145
US-10-008-029-46
; Sequence 46, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, JOEL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 46
; LENGTH: 13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-46
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
Db 12 AACAAACCACC 1
```

```
US-10-008-029-47/c
; Sequence 47, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: LNA monomer
US-10-008-029-47
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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QY 736 AAACAGAACACC 747
    |||||
Db 12 AAACAACACC 1
```

```
RESULT 146
US-10-008-029-48/c
; Sequence 48, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
```

```
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-008-029-48
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 736 AAACAGAACACC 747
    |||||
Db 12 AAACAACACC 1
```

```
RESULT 147
US-10-008-029-71/c
; Sequence 71, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-71
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 736 AAACAGAACACC 747
    |||||
Db 12 AAACAACACC 1
```

```
RESULT 148
US-10-008-029-74/c
; Sequence 74, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
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```
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-74

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      736 AAACAGAACACC 747
Db      12 AAACAAACACC 1

RESULT 149
US-10-008-029-77/c
; Sequence 77, Application US/10008029
; Publication No. US2003013480A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-74

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      736 AAACAGAACACC 747
Db      12 AAACAAACACC 1

RESULT 149
US-10-008-029-77/c
; Sequence 77, Application US/10008029
; Publication No. US2003013480A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
```

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-77

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      736 AAACAGAACACC 747
Db      12 AAACAAACACC 1

RESULT 150
US-10-208-650-3/c
; Sequence 3, Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-3

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      736 AAACAGAACACC 747
Db      12 AAACAAACACC 1

RESULT 151
US-10-208-650-4/c
```

; Sequence 4, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-4

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
| | | | | | | | | |
DB 12 AAACAACACC 1

RESULT 152
US-10-208-650-5/c
; Sequence 5, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-5

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
| | | | | | | | | |
DB 12 AAACAACACC 1

RESULT 153
US-10-208-650-6/c
; Sequence 6, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-6

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;

```

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AAACAACACC 1

RESULT 154
US-10-208-650-7/c
; Sequence 7, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
US-10-208-650-7
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AAACAACACC 1

RESULT 155
US-10-208-650-8/c
; Sequence 8, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05

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; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-8
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AAACAACACC 1

RESULT 156
US-10-208-650-9/c
; Sequence 9, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13

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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-30

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

RESULT 160
US-10-208-650-31/c
; Sequence 31, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-32

```

```

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

```

```

RESULT 161
US-10-208-650-32/c
; Sequence 32, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-32

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

RESULT 162
US-10-208-650-43/c
; Sequence 43, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-32

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; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 43
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-43

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACACC 1

RESULT 163
US-10-208-650-44/c
; Sequence 44, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 44
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-208-650-44

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACACC 1

RESULT 164
US-10-208-650-46/c
; Sequence 46, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 46
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-208-650-46

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACACC 1

RESULT 165
US-10-208-650-47/c
; Sequence 47, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
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; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
;
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: LNA monomer
US-10-208-650-47

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
Db      12 AAACAAACCACC 1

RESULT 166
US-10-208-650-48/c
; Sequence 48, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;
; OTHER INFORMATION: oligonucleotide
US-10-208-650-71

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
Db      12 AAACAAACCACC 1

RESULT 168
US-10-208-650-74/c
; Sequence 74, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-208-650-48

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
Db      12 AAACAAACCACC 1

RESULT 167
US-10-208-650-71/c
; Sequence 71, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;
; OTHER INFORMATION: oligonucleotide
US-10-208-650-71

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
Db      12 AAACAAACCACC 1

RESULT 168
US-10-208-650-74/c
; Sequence 74, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
```

```
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-74

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
      ||||| |||||
Db      12 AAACAAACCACC 1

RESULT 169
US-10-208-650-77/c
; Sequence 77, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGLSEN, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-77

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
      ||||| |||||
Db      12 AAACAAACCACC 1

RESULT 170
US-10-091-281-199
; Sequence 199, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative IRFF/IRF2.01 motif
US-10-091-281-199

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      735 GAACAGAACAC 746
      ||||| |||||
Db      2 GAACGGAACAC 13

RESULT 171
US-10-194-882-5/c
; Sequence 5, Application US/10194882
; Publication No. US20040014042A1
; GENERAL INFORMATION:
; APPLICANT: JU, JINGYUE
; TITLE OF INVENTION: Multiplex Genotyping Using Solid Phase Capturable Dideoxynucleotides
; FILE REFERENCE: 0575/66833/JPW/ADM
; CURRENT APPLICATION NUMBER: US/10/194,882
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: internal mass standard
```

```
US-10-194-882-5
Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 745
DB 13 AGAAAAAGAAA 2
|||||
GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and
; TITLE OF INVENTION: Replicative Capacities
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Influenza B virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)-(13)
; OTHER INFORMATION: n = any nucleotide
US-10-073-377-8

Query Match      39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 1e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
DB 1 AGAGWAACAR 11
|||||
GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.036902
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-021-102

Query Match      38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGA 736
DB 1 TGCGAGGAGA 10
|||||
GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
US-10-033-145-1215

Query Match      38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGA 736
DB 1 TGCGAGGAGA 10
|||||
GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
US-10-033-145-1215
```

```
QY 735 GAAACAGAAC 744
DB 1 GAAACTGAAC 10
|||||
GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 331
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-331

Query Match      38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAA 740
DB 10 AGGATAAACAA 1
|||||
GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1175
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1175

Query Match      38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGA 736
DB 1 TGCGAGGAGA 10
|||||
GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
US-10-033-145-1215

Query Match      38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGA 736
DB 1 TGCGAGGAGA 10
|||||
GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
US-10-033-145-1215
```

; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1215
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-033-145-1215

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 729 CCAGGAGAAA 738
 |||||
 Db 1 CCAGGAGGAA 10

RESULT 177
 US-10-390-045-47/c
 ; Sequence 47, Application US/10390045
 ; Publication No. US20030170713A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SRIVASTAVA, SHIV
 ; APPLICANT: MOUL, JUDD W.
 ; APPLICANT: XU, LINDA L.
 ; APPLICANT: SEGAWA, TAKEHIKO
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
 ; FILE REFERENCE: POYNUCLEOTIDE ARRAY
 ; CURRENT APPLICATION NUMBER: US/10/390,045
 ; CURRENT FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: US/09/769,482
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,772
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/179,045
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: oligonucleotide
 ; US-10-390-045-47

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 731 AGGATAAACCA 740
 |||||
 Db 10 AGGATAAACCA 1

RESULT 178
 US-10-330-627-834
 ; Sequence 834, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert

; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 834
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-330-627-834

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 729 CCAGGAGAAA 738
 |||||
 Db 1 CCAGGAGGAA 10

RESULT 179
 US-10-330-627-1293/c
 ; Sequence 1293, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1293
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-330-627-1293

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 731 AGGATAAACCA 740
 |||||
 Db 10 AGGATAAACCA 1

RESULT 180
 US-10-330-627-1363/c
 ; Sequence 1363, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1363
 ; LENGTH: 10
 ; TYPE: DNA

```
; ORGANISM: Homo sapiens
US-10-330-627-1363

Query Match          38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAGA 742
Db 10 GATAAACAGA 1

RESULT 181
US-10-434-479-47/c
; Sequence 47, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PHEPAL GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-434-479-47

Query Match          38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAAACAGA 740
Db 10 AGGATAACAGA 1

RESULT 182
US-10-450-797-47/c
; Sequence 47, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 47
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-47/c

Query Match          38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 735 AAACAGACAGA 745
Db 10 AATCAGACAGA 1

RESULT 184
US-10-450-797-537
; Sequence 537, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 537
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-537

Query Match          38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACAGACAGA 745
Db 10 AATCAGACAGA 1

RESULT 183
US-10-450-797-532/c
; Sequence 532, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 532
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-532

Query Match          38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAGA 742
Db 10 GATAAACAGA 1
```

OY 739 CAGAACACCG 748
Db 1 CGGAACACCG 10

RESULT 185

US-10-450-797-613/c
; Sequence 613, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 613
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-613

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 734 AGAACACGAA 743
Db 10 AGAACACGAA 1

RESULT 186

US-10-450-797-741
; Sequence 741, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 741
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-741

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 729 CCAGGAGAAA 738
Db 1 CCAGGAGAAA 10

RESULT 187

US-09-179-536B-81

; Sequence 81, Application US/09179536B
; Patent No. US20020042112A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K ster
; APPLICANT: David M. Lough
; APPLICANT: Guobing Xiang

TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
NUMBER OF SEQUENCES: 320
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/179,536B
FILING DATE: 26-Oct-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/20444
FILING DATE: 06-NOV-1997
APPLICATION NUMBER: 08/947,801
FILING DATE: 08-Oct-97
APPLICATION NUMBER: 08/933,792
FILING DATE: 19-Sep-97
APPLICATION NUMBER: 08/787,639
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/786,988
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/746,055
FILING DATE: 06-NO. US20020042112A1-96
APPLICATION NUMBER: 08/746,036
FILING DATE: 06-NO. US20020042112A1-96
APPLICATION NUMBER: 08/744,590
FILING DATE: 06-NO. US20020042112A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-NO. US20020042112A1-96

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2004B
TELEPHONE: 858-450-8400
TELEFAX: 858-587-5360
TELECOMMUNICATION INFORMATION:
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 81

SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 81:
US-09-179-536B-81

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 728 GCCAGGAGAA 737
Db 2 GCCAGGAGAA 11

RESULT 188
US-09-179-536B-86
; Sequence 86, Application US/09179536B
; Patent No. US20020042112A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K ster
; David M. Lough
; Guobing Xiang
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/179,536B
; FILING DATE: 26-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/20444
; FILING DATE: 06-NOV-1997
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20020042112A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-179-536B-86

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-09-179-536B-86

Db 2 GCCAGGACAA 11
|||||
RESULT 189
US-09-263-959-477/c
; Sequence 477, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 477:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-477

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGACAA 745
|||||
Db 12 AACAGACAA 3

RESULT 190
US-09-263-959-492/c
; Sequence 492, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-09-263-959-492

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-09-179-536B-86

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Patentin Release #1.0, Version #1.25
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 492:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-492

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. le+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAACAC 745
DB 11 AACACACAC 2

RESULT 191
US-09-263-959-755/c
Sequence 755, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 755:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-755

Query Match 38.2%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. le+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACAGAACAC 745
DB 11 AACACACAC 2

RESULT 192
US-09-263-959-850/c
Sequence 850, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 850:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-850

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. le+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACAC 746
DB 12 AACACACAC 3

RESULT 193
US-09-845-938A-4/c
Sequence 4, Application US/09845938A
Publication No. US20030118550A1
GENERAL INFORMATION:
APPLICANT: Kabanov, Alexander V
APPLICANT: Lelievre, Pierre
APPLICANT: Yulievich, Valery
TITLE OF INVENTION: Compositions and Methods for Inducing Activation of Dendritic Cell
FILE REFERENCE: 3874-129 US
CURRENT APPLICATION NUMBER: US/09/845,938A
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1

```

; SEQ ID NO 4
; LENGTH: 12
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-09-845-938A-4

Query Match      38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      730 CAGAGGAAC 739
Db      11 CAGAGGAAC 2

RESULT 194
US-09-845-938A-7/c
; Sequence 7, Application US/09845938A
; Publication No. US20030118550A1
; GENERAL INFORMATION:
; APPLICANT: Kabanov, Alexander V
; APPLICANT: Lenieux, Pierre
; APPLICANT: Yulievich, Valery
; APPLICANT: Vinogradov, Sergey V.
; TITLE OF INVENTION: Compositions and Methods for Inducing Activation of Dendritic Cell
; FILE REFERENCE: 3874-129 US
; CURRENT APPLICATION NUMBER: US/09/845,938A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Herpes Simplex Virus type 1
US-09-845-938A-7

Query Match      38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      730 CAGAGGAAC 739
Db      11 CAGAGGAAC 2

RESULT 195
US-09-297-576A-81
; Sequence 81, Application US/09297576A
; Publication No. US20030129589A1
; GENERAL INFORMATION:
; APPLICANT: KOSTER, Hubert
; APPLICANT: LITTLE, Daniel P.
; APPLICANT: BRAUN, Andreas
; APPLICANT: LOUGH, David M.
; APPLICANT: XIANG, Guobing
; APPLICANT: VAN DEN BOOM, Dirk
; APPLICANT: JURINKE, Christian
; APPLICANT: RUPPERT, Andreas
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:

```

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; APPLICATION NUMBER: US/09/297,576A
; FILING DATE: 07-Jun-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20030129589A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-450-8499
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
US-09-297-576A-81

Query Match      38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      728 GCCAGGAGAA 737
Db      2 GCCAGGAGAA 11

RESULT 196
US-09-297-576A-86
; Sequence 86, Application US/09297576A
; Publication No. US20030129589A1
; GENERAL INFORMATION:
; APPLICANT: KOSTER, Hubert
; APPLICANT: LITTLE, Daniel P.
; APPLICANT: BRAUN, Andreas
; APPLICANT: LOUGH, David M.
; APPLICANT: XIANG, Guobing
; APPLICANT: VAN DEN BOOM, Dirk
; APPLICANT: JURINKE, Christian
; APPLICANT: RUPPERT, Andreas
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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/
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/297,576A
/ FILING DATE: 07-Jun-2000
/ CLASSIFICATION:
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/947,801
/ FILING DATE: 08-Oct-97
/ APPLICATION NUMBER: 08/933,792
/ FILING DATE: 19-Sep-97
/ APPLICATION NUMBER: 08/787,639
/ FILING DATE: 23-Jan-97
/ APPLICATION NUMBER: 08/786,988
/ FILING DATE: 23-Jan-97
/ APPLICATION NUMBER: 08/746,055
/ FILING DATE: 06-No. US20030129589A1-96
/ APPLICATION NUMBER: 08/746,036
/ FILING DATE: 06-No. US20030129589A1-96
/ APPLICATION NUMBER: 08/744,590
/ FILING DATE: 06-No. US20030129589A1-96
/ APPLICATION NUMBER: 08/744,481
/ FILING DATE: 06-No. US20030129589A1-96
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seidman, Stephanie L.
/ REGISTRATION NUMBER: 33,779
/ REFERENCE/DOCKET NUMBER: 24736-2004
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 858-450-8400
/ TELEFAX: 858-450-8499
/ INFORMATION FOR SEQ ID NO: 86:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: <Unknown>
/ ORIGINAL SOURCE:
/ US-09-297-576A-86

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 728 GCCAGGAGAA 737
Db 2 GCCAGGAGAA 11

RESULT 197
US-10-164-875C-3/C
; Sequence 3, Application US/10164875C
; Publication No. US20030198678A1
; GENERAL INFORMATION:
; APPLICANT: Alakov, Alexander V.
; APPLICANT: Kabanov, Alexander V.
; TITLE OF INVENTION: Polynucleotide Compositions
; FILE REFERENCE: 3874.118.1.2.1.US
; CURRENT APPLICATION NUMBER: US/10/164,875C
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/320,640
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/124,943
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 08/912,968
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/342,209
; PRIOR FILING DATE: 1994-11-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Herpes Simplex Virus 1
; US-09-297-576A-86

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 730 CAGGAGAAAC 739
Db 11 CAGGAGAAAC 2

RESULT 198
US-10-164-875C-5/c
; Sequence 5, Application US/10164875C
; Publication No. US20030198678A1
; GENERAL INFORMATION:
; APPLICANT: Kabanov, Alexander V.
; APPLICANT: Alakov, Valery Y.
; APPLICANT: Vinogradov, Sergey V.
; TITLE OF INVENTION: Polynucleotide Compositions
; FILE REFERENCE: 3874.118.1.2.1.US
; CURRENT APPLICATION NUMBER: US/10/164,875C
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/320,640
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/124,943
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 08/912,968
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/342,209
; PRIOR FILING DATE: 1994-11-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Herpes Simplex Virus 1
; US-10-164-875C-5

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 730 CAGGAGAAAC 739
Db 11 CAGGAGAAAC 2

RESULT 199
US-10-165-433/c
; Sequence 433, Application US/10661165
; Publication No. US20040137470A1
; GENERAL INFORMATION:
; APPLICANT: Dhallan, Ravinder S.
; TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
; FILE REFERENCE: 543312000420
; CURRENT APPLICATION NUMBER: US/10/661,165
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: PCT/US03/06198
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/378,354
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 10/093,618
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/360,232
; PRIOR FILING DATE: 2002-03-01
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; PRIOR APPLICATION NUMBER: PCT/US03/27308
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 10/376,770
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 628
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 433
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-661-165-433

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACACAAACAC 746
| | | | |
DB 10 AACACAAACAC 1

RESULT 200
US-10-667-891-32
; Sequence 32, Application US/10667891
; Publication No. US20040171024A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, CHARLES W.
; APPLICANT: BRBY, PAUL T.
; APPLICANT: HOLM, INGE
; APPLICANT: GRAILLES, MARINE
; APPLICANT: RHETSKY, ANDREY
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND
; FILE REFERENCE: 03495.0294-00000
; CURRENT APPLICATION NUMBER: US/10/667,891
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/413,469
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-667-891-32

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACACAAACAC 746
| | | | |
DB 2 AACACAAACGC 11

RESULT 201
US-10-091-281-222/c
; Sequence 222, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 222
; LENGTH: 9

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative AREB/AREB6.04 motif
US-10-091-281-222

Query Match 36.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAG 741
| | | | |
DB 8 AGAAACAG 1

RESULT 202
US-10-293-222-96/c
; Sequence 96, Application US/10293222
; Publication No. US2004003932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-96

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAG 735
| | | | |
DB 10 GCCAGGAG 3

RESULT 203
US-10-033-145-537
; Sequence 537, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 537
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-537

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 GAACACCG 748
Db 1 GAACACCG 8

RESULT 204

US-10-329-465-139
; Sequence 139, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
; TITLE OF INVENTION: FUSION
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-139

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAA 738
Db 2 AGGAGAAA 9

RESULT 205

US-10-355-820-2
; Sequence 2, Application US/10355820
; Publication No. US20030166282A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, DAVID
; APPLICANT: FORD, LANCE
; APPLICANT: JARVIS, RICH
; APPLICANT: PALLOTTA, VINCE
; APPLICANT: PASLOSKE, BRITTAN
; TITLE OF INVENTION: HIGH POTENCY siRNAs FOR REDUCING THE EXPRESSION OF
; TITLE OF INVENTION: TARGET GENES
; FILE REFERENCE: AM61-077US
; CURRENT APPLICATION NUMBER: US/10/355,820
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/353,332
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-355-820-2

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAAC 739
Db 1 GGAGAAAC 8

Db 2 GGAGAAAC 9

RESULT 206

US-10-330-627-26
; Sequence 26, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-26

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 740 AGAACACCC 747
Db 1 AGAACACCC 8

RESULT 207

US-10-330-627-77
; Sequence 77, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-77

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGAA 743
Db 3 AAACAGAA 10

RESULT 208

US-10-330-627-79
; Sequence 79, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert

```
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-79

Query Match          36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      736 AAACAGAA 743
Db      3 AAACAGAA 10
      |||||
      |||||

RESULT 209
US-10-330-627-85
; Sequence 85, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-85

Query Match          36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      736 AAACAGAA 743
Db      3 AAACAGAA 10
      |||||
      |||||

RESULT 210
US-10-330-627-1321/c
; Sequence 1321, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1321
; LENGTH: 10
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-330-627-1321

Query Match          36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      736 AAACAGAA 743
Db      3 AAACAGAA 10
      |||||
      |||||

RESULT 211
US-10-302-547-55/c
; Sequence 55, Application US/10302547
; Publication No. US20040142448A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, BRIAN R.
; APPLICANT: COLLINS, PETER L.
; APPLICANT: SKIADPOULOS, MARIO H.
; APPLICANT: NEWMAN, JASON T.
; TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE
; TITLE OF INVENTION: 1 (HPV1) FROM CDNA AND USE OF RECOMBINANT HPV1 IN
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT
; TITLE OF INVENTION: IMMUNE RESPONSES AGAINST PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 2303-37-3
; CURRENT APPLICATION NUMBER: US/10/302,547
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/331,961
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 55
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Bovine parainfluenza virus 3
US-10-302-547-55

Query Match          36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      731 AGGAGAAA 738
Db      10 AGGAGAAA 3
      |||||
      |||||

RESULT 212
US-09-828-211A-8/c
; Sequence 8, Application US/09828211A
; Publication No. US20010034029A1
; GENERAL INFORMATION:
; APPLICANT: FUJIWAKE, Hideshi
; TITLE OF INVENTION: Method of Detecting Mutation in Base Sequence of Nucleic Acid
; FILE REFERENCE: NOG-0009
; CURRENT APPLICATION NUMBER: US/09/828,211A
; CURRENT FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence 17a in Fig. 3 (5' to 3')
US-09-828-211A-8

Query Match          36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      735 GAACAGAA 742
Db      |||||
      |||||
```

```

Db      8 GAAACAGA 1

RESULT 213
US-09-918-715-65/c
; Sequence 65, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOGENOUS CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-65

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      |||||
Db      11 GCCAGGAG 4

RESULT 214
US-10-266-138B-6
; Sequence 6, Application US/10266138B
; Publication No. US20030152964A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE
; FILE REFERENCE: J6664US(ED;BP/JVT)seq13Sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/266,138B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/338,272
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq. # 56 of
; OTHER INFORMATION: Table I
US-10-266-138B-6

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      |||||
Db      1 GCCAGGAG 8

RESULT 215
US-10-055-728-27
; Sequence 27, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
; APPLICANT: van der Kuyt, Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
; FILE REFERENCE: 5244US (REN/P55190US00)
; CURRENT APPLICATION NUMBER: US/10/055,728
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,722
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 0120373.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TAG sequence Hs23579
US-10-055-728-27

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
      |||||
Db      4 CAGGAGAA 11

RESULT 216
US-10-265-509B-6
; Sequence 6, Application US/10265509B
; Publication No. US20030170739A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: GENE EXPRESSION FOR ANALYZING PHOTODAMAGE
; FILE REFERENCE: J6663US(ED;BP/JVT)seq13Sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/265,509B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/337,856
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq. # 56 of
; OTHER INFORMATION: Table I
US-10-265-509B-6

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      |||||
Db      1 GCCAGGAG 8

RESULT 217
US-10-266-138B-6
; Sequence 6, Application US/10266138B
; Publication No. US20030152964A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE
; FILE REFERENCE: J6664US(ED;BP/JVT)seq13Sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/266,138B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/338,272
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq. # 56 of
; OTHER INFORMATION: Table I
US-10-266-138B-6

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      |||||
Db      1 GCCAGGAG 8

```


US-10-310-677-27
; Sequence 27, Application US/10310677
; Publication No. US20030219772A1
; GENERAL INFORMATION:
; APPLICANT: Kuyil V.d., Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: Means and methods for treatment evaluation
; FILE REFERENCE: P55190US10
; CURRENT APPLICATION NUMBER: US/10/310,677
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: EP 01203703.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/325,722
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TAG sequence
; OTHER INFORMATION: Hs23579
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(11)
US-10-310-677-27
Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 730 CAGGAGAA 737
Db 4 CAGGAGAA 11
RESULT 218
US-10-450-797-452/c
; Sequence 452, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 452
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-452
Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 736 AAACAGAA 743
Db 11 AAACAGAA 4
RESULT 219

US-10-450-797-714
; Sequence 714, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 714
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-714
Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 728 GCCAGGAG 735
Db 1 GCCAGGAG 8
RESULT 220
US-10-450-797-1387
; Sequence 1387, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1387
Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 733 GAGAAACA 740
Db 1 GAGAAACA 8
RESULT 221
US-10-723-940-88/c
; Sequence 88, Application US/10723940
; Publication No. US20040195468A1
; GENERAL INFORMATION:
; APPLICANT: Leonard, Sherry
; APPLICANT: Freeman, Robert
; TITLE OF INVENTION: Promoter Variants in the Alpha-7 Nicotinic Acetylcholine Receptor

;/ TITLE OF INVENTION: Gene
;/ FILE REFERENCE: VARD-07989
;/ CURRENT APPLICATION NUMBER: US/10/723,940
;/ CURRENT FILING DATE: 2003-11-26
;/ PRIOR APPLICATION NUMBER: 08/956,518
;/ PRIOR FILING DATE: 1997-10-23
;/ NUMBER OF SEQ ID NOS: 180
;/ SOFTWARE: PatentIn version 3.2
;/ SEQ ID NO 86
;/ LENGTH: 11
;/ TYPE: DNA
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Synthetic
US-10-723-940-88

Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAG 741
DB 8 AGAAACAG 1
|||||

RESULT 222

US-09-765-061B-30/c
;/ Sequence 30, Application US/09765061B
;/ Publication No. US2003002165A1
;/ GENERAL INFORMATION:

;/ APPLICANT: Board of Regents of the University of Texas System
;/ TITLE OF INVENTION: Mutations in a No. US20030022165A1el Photoreceptor-pineal gene 17
;/ FILE REFERENCE: 96606/16UTL
;/ CURRENT APPLICATION NUMBER: US/09/765,061B
;/ CURRENT FILING DATE: 2001-01-17
;/ NUMBER OF SEQ ID NOS: 78
;/ SOFTWARE: PatentIn version 3.1
;/ SEQ ID NO 30
;/ LENGTH: 12
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: mutation
;/ LOCATION: (4)...(4)
;/ OTHER INFORMATION: a to c mutation: IVS2-10A to C Benign

US-09-765-061B-30

Query Match 36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAAC 739
DB 9 GGAGAAAC 2
|||||

RESULT 223

US-09-249-155-73/c
;/ Sequence 73, Application US/09249155
;/ Publication No. US20030037345A1
;/ GENERAL INFORMATION:

;/ APPLICANT: Heber-Katz, Ellen
;/ TITLE OF INVENTION: Compositions and Methods for Wound
;/ FILE REFERENCE: 00486.78503
;/ CURRENT APPLICATION NUMBER: US/09/249,155
;/ CURRENT FILING DATE: 1999-02-12
;/ EARLIER APPLICATION NUMBER: 60/074,737
;/ EARLIER FILING DATE: 1998-02-13
;/ EARLIER APPLICATION NUMBER: 60/097,937
;/ EARLIER FILING DATE: 1998-08-26
;/ EARLIER APPLICATION NUMBER: 60/102,051

;/ EARLIER FILING DATE: 1998-09-28
;/ NUMBER OF SEQ ID NOS: 254
;/ SOFTWARE: FastSeq for Windows Version 3.0
;/ SEQ ID NO 73
;/ LENGTH: 11
;/ TYPE: DNA
;/ ORGANISM: Mus musculus
US-09-249-155-73

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
DB 11 GCAGAAACCGA 1
|||||

RESULT 224

US-09-918-715-49
;/ Sequence 49, Application US/09918715
;/ Publication No. US20030017157A1
;/ GENERAL INFORMATION:

;/ APPLICANT: Brad St. Croix
;/ APPLICANT: Bert Vogelstein
;/ APPLICANT: Kenneth Kinzler
;/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
;/ FILE REFERENCE: 1107.00134
;/ CURRENT APPLICATION NUMBER: US/09/918,715
;/ CURRENT FILING DATE: 2001-08-01
;/ PRIOR APPLICATION NUMBER: 60/222,599
;/ PRIOR FILING DATE: 2000-08-02
;/ PRIOR APPLICATION NUMBER: 60/224,360
;/ PRIOR FILING DATE: 2000-08-11
;/ PRIOR APPLICATION NUMBER: 60/282,850
;/ PRIOR FILING DATE: 2000-04-11
;/ NUMBER OF SEQ ID NOS: 358
;/ SOFTWARE: FastSeq for Windows Version 3.0
;/ SEQ ID NO 49
;/ LENGTH: 11
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
US-09-918-715-49

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
DB 1 TGCCAGGTGCA 11
|||||

RESULT 225

US-10-620-514-6
;/ Sequence 6, Application US/10620514
;/ Publication No. US20040068762A1
;/ GENERAL INFORMATION:

;/ APPLICANT: Attar, Ricardo M.
;/ APPLICANT: Bol, David K.
;/ APPLICANT: Gottardis, Marco
;/ APPLICANT: Mookhtiar, Kasim
;/ APPLICANT: Rowley, Ronald B.
;/ APPLICANT: Ostrowski, Jacek
;/ TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING A REPORTER NUCLEIC ACID
;/ FILE REFERENCE: D0287 NP
;/ CURRENT APPLICATION NUMBER: US/10/620,514
;/ CURRENT FILING DATE: 2003-07-16
;/ PRIOR APPLICATION NUMBER: US 60/396,501
;/ PRIOR FILING DATE: 2002-07-17
;/ NUMBER OF SEQ ID NOS: 14
;/ SOFTWARE: PatentIn version 3.2

```
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: DR-1
US-10-620-514-6

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      735 GGAACGAGACA 745
DB      1 GGAACGAGACA 11
      |||||
RESULT 226
US-10-314-322-73/c
; Sequence 73, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; HEALING
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-73

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 GGAGAAACAGA 742
DB      11 GGAGAAACCGA 1
      |||||
RESULT 227
US-10-450-797-297/c
; Sequence 297, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 297
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF antisense
US-09-365-029-21

; SEQ ID NO 21
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF antisense
US-09-365-029-21

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-297

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      727 TGCCAGAGAGAA 737
DB      11 TGCCAGAGAGTA 1
      |||||
RESULT 228
US-10-450-797-1044/c
; Sequence 1044, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1044
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1044

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 GGAGAAACAGA 742
DB      11 GGAGATACAGA 1
      |||||
RESULT 229
US-09-365-029-21
; Sequence 21, Application US/09365029
; Patent No. US20010021772A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, Eugen
; APPLICANT: PEYMAN, Anuschirwan
; APPLICANT: BITONTI, Alan J.
; APPLICANT: WOESSNER, Richard D.
; TITLE OF INVENTION: SHORT OLIGONUCLEOTIDES FOR THE INHIBITION OF VEGF
; FILE REFERENCE: 26083/208
; CURRENT APPLICATION NUMBER: US/09/365,029
; CURRENT FILING DATE: 1999-08-02
; EARLIER APPLICATION NUMBER: EP 98114853.9
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF antisense
US-09-365-029-21
```

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Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCACGAGAAA 738
DB 1 GACAGACAAA 11

RESULT 230
US-09-804-481-9
; Sequence 9, Application US/09804481
; Patent No. US20020058287A1
; GENERAL INFORMATION:
; APPLICANT: de Graaf, David
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: No. US20020058287A1el Small Nuclear RNA Vectors and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 2825.1023-001
; CURRENT APPLICATION NUMBER: US/09/804,481
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/188,304
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modification fragment
US-09-804-481-9

Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGAAC 744
DB 2 ACAACACAGAAC 12

RESULT 231
US-09-828-034-24
; Sequence 24, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-24

Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGAAC 744
DB 2 AAAACAGUAC 12

```

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RESULT 232
US-10-100-957A-65
; Sequence 65, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1A
; CURRENT APPLICATION NUMBER: US/10/100,957A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase-6
; OTHER INFORMATION: substrate recognition sequence
US-10-100-957A-65

Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GCAGAACAGAC 742
DB 1 GTAGAAATAGA 11

RESULT 233
US-10-073-377-3/c
; Sequence 3, Application US/10073377
; Publication No. US20030099670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Influenza C virus
US-10-073-377-3

Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
DB 12 AGCAGAGCAG 2

RESULT 234
US-10-073-377-4/c
; Sequence 4, Application US/10073377
; Publication No. US20030099670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377

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; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified
; OTHER INFORMATION: Influenza A 3'-sequence
US-10-073-377-4

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAAACACG 2

RESULT 235
US-10-088-359/c
; Sequence 359, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular B
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 359
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence encoding post-translational modification site
US-10-211-088-359

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACAC 746
Db 12 AGACAGACGC 2

RESULT 236
US-10-273-334-41/c
; Sequence 41, Application US/10273334
; Publication No. US20030129631A1
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11

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; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recognition sequence
US-10-273-334-41

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 745
Db 12 GAAAGAGAAA 2

RESULT 237
US-10-427-629-14
; Sequence 14, Application US/10427629
; Publication No. US20040078834A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; TITLE OF INVENTION: Human Chronic Lymphocytic Leukemia Modeled In Mouse By Targeted
; FILE REFERENCE: TJU2851
; CURRENT APPLICATION NUMBER: US/10/427,629
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 60/376,464
; PRIOR FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Mus musculus
; OTHER INFORMATION:
US-10-427-629-14

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAC 740
Db 2 CAGGAGACAGA 12

RESULT 238
US-10-455-101-13
; Sequence 13, Application US/10455101
; Publication No. US20040038405A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Dakai
; APPLICANT: Rabbani, Elazar
; TITLE OF INVENTION: VECTORS AND VIRAL VECTORS, AND PACKAGING CELL LINES FOR
; TITLE OF INVENTION: PROPAGATING SAME
; FILE REFERENCE: Enz-56(D2)SequenceListing051199
; CURRENT APPLICATION NUMBER: US/10/455,101
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/046,841
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/822,963
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: DNA
; ORGANISM: human glucocorticoid

```

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:nucleic acid,
; OTHER INFORMATION: double stranded, linear topology
US-10-455-101-13

Query Match 33.6%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred.No. 8.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
||| |||||
Db 1 CAGAACATC 9

RESULT 239

US-10-283-741-14/c
; Sequence 14, Application US/10283741
; Publication No. US20030182068A1

GENERAL INFORMATION:

APPLICANT: Battersby, Bronwyn J.
APPLICANT: Miller, Christopher R.

APPLICANT: Trau, Matthias
APPLICANT: Way, Jeffery C.

APPLICANT: Johnston, Angus

TITLE OF INVENTION: Device and Methods For Directed
FILE REFERENCE: 50277/003002

CURRENT APPLICATION NUMBER: US/10/283,741
CURRENT FILING DATE: 2002-10-30

PRIOR APPLICATION NUMBER: US 60/330,759
PRIOR FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14

LENGTH: 9

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-283-741-14

Query Match 33.6%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred.No. 8.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
||| |||||
Db 9 GAGTAACAG 1

RESULT 240

US-09-910-469-55/c

Sequence 55, Application US/09910469
Publication No. US20030175702A1

GENERAL INFORMATION:

APPLICANT: Schweitzer, Markus
APPLICANT: Anderson, Richard R.

APPLICANT: Mueller, Jochen

APPLICANT: Fiechter, Michael

APPLICANT: Bruecher, Christoph

APPLICANT: Kienle, Stefan

APPLICANT: Orwick, Jill

APPLICANT: Pignot, Marc

APPLICANT: Raddatz, Stefan

APPLICANT: Schneider, Eberhard

APPLICANT: Windhab, No. US20030175702Albert

TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthetic

TITLE OF INVENTION: Binding Systems

FILE REFERENCE: 264/217 Nanogen Recognomics

CURRENT APPLICATION NUMBER: US/09/910,469

CURRENT FILING DATE: 2001-07-19

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PatentIn version 3.1

SEQ ID NO 55
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic binding system
NAME/KEY: modified base
LOCATION: (1)..(10)
OTHER INFORMATION: pyranosyl RNA
US-09-910-469-55

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
||| |||||
Db 9 GATACAGAA 1

RESULT 241

US-09-910-469-56

Sequence 56, Application US/09910469
Publication No. US20030175702A1

GENERAL INFORMATION:

APPLICANT: Schweitzer, Markus

APPLICANT: Anderson, Richard R.

APPLICANT: Mueller, Jochen

APPLICANT: Fiechter, Michael

APPLICANT: Bruecher, Christoph

APPLICANT: Kienle, Stefan

APPLICANT: Orwick, Jill

APPLICANT: Pignot, Marc

APPLICANT: Raddatz, Stefan

APPLICANT: Schneider, Eberhard

APPLICANT: Windhab, No. US20030175702Albert

TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthetic

TITLE OF INVENTION: Binding Systems

FILE REFERENCE: 264/217 Nanogen Recognomics

CURRENT APPLICATION NUMBER: US/09/910,469

CURRENT FILING DATE: 2001-07-19

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PatentIn version 3.1

SEQ ID NO 56

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic binding system

NAME/KEY: modified base

LOCATION: (1)..(10)

OTHER INFORMATION: pyranosyl RNA

US-09-910-469-56

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
||| |||||
Db 2 GATACAGAA 10

RESULT 242

US-10-293-222-212

Sequence 212, Application US/10293222

Publication No. US2004003932A1

GENERAL INFORMATION:

APPLICANT: Versteeg, Rogier

APPLICANT: Caron, Hubertus N.

TITLE OF INVENTION: MYC targets

FILE REFERENCE: 2183-5580US

CURRENT APPLICATION NUMBER: US/10/293,222

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-196

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      740 AGAACACCG 748
Db      1 AGGACACCG 9
      ||| |||||
      ||| |||||

RESULT 245
US-10-033-145-236/c
; Sequence 236, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 236
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-236

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      736 AACACAGAAC 744
Db      10 ACACAGAAC 2
      ||| |||||
      ||| |||||

RESULT 246
US-10-033-145-339/c
; Sequence 339, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 339
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-339

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      729 CCAGGAGAA 737
Db      10 CCAGCAGAA 2
      ||| |||||
      ||| |||||

; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 212
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-212

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGGAAC 739
Db      2 AGGGAAC 10
      ||| |||||
      ||| |||||

RESULT 243
US-10-033-145-75
; Sequence 75, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-75

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      733 GAGAAACAG 741
Db      1 GGAACAG 9
      ||| |||||
      ||| |||||

RESULT 244
US-10-033-145-196
; Sequence 196, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 10

```

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RESULT 247
US-10-033-145-373/c
; Sequence 373, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 373
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-373

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      735 GAGACAGAA 743
DB      10 GAGACAGAA 2
|||||
|

RESULT 248
US-10-033-145-595/c
; Sequence 595, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 595
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-595

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      730 CAGCAGAAA 738
DB      10 CAGCAGAAA 2
|||||
|

RESULT 249
US-10-033-145-780/c
; Sequence 780, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

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; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 780
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-780

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      727 TGCCAGGAG 735
DB      9 TTCCAGGAG 1
|||||
|

RESULT 250
US-10-033-145-794
; Sequence 794, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 794
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-794

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      735 GAAACAGAA 743
DB      1 GAAACTGAA 9
|||||
|

RESULT 251
US-10-033-145-813/c
; Sequence 813, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 813
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-10-033-145-813

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
|||||
DB 9 GCCAGGATA 1

RESULT 252

US-10-033-145-835
; Sequence 835, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 835
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-835

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAC 739
|||||
DB 2 AGGAGATC 10

RESULT 253

US-10-033-145-1342/c
; Sequence 1342, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1342
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1342

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAAGAGAA 743
|||||
DB 9 GAAAGAGAA 1

RESULT 254

US-10-033-145-1396
; Sequence 1396, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1396
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1396

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAA 738
|||||
DB 1 CAGGAGACA 9

RESULT 255

US-10-033-145-1419
; Sequence 1419, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1419
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1419

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAAACA 745
|||||
DB 1 AACAGAAATA 9

RESULT 256

US-10-033-145-1496
; Sequence 1496, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145

; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1496
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1496

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGACA 745
 Db 1 ACCAGACA 9

RESULT 257

US-10-033-145-1773
 ; Sequence 1773, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1773
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1773

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
 Db 2 GAGAAACAG 10

RESULT 258

US-10-033-145-1999/c
 ; Sequence 1999, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1999
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1999

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
 Db 9 GAGAAACAG 1

RESULT 259

US-10-010-802-261/c
 ; Sequence 261, Application US/10010802
 ; Publication No. US20030078220A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genaisance Pharmaceuticals
 ; APPLICANT: Chew, Anne
 ; APPLICANT: Denton, R. Rex
 ; APPLICANT: Duda, Amy
 ; APPLICANT: Nandabalan, Krishnan
 ; APPLICANT: Stephens, J. Claiborne
 ; APPLICANT: Windemuth, Andreas
 ; TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the Interleukin
 ; TITLE OF INVENTION: 4 Receptor Alpha Gene
 ; FILE REFERENCE: MMH-0002US2 IL4R alpha
 ; CURRENT APPLICATION NUMBER: US/10/010,802
 ; CURRENT FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/19094
 ; PRIOR FILING DATE: 2000-07-13
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 261
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-010-802-261

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAG 735
 Db 10 TGCCAGGAG 2

RESULT 260

US-10-010-802-287/c
 ; Sequence 287, Application US/10010802
 ; Publication No. US20030078220A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genaisance Pharmaceuticals
 ; APPLICANT: Chew, Anne
 ; APPLICANT: Denton, R. Rex
 ; APPLICANT: Duda, Amy
 ; APPLICANT: Nandabalan, Krishnan
 ; APPLICANT: Stephens, J. Claiborne
 ; APPLICANT: Windemuth, Andreas
 ; TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the Interleukin
 ; TITLE OF INVENTION: 4 Receptor Alpha Gene
 ; FILE REFERENCE: MMH-0002US2 IL4R alpha
 ; CURRENT APPLICATION NUMBER: US/10/010,802
 ; CURRENT FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/19094
 ; PRIOR FILING DATE: 2000-07-13
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 287
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-010-802-287

Query Match 33.6%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1;

Qy 739 CAGAACACC 747
Db 10 CAGAGCACC 2

RESULT 261

US-10-176-464A-59
; Sequence 59, Application US/10176464A
; Publication No. US20030165902A1
; GENERAL INFORMATION:
; APPLICANT: Bieganski, Karyn
; APPLICANT: Lee, Helen
; APPLICANT: Messer, Chad
; APPLICANT: Monroe, Glen
; TITLE OF INVENTION: HAPLOTYPES OF THE F2R GENE
; FILE REFERENCE: F2R MWH-1457US
; CURRENT APPLICATION NUMBER: US/10/176,464A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/30876
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/236,603
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-176-464A-59

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 734 AGAACACAGA 742
Db 1 AGACACAGA 9

RESULT 262

US-10-329-465-95/c
; Sequence 95, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
; TITLE OF INVENTION: FUSION
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-95

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAA 738
Db 10 CAGCAGAAA 2

RESULT 263

US-10-330-627-238/c
; Sequence 238, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-238

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TCCACGAG 735
Db 9 TTCCAGGAG 1

RESULT 264

US-10-330-627-399/c
; Sequence 399, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-399

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAA 738
Db 10 CAGCAGAAA 2

RESULT 265

US-10-193-507-79
; Sequence 79, Application US/10193507
; Publication No. US20040018493A1
; GENERAL INFORMATION:
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Kazemi, Amir
; APPLICANT: Lachowicz, Michael F.
; APPLICANT: Pabon, Vicente
; APPLICANT: Shah, Nisha

```

; TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE
; FILE REFERENCE: MW-2790US
; CURRENT APPLICATION NUMBER: US/10/193,507
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/304,573
; PRIOR FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-193-507-79

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAC 739
Db      2 AGGGAAC 10

RESULT 266
US-09-735-363A-82/c
; Sequence 82, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-82

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      736 AACAGAAC 744
Db      10 AACAAAC 2

RESULT 267
US-09-249-155-86
; Sequence 86, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/097,937
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-86

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      738 ACAGAACAC 746
Db      3 ACCGAACAC 11

RESULT 268
US-09-249-155-124
; Sequence 124, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/097,937
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 124
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-124

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      738 ACAGAACAC 746
Db      3 ACCGAACAC 11

RESULT 269
US-09-918-715-66/c
; Sequence 66, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66

```

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; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-66

Query Match          33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      734 AGAAGACAGA 742
      |||||
Db      9 AGAAGCAGA 1

RESULT 270
US-10-191-302-8
; Sequence 8, Application US/10191302
; Publication No. US20030092065A1
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, K. T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/191.302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,528
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: VITO, CHRISTINE C.
; REGISTRATION NUMBER: 39,061
; REFERENCE/DOCKET NUMBER: CRP-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..11
; OTHER INFORMATION: /product= "MEF-2 MUTANT CONSENSUS"
US-10-191-302-8

Query Match          33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      736 AAACAGAAC 744
      |||||
Db      3 AAACATAAC 11

RESULT 271
US-10-314-322-86
; Sequence 86, Application US/10314322
; Publication No. US20040137011A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-86

Query Match          33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      738 ACAGAACAC 746
      |||||
Db      1 ACAGAACTC 9

RESULT 272
US-10-314-322-124
; Sequence 124, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-124

Query Match          33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      738 ACAGAACAC 746
      |||||
Db      3 ACCGAACAC 11

RESULT 273
US-10-612-224-78
; Sequence 78, Application US/10612224
; Publication No. US20040137011A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Cunningham, Philip R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; IDENTIFICATION OF ANTIBIOTICS THAT ARE NOT SUSCEPTIBLE TO
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE
; FILE REFERENCE: MSV-2597
; CURRENT APPLICATION NUMBER: US/10/612,224
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 60/393237
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/452012
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 11
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-612-224-78

```

```

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      738 ACAGAACAC 746
Db      2 ACAGAACUC 10

```

```

RESULT 274
US-10-450-797-51/c
; Sequence 51, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-51

```

```

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      739 CAGAACACC 747
Db      11 CAGAACACC 3

```

```

RESULT 275
US-10-450-797-110/c
; Sequence 110, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

```

```

; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 110
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-110

```

```

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      732 GGAGAAACA 740
Db      9 GGAGCAACA 1

```

```

RESULT 276
US-10-450-797-284/c
; Sequence 284, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 284
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-284

```

```

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      738 ACAGAACAC 746
Db      9 ACAGAGCAC 1

```

```

RESULT 277
US-10-450-797-285
; Sequence 285, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03

```

; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 285
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-285

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAA 738
Db 1 CAGGAGGAA 9

RESULT 278

US-10-450-797-335/c
; Sequence 335, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 335
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-335

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGACA 745
Db 10 AAGAGACA 2

RESULT 279

US-10-450-797-538
; Sequence 538, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 538
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-538

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 1 GAAACAAAA 9

RESULT 280

US-10-450-797-626
; Sequence 626, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 626
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-626

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 1 GGGAAACAG 9

RESULT 281

US-10-450-797-662/c
; Sequence 662, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 662
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-662

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 1 GAAACAAAA 9


```
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1320
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1320

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      727 TGCCAGGAG 735
Db      2   TGCCAGGAG 10
      |||||
      |||||
```

Search completed: October 18, 2004, 14:11:19
Job time : 1 secs

This Page Blank (uspto)

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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 14:05:37 ; Search time 0.001 Seconds
(without alignments)

333.432 Million cell updates/sec

Title: US-09-695-451-1

Perfect score: 22

Sequence: 1 tggcaggagaacacagaccg 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 634 seqs, 7578 residues

Total number of hits satisfying chosen parameters: 1268

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 634 summaries

Database : rge1-727.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	95.5	21	BD174191	ACCESSION:BD174191
C 2	21	95.5	21	BD185146	ACCESSION:BD185146
C 3	17	77.3	18	AR096376	ACCESSION:AR096376
C 4	17	77.3	18	BD217424	ACCESSION:BD217424
C 5	16.4	74.5	22	AX598452	ACCESSION:AX598452
C 6	15.4	70.0	18	AR175645	ACCESSION:AR175645
C 7	15.4	70.0	18	AR195221	ACCESSION:AR195221
C 8	15.4	70.0	18	AR222303	ACCESSION:AR222303
C 9	15.4	70.0	18	AR241422	ACCESSION:AR241422
C 10	15.4	70.0	18	BD04788	ACCESSION:BD04788
C 11	15.4	70.0	19	AX132046	ACCESSION:AX132046
C 12	15	68.2	18	AG7107	ACCESSION:AG7107
C 13	14.6	66.4	22	AX286278	ACCESSION:AX286278
C 14	14.6	66.4	22	AX286282	ACCESSION:AX286282
C 15	14.6	66.4	22	AX286288	ACCESSION:AX286288
C 16	14.4	65.5	19	AX132045	ACCESSION:AX132045
C 17	14.2	64.5	19	AX132309	ACCESSION:AX132309
C 18	14.2	64.5	21	AX440525	ACCESSION:AX440525
C 19	14	63.6	18	AG7109	ACCESSION:AG7109
C 20	13.4	60.9	18	AG7103	ACCESSION:AG7103
C 21	13.4	60.9	18	AG7105	ACCESSION:AG7105
C 22	13.4	60.9	18	AG7106	ACCESSION:AG7106
C 23	13.4	60.9	20	E26485	ACCESSION:E26485
C 24	13.2	60.0	19	AX132047	ACCESSION:AX132047
C 25	13.2	60.0	19	AX132308	ACCESSION:AX132308
C 26	13.2	60.0	19	AX132310	ACCESSION:AX132310
C 27	12.8	58.2	17	AX499947	ACCESSION:AX499947
C 28	12.8	58.2	17	AX499948	ACCESSION:AX499948
C 29	12.8	58.2	19	AX023982	ACCESSION:AX023982
C 30	12.4	56.4	16	AX255710	ACCESSION:AX255710
C 31	12.4	56.4	17	AX076026	ACCESSION:AX076026
C 32	12.4	56.4	17	AX499949	ACCESSION:AX499949
C 33	12.4	56.4	17	AX499950	ACCESSION:AX499950

C 34	12.4	56.4	18	1	AG7108	ACCESSION:AG7108
C 35	12.4	56.4	18	1	AG7111	ACCESSION:AG7111
C 36	12.4	56.4	18	1	AR065607	ACCESSION:AR065607
C 37	12.2	55.5	18	1	IO6264	ACCESSION:IO6264
C 38	12.2	55.5	18	1	AR292914	ACCESSION:AR292914
C 39	12	54.5	17	1	BD241241	ACCESSION:BD241241
C 40	11.8	53.6	17	1	AX499946	ACCESSION:AX499946
C 41	11.8	53.6	17	1	AX674572	ACCESSION:AX674572
C 42	11.8	53.6	17	1	AX729839	ACCESSION:AX729839
C 43	11.8	53.6	17	1	AX762877	ACCESSION:AX762877
C 44	11.8	53.6	18	1	AG7102	ACCESSION:AG7102
C 45	11.8	53.6	18	1	AG7104	ACCESSION:AG7104
C 46	11.4	51.8	17	1	AR190011	ACCESSION:AR190011
C 47	11.4	51.8	17	1	AR324988	ACCESSION:AR324988
C 48	11.4	51.8	17	1	AX499951	ACCESSION:AX499951
C 49	11.4	51.8	17	1	AX674143	ACCESSION:AX674143
C 50	11.4	51.8	17	1	AX732557	ACCESSION:AX732557
C 51	11.2	50.9	17	1	BD266301	ACCESSION:BD266301
C 52	11.2	50.9	17	1	E54495	ACCESSION:E54495
C 53	11.2	50.9	17	1	AR190548	ACCESSION:AR190548
C 54	11.2	50.9	17	1	AR325471	ACCESSION:AR325471
C 55	11.2	50.9	17	1	AX227611	ACCESSION:AX227611
C 56	11.2	50.9	17	1	AX692031	ACCESSION:AX692031
C 57	11.2	50.9	17	1	AX692032	ACCESSION:AX692032
C 58	11.2	50.9	17	1	BD105092	ACCESSION:BD105092
C 59	11	50.0	15	1	AI1101	ACCESSION:AI1101
C 60	11	50.0	15	1	AR362726	ACCESSION:AR362726
C 61	10.8	49.1	15	1	IG1456	ACCESSION:IG1456
C 62	10.8	49.1	15	1	AX635865	ACCESSION:AX635865
C 63	10.8	49.1	15	1	BD208396	ACCESSION:BD208396
C 64	10.8	49.1	16	1	A09424	ACCESSION:A09424
C 65	10.8	49.1	16	1	AI0627	ACCESSION:AI0627
C 66	10.8	49.1	16	1	AI1575	ACCESSION:AI1575
C 67	10.8	49.1	16	1	A35095	ACCESSION:A35095
C 68	10.8	49.1	16	1	AX076025	ACCESSION:AX076025
C 69	10.4	47.3	12	1	I28559	ACCESSION:I28559
C 70	10.4	47.3	12	1	I58721	ACCESSION:I58721
C 71	10.4	47.3	14	1	A40588	ACCESSION:A40588
C 72	10.4	47.3	14	1	A89112	ACCESSION:A89112
C 73	10.4	47.3	14	1	A89603	ACCESSION:A89603
C 74	10.4	47.3	14	1	AR061873	ACCESSION:AR061873
C 75	10.4	47.3	14	1	AR232868	ACCESSION:AR232868
C 76	10.4	47.3	14	1	AR407925	ACCESSION:AR407925
C 77	10.4	47.3	14	1	AX030163	ACCESSION:AX030163
C 78	10.4	47.3	14	1	AX316484	ACCESSION:AX316484
C 79	10.4	47.3	14	1	BD066625	ACCESSION:BD066625
C 80	10.4	47.3	14	1	BD067116	ACCESSION:BD067116
C 81	10.4	47.3	15	1	IG1457	ACCESSION:IG1457
C 82	10.4	47.3	15	1	AR180064	ACCESSION:AR180064
C 83	10.4	47.3	15	1	AR180799	ACCESSION:AR180799
C 84	10.4	47.3	15	1	AX635867	ACCESSION:AX635867
C 85	10.4	47.3	15	1	A22593	ACCESSION:A22593
C 86	10.4	47.3	16	1	AR096276	ACCESSION:AR096276
C 87	10.4	47.3	16	1	AX076029	ACCESSION:AX076029
C 88	10.4	47.3	16	1	AX255620	ACCESSION:AX255620
C 89	10.4	47.3	16	1	AX255663	ACCESSION:AX255663
C 90	10.4	47.3	16	1	AX452095	ACCESSION:AX452095
C 91	10.2	46.4	15	1	BD208458	ACCESSION:BD208458
C 92	10.2	46.4	15	1	BD208459	ACCESSION:BD208459
C 93	10	45.5	11	1	AR123024	ACCESSION:AR123024
C 94	10	45.5	11	1	AX626398	ACCESSION:AX626398
C 95	10	45.5	11	1	AR180388	ACCESSION:AR180388
C 96	10	45.5	15	1	BD208460	ACCESSION:BD208460
C 97	9.8	44.5	14	1	AX5806	ACCESSION:AX5806
C 98	9.8	44.5	14	1	A40589	ACCESSION:A40589
C 99	9.8	44.5	14	1	A87922	ACCESSION:A87922
C 100	9.8	44.5	14	1	A89113	ACCESSION:A89113
C 101	9.8	44.5	14	1	A89889	ACCESSION:A89889
C 102	9.8	44.5	14	1	AR029997	ACCESSION:AR029997
C 103	9.8	44.5	14	1	AR030009	ACCESSION:AR030009
C 104	9.8	44.5	14	1	I26228	ACCESSION:I26228
C 105	9.8	44.5	14	1	I52188	ACCESSION:I52188
C 106	9.8	44.5	14	1	I52193	ACCESSION:I52193

107	9.8	44.5	14	1	AR232869	ACCESSION:AR232869	C 180	9	40.9	11	1	AX630559	ACCESSION:AX630559
108	9.8	44.5	14	1	AX030164	ACCESSION:AX030164	C 181	9	40.9	11	1	AX632264	ACCESSION:AX632264
109	9.8	44.5	14	1	AX316485	ACCESSION:AX316485	C 182	9	40.9	11	1	AX632552	ACCESSION:AX632552
110	9.8	44.5	14	1	AX571850	ACCESSION:AX571850	C 183	9	40.9	11	1	BD242525	ACCESSION:BD242525
111	9.8	44.5	14	1	BD065435	ACCESSION:BD065435	C 184	9	40.9	12	1	BD242532	ACCESSION:BD242532
112	9.8	44.5	14	1	BD066626	ACCESSION:BD066626	C 185	9	40.9	12	1	AR217450	ACCESSION:AR217450
113	9.8	44.5	14	1	BD209300	ACCESSION:BD209300	C 186	9	40.9	12	1	AR217457	ACCESSION:AR217457
114	9.8	44.5	15	1	AR130724	ACCESSION:AR130724	C 187	9	40.9	12	1	AX766772	ACCESSION:AX766772
115	9.8	44.5	15	1	AR180392	ACCESSION:AR180392	C 188	9	40.9	12	1	AX766786	ACCESSION:AX766786
116	9.8	44.5	15	1	AR235561	ACCESSION:AR235561	C 189	9	40.9	13	1	AR364664	ACCESSION:AR364664
117	9.8	44.5	15	1	AR370348	ACCESSION:AR370348	C 190	8.8	40.0	13	1	AR123872	ACCESSION:AR123872
118	9.8	44.5	15	1	AX009449	ACCESSION:AX009449	C 191	8.8	40.0	12	1	AR123873	ACCESSION:AR123873
119	9.8	44.5	15	1	BD005884	ACCESSION:BD005884	C 192	8.8	40.0	12	1	AR123877	ACCESSION:AR123877
120	9.8	44.5	15	1	BD208397	ACCESSION:BD208397	C 193	8.8	40.0	12	1	AR178311	ACCESSION:AR178311
121	9.8	44.5	15	1	AX471642	ACCESSION:AX471642	C 194	8.8	40.0	12	1	AX323393	ACCESSION:AX323393
122	9.4	42.7	11	1	AX627643	ACCESSION:AX627643	C 195	8.8	40.0	13	1	AR021478	ACCESSION:AR021478
123	9.4	42.7	12	1	AR011923	ACCESSION:AR011923	C 196	8.8	40.0	13	1	AR061316	ACCESSION:AR061316
124	9.4	42.7	12	1	AR017794	ACCESSION:AR017794	C 197	8.8	40.0	13	1	AR100114	ACCESSION:AR100114
125	9.4	42.7	12	1	AR077199	ACCESSION:AR077199	C 198	8.8	40.0	13	1	AR100119	ACCESSION:AR100119
126	9.4	42.7	12	1	AR087821	ACCESSION:AR087821	C 199	8.8	40.0	13	1	AR175971	ACCESSION:AR175971
127	9.4	42.7	12	1	AR167798	ACCESSION:AR167798	C 200	8.6	39.1	13	1	BD269493	ACCESSION:BD269493
128	9.4	42.7	12	1	BD242531	ACCESSION:BD242531	C 201	8.6	39.1	13	1	AX035442	ACCESSION:AX035442
129	9.4	42.7	12	1	BD269489	ACCESSION:BD269489	C 202	8.6	39.1	13	1	AX100748	ACCESSION:AX100748
130	9.4	42.7	12	1	E29682	ACCESSION:E29682	C 203	8.6	39.1	13	1	AX352663	ACCESSION:AX352663
131	9.4	42.7	12	1	E38120	ACCESSION:E38120	C 204	8.6	39.1	13	1	AX362221	ACCESSION:AX362221
132	9.4	42.7	12	1	E38788	ACCESSION:E38788	C 205	8.6	39.1	13	1	AX428934	ACCESSION:AX428934
133	9.4	42.7	12	1	E64214	ACCESSION:E64214	C 206	8.6	39.1	13	1	AX512617	ACCESSION:AX512617
134	9.4	42.7	12	1	AR217456	ACCESSION:AR217456	C 207	8.6	39.1	13	1	AX522268	ACCESSION:AX522268
135	9.4	42.7	12	1	AR282763	ACCESSION:AR282763	C 208	8.4	38.2	10	1	AR026539	ACCESSION:AR026539
136	9.4	42.7	12	1	AX035438	ACCESSION:AX035438	C 209	8.4	38.2	10	1	BD238913	ACCESSION:BD238913
137	9.4	42.7	12	1	AX100750	ACCESSION:AX100750	C 210	8.4	38.2	10	1	BD239757	ACCESSION:BD239757
138	9.4	42.7	12	1	AX100751	ACCESSION:AX100751	C 211	8.4	38.2	10	1	BD239797	ACCESSION:BD239797
139	9.4	42.7	12	1	AX352660	ACCESSION:AX352660	C 212	8.4	38.2	10	1	E39660	ACCESSION:E39660
140	9.4	42.7	12	1	AX352661	ACCESSION:AX352661	C 213	8.4	38.2	10	1	AR303316	ACCESSION:AR303316
141	9.4	42.7	12	1	AX362218	ACCESSION:AX362218	C 214	8.4	38.2	10	1	AR303402	ACCESSION:AR303402
142	9.4	42.7	12	1	AX362219	ACCESSION:AX362219	C 215	8.4	38.2	10	1	AR336872	ACCESSION:AR336872
143	9.4	42.7	12	1	AX428931	ACCESSION:AX428931	C 216	8.4	38.2	10	1	AX152919	ACCESSION:AX152919
144	9.4	42.7	12	1	AX428932	ACCESSION:AX428932	C 217	8.4	38.2	10	1	AX153378	ACCESSION:AX153378
145	9.4	42.7	12	1	AX512614	ACCESSION:AX512614	C 218	8.4	38.2	10	1	AX153448	ACCESSION:AX153448
146	9.4	42.7	12	1	AX512615	ACCESSION:AX512615	C 219	8.4	38.2	10	1	AX302584	ACCESSION:AX302584
147	9.4	42.7	12	1	AX522265	ACCESSION:AX522265	C 220	8.4	38.2	10	1	BD083216	ACCESSION:BD083216
148	9.4	42.7	12	1	AX522266	ACCESSION:AX522266	C 221	8.4	38.2	10	1	BD166609	ACCESSION:BD166609
149	9.4	42.7	12	1	AX766784	ACCESSION:AX766784	C 222	8.4	38.2	10	1	BD166675	ACCESSION:BD166675
150	9.4	42.7	13	1	AR282758	ACCESSION:AR282758	C 223	8.4	38.2	10	1	BD166874	ACCESSION:BD166874
151	9.4	42.7	13	1	AR407966	ACCESSION:AR407966	C 224	8.4	38.2	10	1	AX470470	ACCESSION:AX470470
152	9.4	42.7	13	1	BD237463	ACCESSION:BD237463	C 225	8.4	38.2	11	1	AX470955	ACCESSION:AX470955
153	9.4	42.7	14	1	BD261338	ACCESSION:BD261338	C 226	8.4	38.2	11	1	AX470960	ACCESSION:AX470960
154	9.4	42.7	14	1	BD269502	ACCESSION:BD269502	C 227	8.4	38.2	11	1	AX471036	ACCESSION:AX471036
155	9.4	42.7	14	1	AX035451	ACCESSION:AX035451	C 228	8.4	38.2	11	1	AX471164	ACCESSION:AX471164
156	9.4	42.7	14	1	AX352673	ACCESSION:AX352673	C 229	8.4	38.2	11	1	AX623587	ACCESSION:AX623587
157	9.4	42.7	14	1	AX362231	ACCESSION:AX362231	C 230	8.4	38.2	11	1	AX623632	ACCESSION:AX623632
158	9.4	42.7	14	1	AX428944	ACCESSION:AX428944	C 231	8.4	38.2	11	1	AX624564	ACCESSION:AX624564
159	9.4	42.7	14	1	AX512628	ACCESSION:AX512628	C 232	8.4	38.2	11	1	AX624971	ACCESSION:AX624971
160	9.4	42.7	14	1	AX522279	ACCESSION:AX522279	C 233	8.4	38.2	11	1	AX626122	ACCESSION:AX626122
161	9.2	41.8	14	1	A40498	ACCESSION:A40498	C 234	8.4	38.2	11	1	AX627227	ACCESSION:AX627227
162	9.2	41.8	14	1	AS9025	ACCESSION:AS9025	C 235	8.4	38.2	11	1	AX627341	ACCESSION:AX627341
163	9.2	41.8	14	1	AR233778	ACCESSION:AR233778	C 236	8.4	38.2	11	1	AX627766	ACCESSION:AX627766
164	9.2	41.8	14	1	AX316394	ACCESSION:AX316394	C 237	8.4	38.2	11	1	AX628298	ACCESSION:AX628298
165	9.2	41.8	14	1	BD066538	ACCESSION:BD066538	C 238	8.4	38.2	11	1	AX628930	ACCESSION:AX628930
166	9.2	41.8	14	1	BD193255	ACCESSION:BD193255	C 239	8.4	38.2	11	1	AX629191	ACCESSION:AX629191
167	9.2	41.8	14	1	S59977S1	ACCESSION:S59977S1	C 240	8.4	38.2	11	1	AX630040	ACCESSION:AX630040
168	9	40.9	10	1	BD240369	ACCESSION:BD240369	C 241	8.4	38.2	11	1	AX630299	ACCESSION:AX630299
169	9	40.9	10	1	BD240503	ACCESSION:BD240503	C 242	8.4	38.2	11	1	AX631008	ACCESSION:AX631008
170	9	40.9	10	1	AR303296	ACCESSION:AR303296	C 243	8.4	38.2	11	1	AX631053	ACCESSION:AX631053
171	9	40.9	10	1	AR303305	ACCESSION:AR303305	C 244	8.4	38.2	11	1	AX632085	ACCESSION:AX632085
172	9	40.9	10	1	AR303339	ACCESSION:AR303339	C 245	8.4	38.2	11	1	AX632392	ACCESSION:AX632392
173	9	40.9	10	1	BD161212	ACCESSION:BD161212	C 246	8.4	38.2	12	1	AR123885	ACCESSION:AR123885
174	9	40.9	11	1	AX470590	ACCESSION:AX470590	C 247	8.4	38.2	12	1	AX328584	ACCESSION:AX328584
175	9	40.9	11	1	AX623138	ACCESSION:AX623138	C 248	8.4	38.2	12	1	AX328589	ACCESSION:AX328589
176	9	40.9	11	1	AX624843	ACCESSION:AX624843	C 249	8.4	38.2	12	1	BD132149	ACCESSION:BD132149
177	9	40.9	11	1	AX625131	ACCESSION:AX625131	C 250	8.4	38.2	12	1	BD132154	ACCESSION:BD132154
178	9	40.9	11	1	AX626407	ACCESSION:AX626407	C 251	8.4	38.2	12	1	S73118S1	ACCESSION:S73118S1
179	9	40.9	11	1	AX628047	ACCESSION:AX628047	C 252	8.4	38.2	12	1		

253	8	36.4	10	1	BD239119	ACCESSION:BD239119	C 325	7.8	35.5	11	1	AX629695
254	8	36.4	10	1	AR300461	ACCESSION:AR300461	C 327	7.8	35.5	11	1	AX629821
255	8	36.4	10	1	AX152111	ACCESSION:AX152111	328	7.8	35.5	11	1	AX629849
256	8	36.4	10	1	AX152162	ACCESSION:AX152162	C 329	7.8	35.5	11	1	AX630158
257	8	36.4	10	1	AX152164	ACCESSION:AX152164	C 330	7.8	35.5	11	1	AX630160
258	8	36.4	10	1	AX152170	ACCESSION:AX152170	331	7.8	35.5	11	1	AX630631
259	8	36.4	10	1	AX153406	ACCESSION:AX153406	332	7.8	35.5	11	1	AX630810
260	8	36.4	10	1	AX301382	ACCESSION:AX301382	333	7.8	35.5	11	1	AX630810
261	8	36.4	10	1	BD083241	ACCESSION:BD083241	C 334	7.8	35.5	11	1	AX631236
262	8	36.4	10	1	BD161382	ACCESSION:BD161382	C 335	7.8	35.5	11	1	AX631287
263	8	36.4	11	1	AX393135	ACCESSION:AX393135	336	7.8	35.5	11	1	AX631662
264	8	36.4	11	1	AX470875	ACCESSION:AX470875	337	7.8	35.5	11	1	AX631787
265	8	36.4	11	1	AX471137	ACCESSION:AX471137	C 338	7.8	35.5	11	1	AX632664
266	8	36.4	11	1	AX471810	ACCESSION:AX471810	C 339	7.8	35.5	11	1	AX632754
267	8	36.4	11	1	AX482050	ACCESSION:AX482050	C 340	7.8	35.5	11	1	AX632754
268	8	36.4	11	1	AX511289	ACCESSION:AX511289	341	7.8	35.5	11	1	BD124242
269	8	36.4	11	1	AX623051	ACCESSION:AX623051	342	7.8	35.5	11	1	BD174612
270	8	36.4	11	1	AX623196	ACCESSION:AX623196	343	7.8	35.5	11	1	BD174617
271	8	36.4	11	1	AX623555	ACCESSION:AX623555	C 344	7.8	35.5	12	1	AX630661
272	8	36.4	11	1	AX624933	ACCESSION:AX624933	345	7.8	35.5	12	1	AX630661
273	8	36.4	11	1	AX624958	ACCESSION:AX624958	C 346	7.8	35.5	12	1	AX630661
274	8	36.4	11	1	AX624999	ACCESSION:AX624999	C 347	7.8	35.5	12	1	AX630661
275	8	36.4	11	1	AX625252	ACCESSION:AX625252	C 348	7.8	35.5	12	1	AX630661
276	8	36.4	11	1	AX625448	ACCESSION:AX625448	349	7.8	35.5	12	1	AX630661
277	8	36.4	11	1	AX625885	ACCESSION:AX625885	350	7.8	35.5	12	1	AX630661
278	8	36.4	11	1	AX626273	ACCESSION:AX626273	351	7.8	35.5	12	1	AX630661
279	8	36.4	11	1	AX626400	ACCESSION:AX626400	352	7.8	35.5	12	1	AX630661
280	8	36.4	11	1	AX626990	ACCESSION:AX626990	C 353	7.8	35.5	12	1	AX630661
281	8	36.4	11	1	AX627679	ACCESSION:AX627679	C 354	7.8	35.5	12	1	AX630661
282	8	36.4	11	1	AX627723	ACCESSION:AX627723	355	7.8	35.5	12	1	AX630661
283	8	36.4	11	1	AX628113	ACCESSION:AX628113	C 356	7.8	35.5	12	1	AX630661
284	8	36.4	11	1	AX628247	ACCESSION:AX628247	C 357	7.8	35.5	12	1	AX630661
285	8	36.4	11	1	AX628626	ACCESSION:AX628626	C 358	7.8	35.5	12	1	AX630661
286	8	36.4	11	1	AX628755	ACCESSION:AX628755	C 359	7.8	35.5	12	1	AX630661
287	8	36.4	11	1	AX629350	ACCESSION:AX629350	360	7.8	35.5	12	1	AX630661
288	8	36.4	11	1	AX629616	ACCESSION:AX629616	361	7.8	35.5	12	1	AX630661
289	8	36.4	11	1	AX630472	ACCESSION:AX630472	C 362	7.8	35.5	12	1	AX630661
290	8	36.4	11	1	AX630617	ACCESSION:AX630617	C 363	7.8	35.5	12	1	AX630661
291	8	36.4	11	1	AX630976	ACCESSION:AX630976	364	7.8	35.5	12	1	AX630661
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10/18/04

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SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Hikichi, Y., Shintani, Y. and Matsui, H.
TITLE       Cell differentiating agent
JOURNAL     Patent: JP 2002356438-A 37 13-DEC-2002;
            TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT     OS Artificial Sequence
            PN JP 2002356438-A/37
            PD 13-DEC-2002
            PF 21-FEB-2002 JP 2002044741
            PI YUKIKO HIKICHI, YASUSHI SHINTANI, HIDEKI MATSUI PC
            A61K38/00, A61K31/7088, A61F15/00, A61E21/04, A61P35/00, C12N15/09// PC
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DB 21 TGCCAGGAGAAACAGACACC 1
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ACCESSION  AR096376
VERSION     AR096376.1 GI:100251133
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Baker, B.F. and Cowsert, L.M.
TITLE       Antisense inhibition of TNFR1 expression
JOURNAL     Patent: US 6007995-A 47 28-DEC-1999;
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ORGANISM    unidentified.
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REFERENCE   1 (bases 1 to 18)
AUTHORS     Baker, B.F. and Cowsert, L.M.
TITLE       Antisense modulation of TNFR1 expression
JOURNAL     Patent: JP 2002519015-A 47 02-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS Unidentified
            PN JP 2002519015-A/47
            PD 02-JUL-2002
            PF 17-JUN-1999 JP 2000557265
            PR 26-JUN-1998 US 09/106038
            PI BRENDA F BAKER, LEX M COWSERT
            PC
            C12N15/09, A61K31/7105, A61K31/711, A61K48/00, A61P29/00, A61P43/00, PC
            C12Q1/68,
            CC C12N15/00
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VERSION     AX598452.1 GI:28398628
KEYWORDS    synthetic construct
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            artificial sequences.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Brower, A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de arruda
            Indig, M., Kurensky, D., Luedtke, C., Lukowiak, A.A., Lyamichev, V.,
            Neri, B.P., Reimer, N.D., Roever, R.T., Skrzypczynski, Z., Ziarno, W.A.,
            Comerford, J., Stump, S. and Viegut, D.D.
            Systems and method for detection assay production and sale
            Patent: WO 0244994-A 726 06-JUN-2002;
            THIRD WAVE TECHNOLOGIES, INC. (US)
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DEFINITION Sequence 45 from patent US 6309853.

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Best Local Similarity   94.1%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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VERSION   AR241422.1 GI:27287112
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SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE
  1 (bases 1 to 18)
AUTHORS   Friedman,J.M., Zhang,Y. and Proenca,R.
TITLE     Ob polypeptides, modified forms and compositions thereto
JOURNAL   Patent: US 6471956-A 45 29-OCT-2002;
FEATURES   Location/Qualifiers
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DEFINITION Modulator of weight, corresponding nucleic acid and protein, and
ACCESSION BD014788
VERSION   BD014788.1 GI:22555571
KEYWORDS  JP 2001157591-A/29.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE
  1 (bases 1 to 18)
AUTHORS   Friednan,J.M., Zhang,Y., Proenca,R., Maffei,M., Halaas,J.L.,
          Kajiwara,K. and Burley,S.K.
TITLE     Modulator of weight, corresponding nucleic acid and protein, and
          diagnosis and remedy utilization thereof
JOURNAL   Patent: JP 2001157591-A 29 12-JUN-2001;
          THE ROCKEFELLER UNIVERSITY
COMMENT   OS Homo sapiens (human)
          PN JP 2001157591-A/29
          PD 12-JUN-2001
          PF 29-SEP-2000 JP 2000301496
          PR 30-NOV-1994 US 08/347563,10-MAY-1995 US 08/438431 PR
          P1 JEFFERY M FRIEDMAN,YIYING ZHANG,RICARDO PROENCA,MARGHERITA PI
             MAFFEI,
             PI JEFFRY L HALAAS,KETAN KAJIWARA,STEPHEN K BURLEY PC
             C12N15/09,A61K31/711,A61K38/00,A61K39/395,A61K45/00,A61K48/00,PC
             A61P3/04.
             PC A61P3/06,A61P3/10,A61P9/12,C07K14/47,C07K16/18,C12N1/19,C12N1/
             PC 21,C12N5/10,
             PC C12N5/10,C12P21/02,C12P21/08,C12Q1/69// (C12N1/19,C12R1:72),PC
             (C12N1/19,C12R1:185),(C12N1/19,C12R1:19),(C12N1/19,C12R1:07),PC
             (C12N1/21,C12R1:465),(C12N1/21,C12R1:38),(C12N5/10,C12R1:91),PC
             (C12P21/02,C12R1:19),(C12N15/00,A61K37/02,C12N5/00,C12N5/00,PC
             (C12N5/00,C12R1:91)

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CC Strandedness: Single;
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Best Local Similarity 94.1%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 730 CAGGAGAAACAGACAC 746
Db 18 CAGGAGAAACAGACAC 2
RESULT 11
AX132046/c
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DEFINITION Sequence 3264 from Patent WO0130362.
ACCESSION AX132046
VERSION AX132046.1 GI:14138351
KEYWORDS
SOURCE
    ORGANISM
        Homo sapiens (human)
REFERENCE
    AUTHORS Robbins, J.M. and Tritz, R.
    TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
    JOURNAL Patent: WO 0130362-A 3264 03-MAY-2001; IMMUSOL, INC. (US)
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Query Match 70.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAACCCG 748
Db 19 GGAGAGCAGAACACCG 3
RESULT 12
A67107/c
LOCUS A67107
DEFINITION Sequence 274 from Patent WO9740193.
ACCESSION A67107
VERSION A67107.1 GI:4538478
KEYWORDS
SOURCE
    ORGANISM
        unidentified
        unidentified
        unclassified.
REFERENCE
    1 (bases 1 to 18)
    AUTHORS Stuyver, L., Rossau, R. and Maertens, G.
    TITLE METHOD FOR TYPING AND DETECTING HBV
    JOURNAL Patent: WO 9740193-A 274 30-OCT-1997; INNOGENETICS NV (BE)
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACAGA 4
RESULT 13
AX286278/c
LOCUS AX286278
DEFINITION Sequence 7 from Patent WO0179296.
ACCESSION AX286278
VERSION AX286278.1 GI:17048526
KEYWORDS
SOURCE
    ORGANISM
        Homo sapiens (human)
        Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1
    AUTHORS Lin, H.H., Gordon, D.S., McKnight, A.J. and Stacey, M.S.
    TITLE Human emr2, a G-protein coupled receptor from the egf-tm7 family
    JOURNAL Patent: WO 0179296-A 7 25-OCT-2001; Isis Innovation Limited (GB)
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Best Local Similarity 81.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 727 TCCGAGGAGAACAGACACC 747
Db 22 TCCGAGAGACAGACAGCACC 2
RESULT 14
AX286282/c
LOCUS AX286282
DEFINITION Sequence 11 from Patent WO0179296.
ACCESSION AX286282
VERSION AX286282.1 GI:17048530
KEYWORDS
SOURCE
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        Homo sapiens (human)
        Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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    AUTHORS Lin, H.H., Gordon, D.S., McKnight, A.J. and Stacey, M.S.
    TITLE Human emr2, a G-protein coupled receptor from the egf-tm7 family
    JOURNAL Patent: WO 0179296-A 11 25-OCT-2001; Isis Innovation Limited (GB)
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Best Local Similarity 81.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 727 TCCGAGGAGAACAGACACC 747
Db 22 TCCGAGAGACAGACAGCACC 2
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DEFINITION Sequence 11 from Patent WO0179296.
ACCESSION AX286282
VERSION AX286282.1 GI:17048530
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        Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1
    AUTHORS Lin, H.H., Gordon, D.S., McKnight, A.J. and Stacey, M.S.
    TITLE Human emr2, a G-protein coupled receptor from the egf-tm7 family
    JOURNAL Patent: WO 0179296-A 11 25-OCT-2001; Isis Innovation Limited (GB)
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Best Local Similarity 81.0%; Pred. No. 29;
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QY 727 TCCGAGGAGAACAGACACC 747
Db 22 TCCGAGAGACAGACAGCACC 2

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RESULT 15
AX286288/c
LOCUS AX286288 22 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 17 from Patent WO0175296.
ACCESSION AX286288
VERSION AX286288.1 GI:17048536
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Lin, H.H., Gordon, D.S., McKnight, A.J. and Stacey, M.S.
TITLE Human emt2, a g-protein coupled receptor from the egf-tm7 family
JOURNAL Patent: WO 0179296-A 17 25-OCT-2001;
Isis Innovation Limited (GB)
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Query Match 66.4%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAAACAGAACACC 747
Db 22 TCCAGAGACACAGAGCACC 2

RESULT 16
AX132045/c
LOCUS AX132045 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3263 from Patent WO0130362.
ACCESSION AX132045
VERSION AX132045.1 GI:14138350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 3263 03-MAY-2001;
IMMUSOL, INC. (US)
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/Note="Cyclin B1 ribozyme binding site"
Query Match 65.5%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAGAACACCG 748
Db 19 GAGAAACAGAACACCG 4

RESULT 17
AX132309/c
LOCUS AX132309 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3527 from Patent WO0130362.
ACCESSION AX132309
VERSION AX132309.1 GI:14138614
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 3527 03-MAY-2001;
IMMUSOL, INC. (US)
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Best Local Similarity 84.2%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 729 CCAGGAGAAACAGAACACC 747
Db 19 CCAGGAGAAACAGAACACC 1

RESULT 18
AX440525
LOCUS AX440525 21 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 29 from Patent WO0206529.
ACCESSION AX440525
VERSION AX440525.1 GI:21665328
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Germino, G.G., Watnick, T.J. and Phakdeekitcharoen, B.
TITLE Detection and treatment of polycystic kidney disease
JOURNAL Patent: WO 0206529-A 29 24-JAN-2002;
The Johns Hopkins University School of Medicine (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="PCR primer 5F1"
Query Match 64.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGAACAC 746
Db 3 GCCAGGAGGAGCAGAACCC 21

RESULT 19
A67109/c
LOCUS A67109 18 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 276 from Patent WO9740193.
ACCESSION A67109
VERSION A67109.1 GI:4538480
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
AUTHORS Stuyver, L., Rossau, R. and Maertens, G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 276 30-OCT-1997;
INNOGENETICS NV (BE)
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/mol_type="unassigned DNA"
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Query Match      63.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
Db 18 GCCAGGAGAAACAG 5

RESULT 20
A67103/c
LOCUS      A67103      18 bp      DNA
DEFINITION Sequence 270 from Patent WO9740193.
ACCESSION  A67103
VERSION     A67103.1 GI:4538474
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
TITLE     METHOD FOR TYPING AND DETECTING HBV
JOURNAL   Patent: WO 9740193-A 270 30-OCT-1997;
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Query Match      60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 742
Db 18 GCCAGGAGAAACAG 4

RESULT 21
A67105/c
LOCUS      A67105      18 bp      DNA
DEFINITION Sequence 272 from Patent WO9740193.
ACCESSION  A67105
VERSION     A67105.1 GI:4538476
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
TITLE     METHOD FOR TYPING AND DETECTING HBV
JOURNAL   Patent: WO 9740193-A 272 30-OCT-1997;
          INNOGENETICS NV (BE)
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Query Match      60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 742
Db 18 GCCATGAGAAACAG 4

RESULT 22
A67106/c
LOCUS      A67106      18 bp      DNA
DEFINITION Sequence 273 from Patent WO9740193.
ACCESSION  A67106
VERSION     A67106.1 GI:4538477
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
TITLE     METHOD FOR TYPING AND DETECTING HBV
JOURNAL   Patent: WO 9740193-A 273 30-OCT-1997;
          INNOGENETICS NV (BE)
FEATURES   Location/Qualifiers
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Query Match      60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 742
Db 18 GCCAGGAGAAACGG 4

RESULT 23
E26485/c
LOCUS      E26485      20 bp      DNA
DEFINITION Highly sensitive method for detecting lamivudine-tolerant hepatitis
          B virus.
ACCESSION  E26485
VERSION     E26485.1 GI:13025095
KEYWORDS   JP 1999127860-A/1.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Kazuaki,S. and Hiromitsu,K.
TITLE     Highly sensitive method for detecting lamivudine-tolerant hepatitis
          B virus
JOURNAL   Patent: JP 1999127860-A 1 18-MAY-1999;
          KAZUAKI SAYAMA
COMMENT    OS Unidentified
          PN JP 1999127860-A/1
          PD 18-MAY-1999
          PF 28-OCT-1997 JP 1997296042
          PR
          PT KAZUAKI SAYAMA,HIROMITSU KUMADA
          PC C12N15/09,C12Q1/70//(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,
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          CC Topology: Linear;
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Best Local Similarity 93.3%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 742
Db 17 GCCAGGAGAAACGG 3

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RESULT 24
AX132047/c
LOCUS AX132047 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3265 from Patent WO0130362.
ACCESSION AX132047
VERSION AX132047.1 GI:14138952
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL IMMUSOL, INC. (US)
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/organism="Homo sapiens"
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/note="Cyclin B1 ribozyme binding site"

Query Match 60.0%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGAACAC 745
Db 18 GCGGGGAGAAACAGAACAC 1

RESULT 25
AX132308/c
LOCUS AX132308 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3526 from Patent WO0130362.
ACCESSION AX132308
VERSION AX132308.1 GI:14138613
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL IMMUSOL, INC. (US)
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/organism="Homo sapiens"
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/note="Cdc25 hs ribozyme binding site"

Query Match 60.0%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAACACC 747
Db 19 CAGGAGAAACAGAACACC 2

RESULT 26
AX132310/c
LOCUS AX132310 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3528 from Patent WO0130362.
ACCESSION AX132310
VERSION AX132310.1 GI:14138615

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KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL IMMUSOL, INC. (US)
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/note="Cdc25 hs ribozyme binding site"

Query Match 60.0%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAGAACAC 746
Db 18 CCAGGAGAAACAGAACAC 1

RESULT 27
AX499947/c
LOCUS AX499947 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 1254 from Patent EP1229046.
ACCESSION AX499947
VERSION AX499947.1 GI:23382240
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 1254 07-AUG-2002;
Aeomica, Inc. (US)
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Query Match 58.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCGAGGAGAAACAGAC 742
Db 17 TCCGAGGAGAAACAGAC 2

RESULT 28
AX499948/c
LOCUS AX499948 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 1255 from Patent EP1229046.
ACCESSION AX499948
VERSION AX499948.1 GI:23382241
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 1255 07-AUG-2002;

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACACA 742
Db 16 TCCAGGAGAAACACA 1

RESULT 29
AX023982
LOCUS AX023982 19 bp DNA PAT 15-SEP-2000
DEFINITION Sequence 3 from Patent WO0004918.
ACCESSION AX023982
VERSION AX023982.1 GI:10184299
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kerkmann-Tucek,A.
TITLE Agents for the immunotherapy of tumoral diseases
JOURNAL Patent: WO 0004918-A 3 03-FEB-2000;
KERMANN TUCEK AIDA (DE)
FEATURES
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        /mol_type="unassigned DNA"
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Best Local Similarity 58.2%; Score 12.8; DB 1; Length 19;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAGAAC 744
Db 4 CCAGGAGAAACAGAAC 19

RESULT 30
AX255710/c
LOCUS AX255710 16 bp DNA PAT 10-OCT-2001
DEFINITION Sequence 131 from Patent WO0170982.
ACCESSION AX255710
VERSION AX255710.1 GI:16074765
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Beger,C., Barber,J. and Wong-Staal,F.
TITLE Bcr-a1 regulators and methods of use
JOURNAL Patent: WO 0170982-A 131 27-SEP-2001;
Immusol Incorporated (US) ; Beger, Carmela (DE)
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        /db_xref="taxon:32630"
        /note="Synthetic oligonucleotide"

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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAACAGAACACC 747

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FEATURES
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RESULT 31
AX076026/c
LOCUS AX076026 17 bp DNA PAT 06-FEB-2001
DEFINITION Sequence 2 from Patent WO0104358.
ACCESSION AX076026
VERSION AX076026.1 GI:12710679
KEYWORDS Hepatitis B virus
SOURCE Hepatitis B virus
ORGANISM Hepatitis B virus
REFERENCE 1
AUTHORS Stuyver,L., Maertens,G. and van Geyt,C.
TITLE Detection of anti-hepatitis b drug resistance
JOURNAL Patent: WO 0104358-A 2 18-JAN-2001;
INNOGENETICS N.V. (BE)
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Query Match
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
Db 14 GCCAGGAGAAACGG 1

RESULT 32
AX499949/c
LOCUS AX499949 17 bp DNA PAT 27-SEP-2002
DEFINITION Sequence 1256 from Patent EP1229046.
ACCESSION AX499949
VERSION AX499949.1 GI:23382242
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 1256 07-AUG-2002;
Aeomica, Inc. (US)
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        /db_xref="taxon:9606"

Query Match
Best Local Similarity 56.4%; Score 12.4; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACACA 740
Db 15 TCCAGGAGAAACACA 2

RESULT 33
AX499950/c
LOCUS AX499950 17 bp DNA PAT 27-SEP-2002
DEFINITION Sequence 1257 from Patent EP1229046.
ACCESSION AX499950
VERSION AX499950.1 GI:23382243
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

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Query Match	56.4%;	Score 12.4;	DB 1;	Length 18;	
Best Local Similarity	92.9%;	Pred. No. 59;			
Matches	13;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
Qy	728	GCACGAGAGAAACAG	741		
Db	18	GCATGAGAAACAG	5		
RESULT 36					
AR065607/c					
LOCUS	AR065607	18 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence 6 from patent US 5849534.				
ACCESSION	AR065607				
VERSION	AR065607.1	GI:5995823			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Grotendorst,G.R. and Iida,N.				
TITLE	DNA encoding leukocyte derived growth factor-2 (LDGF-2)				
JOURNAL	Patent: US 5849534-A 6 15-DEC-1998;				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	56.4%;	Score 12.4;	DB 1;	Length 18;	
Best Local Similarity	92.9%;	Pred. No. 59;			
Matches	13;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
Qy	732	GGAGAAACAGAAC	745		
Db	16	GCAGAAACAGAAC	3		
RESULT 37					
I06264/c					
LOCUS	I06264	18 bp	DNA	linear	PAT 02-DEC-1994
DEFINITION	Sequence 22 from Patent EP 0319052.				
ACCESSION	I06264				
VERSION	I06264.1	GI:590255			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Thomas Jnr,K.A. and Linemeyer,D.L.				
TITLE	Mutant acidic fibroblast growth factor				
JOURNAL	Patent: EP 0319052-A2 22 07-JUN-1989;				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	55.5%;	Score 12.2;	DB 1;	Length 18;	
Best Local Similarity	82.4%;	Pred. No. 64;			
Matches	14;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
Qy	732	GGAGAAACAGAACCG	748		
Db	17	GGAGAAAGTGACCCCG	1		
RESULT 38					
AR292914/c					
LOCUS	AR292914	18 bp	DNA	linear	PAT 12-JUN-2003
DEFINITION	Sequence 4649 from patent US 6537751.				
ACCESSION	AR292914				
VERSION	AR292914.1	GI:31680198			
KEYWORDS	Unknown.				


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JOURNAL Patent: WO 03025175-A 1473 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGAGAACAGAC 744
Db 15 CAGGAGACAGATC 1

RESULT 43
AX762877
LOCUS AX762877 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 6198 from Patent WO03040369.
ACCESSION AX762877
VERSION AX762877.1 GI:32257493
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 6198 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAACAG 741
Db 3 TCCAGGAGATCAG 17

RESULT 44
A67102/c
LOCUS A67102 18 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 269 from Patent WO9740193.
ACCESSION A67102
VERSION A67102.1 GI:4538473
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stuyver,L., Rossau,R. and Maertens,G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 269 30-OCT-1997;
INNOGENETICS NV (BE)
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAACAG 742
Db 18 GCCATGAGAACGGA 4

RESULT 45
A67104/c
LOCUS A67104 18 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 271 from Patent WO9740193.
ACCESSION A67104
VERSION A67104.1 GI:4538475
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stuyver,L., Rossau,R. and Maertens,G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 271 30-OCT-1997;
INNOGENETICS NV (BE)
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 75;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAACAG 742
Db 18 GCCATGAGAACGGA 4

RESULT 46
AR190011
LOCUS AR190011 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5499 from patent US 6346398.
ACCESSION AR190011
VERSION AR190011.1 GI:20235976
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5499 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAGACA 745
Db 2 GAGAAATAGACA 14

RESULT 47
AR324988
LOCUS AR324988 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2390 from patent US 6566127.
ACCESSION AR324988
VERSION AR324988.1 GI:33710796
KEYWORDS

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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 2390 20-MAY-2003;
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGACACA 745
Db 2 GAGAAATAGAAC 14

RESULT 48
AX499951/c
LOCUS      AX499951
DEFINITION Sequence 1258 from Patent EP1229046.
ACCESSION  AX499951
VERSION     AX499951.1 GI:23382244
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan,J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 1258 07-AUG-2002;
            Aeonica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAC 739
Db 13 TGCCAGGTGAAC 1

RESULT 49
AX674143/c
LOCUS      AX674143
DEFINITION Sequence 2588 from Patent WO03004526.
ACCESSION  AX674143
VERSION     AX674143.1 GI:29332491
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL     Patent: WO 03004526-A 2588 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
            source
            1..17

SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 2390 20-MAY-2003;
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAACACA 742
Db 17 CAGGAAAACACA 5

RESULT 50
AX732557/c
LOCUS      AX732557
DEFINITION Sequence 4191 from Patent WO03025175.
ACCESSION  AX732557
VERSION     AX732557.1 GI:30511900
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025175-A 4191 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGACACA 745
Db 17 GTGAAACAGACA 5

RESULT 51
BD266301/c
LOCUS      BD266301
DEFINITION Universal arrays.
ACCESSION  BD266301
VERSION     BD266301.1 GI:33076069
KEYWORDS    JP 2002539849-A/301.
            synthetic construct
            SOURCE      synthetic construct
            ORGANISM    artificial sequences.
            1 (bases 1 to 17)
            Fan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,E.S.,
            Lockhart,D.J., Ryder,T. and Sklar,P.
            Universal arrays
            Patent: JP 2002539849-A 301 26-NOV-2002;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
            OS Artificial Sequence
            PN JP 2002539849-A/301
            PD 26-NOV-2002
            PF 27-MAR-2000 JP 2000608794
            PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
            JIAN BING PAN,JOEL N HIRSCHHORN,XIAOHUA
            HUANG,PAUL KAPLAN,ERIC
            PI S LANDER,
            PI DAVID J LOCKHART,THOMAS RYDER,PAMELA SKLAR
            PC C12Q1/68,C12M1/00,C12N15/09,C12N15/09,C12N15/09,G01N33/53, PC
            G01N33/566.

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PC GOIN37/00,C12N15/00,C12N15/00,C12N15/00
CC Primer
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
source 1..17
/organism="Artificial Sequence".
Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGAA 743
Db 16 GCCATGAGAGACGGA 1

RESULT 52
E54495/c
LOCUS AR325471/c 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Heat-resistant lysine biosynthesis enzyme gene of thermophilic
coryneform bacterium.
ACCESSION E54495
VERSION E54495.1 GI:22553552
KEYWORDS JP 2001120270-A/19.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Itaya,M., Kimura,E., Kawara,Y. and Sugimoto,S.
TITLE Heat-resistant lysine biosynthesis enzyme gene of thermophilic
coryneform bacterium
JOURNAL Patent: JP 2001120270-A 19 08-MAY-2001;
AJINOMOTO CO INC
COMMENT OS Artificial Sequence
PS JP 2001120270-A/19
PD 08-MAY-2001
PF 01-NOV-1999 JP 1999311148
PI MINORU ITAYA,EICHIRO KIMURA,YOSHIO KAWARA,SHINICHI SUGIMOTO PC
C12N15/09// (C12N15/09,C12R1:15),C12N15/00,(C12N15/00,C12R1:15) CC
Description of Artificial Sequence: primer for LA cloning of CC
lysa

FH Key Location/Qualifiers
FEATURES
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGAA 743
Db 17 GCCACGAGGATCAGAA 2

RESULT 53
AR190548/c
LOCUS AR190548 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6036 from patent US 6346398.
ACCESSION AR190548
VERSION AR190548.1 GI:20236513
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.

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TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6036 12-FEB-2002;
FEATURES
Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGAA 743
Db 16 GCCAGGAGACGTA 1

RESULT 54
AR325471/c
LOCUS AR325471 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2873 from patent US 6566127.
ACCESSION AR325471
VERSION AR325471.1 GI:33711279
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2873 20-MAY-2003;
FEATURES
Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGAA 743
Db 16 GCCAGGAGACGTA 1

RESULT 55
AX227611
LOCUS AX227611 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 983 from Patent WO0157206.
ACCESSION AX227611
VERSION AX227611.1 GI:15556752
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Fattaey,A.R., Jarvis,T., McSwiggen,J., Bocher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 983 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGACAC 746

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LOCUS       AR362726               15 bp      DNA          linear      PAT 03-SEP-2003
DEFINITION   Sequence 60 from patent US 5182195.
ACCESSION   AR362726
VERSION     AR362726.1  GI:34423106
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Nakahama,K., Kaisho,Y. and Yoshimura,K.
TITLE       Method for increasing gene expression using protease deficient
            yeasts
JOURNAL     Patent: US 5182195-A 60 26-JAN-1993;
FEATURES    Location/Qualifiers
            source      1..15
                        /organism="unknown"
                        /mol_type="genomic DNA"
Query Match      50.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAACAGAC 742
Db 2 GGAGAACAGAC 12

RESULT 61
I61456/c
LOCUS       I61456               15 bp      DNA          linear      PAT 07-OCT-1997
DEFINITION   Sequence 10 from patent US 5658780.
ACCESSION   I61456
VERSION     I61456.1  GI:2479404
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE       Real a targeted ribozymes
JOURNAL     Patent: US 5658780-A 10 19-AUG-1997;
FEATURES    Location/Qualifiers
            source      1..15
                        /organism="unknown"
                        /mol_type="unassigned DNA"
Query Match      49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAC 744
Db 14 AGGAGAACAGATC 1

RESULT 62
AX635865/c
LOCUS       AX635865             15 bp      RNA          linear      PAT 21-FEB-2003
DEFINITION   Sequence 3004 from Patent EPI260586.
ACCESSION   AX635865
VERSION     AX635865.1  GI:28471479
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE    1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE       Method and reagent for inhibiting the expression of disease related
            genes

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JOURNAL     Patent: EP 1260586-A 3004 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
            source      1..15
                        /organism="unidentified"
                        /mol_type="unassigned RNA"
                        /db_xref="taxon:32644"
Query Match      49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAC 744
Db 14 AGGAGAACAGATC 1

RESULT 63
BD208396/c
LOCUS       BD208396             15 bp      RNA          linear      PAT 17-JUL-2003
DEFINITION   Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD208396
VERSION     BD208396.1  GI:33018166
KEYWORDS    JP 2002512791-A/1986.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE       Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
JOURNAL     Patent: JP 2002512791-A 1986 09-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Hepatitis virus (hepatitis C virus)
            PN JP 2002512791-A/1986
            PD 08-MAY-2002
            PF 26-APR-1999 JP 2000545991
            PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
            PS 25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
            LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
            PAVCO,
            PI DENNIS MACEJAK
            PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC A61K37/66,
            PC C12N15/00
            CC Enzymatic nucleic acid treatment of diseases or conditions CC
            related to
            CC hepatitis C virus infection.
            FH Key
            FT source      1..15
                        /organism='Hepatitis virus (hepatitis C PT
                        virus)';
            FT Location/Qualifiers
            source      1..15
                        /organism="unidentified"
                        /mol_type="genomic RNA"
                        /db_xref="taxon:32644"
Query Match      49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAACAGAACACCG 748
Db 15 GAACAGTACACTG 2

RESULT 64
A09424/c
LOCUS       A09424
DEFINITION   Oligonucleotide (a6).
ACCESSION   A09424

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VERSION      A09424.1  GI:490529
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Ueda,I., Niwa,M., Saitoh,Y., Sato,S. and Yamada,H.
TITLE        Process for production of somatostatin
JOURNAL      Patent: EP 0197558-A 30 15-OCT-1986;
FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES     Location/Qualifiers
             source
             1..16
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"

Query Match      49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGCAGAAACACC 747
Db      16 AGAAGCAGAAACACC 3

RESULT 67
A35095/c
LOCUS      A35095
DEFINITION Synthetic IGF-I gene oligo.
ACCESSION A35095
VERSION    A35095.1  GI:1926754
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1 (bases 1 to 16)
AUTHORS    Ueda,I., Niwa,M., Saitoh,S., Saitoh,Y. and Kusunoki,C.
TITLE      Process for production of insulin-like growth factor I and plasmid
JOURNAL    Patent: EP 0219814-A 45 29-APR-1987;
FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES    Location/Qualifiers
            source
            1..16
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match      49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGCAGAAACACC 747
Db      16 AGAAGCAGAAACACC 3

RESULT 68
AX076025/c
LOCUS      AX076025
DEFINITION Sequence 1 from Patent WO0104358.
ACCESSION  AX076025
VERSION     AX076025.1  GI:12710678
KEYWORDS    Hepatitis B virus
SOURCE      Hepatitis B virus
ORGANISM    Hepatitis B virus
REFERENCE    1
AUTHORS      Stuyver,L., Maertens,G. and van Geyt,C.
TITLE        Detection of anti-hepatitis b drug resistance
JOURNAL      Patent: WO 0104358-A 1 18-JAN-2001;
              INNOGENETICS N.V. (BE)
FEATURES     Location/Qualifiers
             source
             1..16
               /organism="Hepatitis B virus"
               /mol_type="unassigned DNA"
               /db_xref="taxon:10407"

Query Match      49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      728 GCCAGGAGAAACAG 741
Db      14 GCCAGGAGAAACGG 1

VERSION      A09424.1  GI:490529
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Ueda,I., Niwa,M., Saitoh,Y., Sato,S. and Yamada,H.
TITLE        Process for production of somatostatin
JOURNAL      Patent: EP 0197558-A 30 15-OCT-1986;
FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES     Location/Qualifiers
             source
             1..16
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"

Query Match      49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGCAGAAACACC 747
Db      16 AGAAGCAGAAACACC 3

RESULT 65
A10627/c
LOCUS      A10627
DEFINITION Oligonucleotide (A6).
ACCESSION  A10627
VERSION    A10627.1  GI:490755
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1 (bases 1 to 16)
AUTHORS    Ueda,I., Niwa,M., Saitoh,Y., Sato,S., Ono,H. and Kitaguchi,T.
TITLE      Process for production of gamma-interferon
JOURNAL    Patent: EP 0176916-A 12 09-APR-1986;
FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES    Location/Qualifiers
            source
            1..16
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match      49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGCAGAAACACC 747
Db      16 AGAAGCAGAAACACC 3

RESULT 66
A11575/c
LOCUS      A11575
DEFINITION Oligonucleotide 'a6'.
ACCESSION  A11575
VERSION    A11575.1  GI:491117
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1 (bases 1 to 16)
AUTHORS    Ueda,I., Niwa,M., Saitoh,Y., Sato,S., Ono,H. and Kitaguchi,T.
TITLE      59 Valine insulin-like growth factor I and process for production thereof
JOURNAL    Patent: EP 0158892-A 71 23-OCT-1985;
FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES    Location/Qualifiers
            source
            1..16

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RESULT 69
LOCUS 128559 12 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 12 from patent US 5571937.
ACCESSION 128559
VERSION 128559.1 GI:1819335
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Watanabe, K.A., Ren, W.-Y. and Weil, R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5571937-A 12 05-NOV-1996;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 90;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGA 742
Db 1 AGGAGAAACAGA 12
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RESULT 70
LOCUS 158721 12 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 12 from patent US 5652350.
ACCESSION 158721
VERSION 158721.1 GI:2477959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Watanabe, K.A., Ren, W.-Y. and Weil, R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5652350-A 12 29-JUL-1997;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 90;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGA 742
Db 1 AGGAGAAACAGA 12
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RESULT 71
LOCUS A40588 14 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 125 from Patent WO9425578.
ACCESSION A40588
VERSION A40588.1 GI:2296623
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
TITLE EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 125 10-NOV-1994;
BIOGNOSTIK GES (DE)

FEATURES source Location/Qualifiers
1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGA 742
Db 1 AGGAGAAACAGA 12
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RESULT 72
LOCUS A89112 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1260 from Patent WO9833904.
ACCESSION A89112
VERSION A89112.1 GI:6737682
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1260 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGA 742
Db 1 AGGAGAAACAGA 12
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RESULT 73
LOCUS A89603 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1751 from Patent WO9833904.
ACCESSION A89603
VERSION A89603.1 GI:6738173
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1751 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AAACAGAACACC 747
Db 12 AAACAGAACACC 1
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RESULT 74
LOCUS      AR061873              14 bp      DNA      linear      PAT 28-SEP-1999
DEFINITION Sequence 4 from patent US 5843661.
ACCESSION  AR061873
VERSION     AR061873.1  GI:5989564
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Rothmund,P.W.K.
TITLE      Method for construction universal DNA based molecular turing
machine
JOURNAL    Patent: US 5843661-A 4 01-DEC-1998;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAACAC 746
Db 2 GAAACAGTACAC 13

RESULT 75
LOCUS      AR232868              14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 125 from patent US 6455689.
ACCESSION  AR232868
VERSION     AR232868.1  GI:27275206
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor-.beta.
            (TGF-.beta.)
JOURNAL    Patent: US 6455689-A 125 24-SEP-2002;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 1 AGGAGAGACAGA 12

RESULT 76
LOCUS      AR407925/c              14 bp      RNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6632057.
ACCESSION  AR407925
VERSION     AR407925.1  GI:40157912
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Fauchet,C.R.J.

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TITLE      Fixing unit with an end imprint in a threaded terminal portion
JOURNAL    Patent: US 6632057-A 18 14-OCT-2003;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 14 AGCAGAAACAGA 3

RESULT 77
LOCUS      AX030163              14 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 125 from Patent EP1008649.
ACCESSION  AX030163
VERSION     AX030163.1  GI:10190380
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
            and Schlingensiepen,R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2 (tgf-b2)
JOURNAL    Patent: EP 1008649-A 125 14-JUN-2000;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 1 AGGAGAGACAGA 12

RESULT 78
LOCUS      AX316484              14 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 125 from Patent EP1160319.
ACCESSION  AX316484
VERSION     AX316484.1  GI:17899657
KEYWORDS   .
SOURCE     unidentified
            unclassified.
ORGANISM   unidentified
            unclassified.
REFERENCE  1
AUTHORS    Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for the treatment of immunosuppressive
            effects of transforming growth factor-beta (tgf-beta)
JOURNAL    Patent: EP 1160319-A 125 05-DEC-2001;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="Description of unknown: unknown"

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Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 1 AGGAGAACAGCA 12

RESULT 79
BD066625
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066625
VERSION BD066625.1 GI:22612228
KEYWORDS JP 2001511000-A/1260.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1260 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1260
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source
FT Location/Qualifiers
1..14 /organism='Unknown'

FEATURES
source
1..14 Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 1 AGGAGAACAGCA 12

RESULT 80
BD067116/c
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD067116
VERSION BD067116.1 GI:22612719
KEYWORDS JP 2001511000-A/1751.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1751 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1751
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 1 AGGAGAACAGCA 12

RESULT 81
BD067116/c
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD067116
VERSION BD067116.1 GI:22612719
KEYWORDS JP 2001511000-A/1260.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1260 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1260
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source
FT Location/Qualifiers
1..14 /organism='Unknown'

FEATURES
source
1..14 Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 1 AGGAGAACAGCA 12

RESULT 82
ARI80064
LOCUS 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 132 from patent US 6333152.
ACCESSION ARI80064
VERSION ARI80064.1 GI:20222097
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6333152-A 132 25-DEC-2001;
FEATURES
source
1..15 Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 13 AGGGGAAACAGCA 2

RESULT 82
ARI80064
LOCUS 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 132 from patent US 6333152.
ACCESSION ARI80064
VERSION ARI80064.1 GI:20222097
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6333152-A 132 25-DEC-2001;
FEATURES
source
1..15 Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGAGGAAA 738
Db 3 TCCAGGAGGAAA 14

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RESULT 83
ARI180799
LOCUS       ARI180799             15 bp    DNA             linear    PAT 20-APR-2002
DEFINITION   Sequence 867 from patent US 633152.
ACCESSION    ARI180799
VERSION      ARI180799.1  GI:20222832
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE        Gene expression profiles in normal and cancer cells
JOURNAL      Patent: US 633152-A 867 25-DEC-2001;
FEATURES     Location/Qualifiers
             source          1..15
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      727  TGGCAGGAGGAA 738
Db      3  TGGCAGGAGGAA 14

RESULT 84
AX635867/c
LOCUS       AX635867             15 bp    RNA             linear    PAT 21-FEB-2003
DEFINITION   Sequence 3006 from Patent EP1260586.
ACCESSION    AX635867
VERSION      AX635867.1  GI:28471481
KEYWORDS     .
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1
AUTHORS      Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
             Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
             Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
             Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
             Woolf,T.
TITLE        Method and reagent for inhibiting the expression of disease related
JOURNAL      Genes
PATENT       Patent: EP 1260586-A 3006 27-NOV-2002;
FEATURES     RIBOZYME PHARMACEUTICALS, INC. (US)
             Location/Qualifiers
             source          1..15
             /organism="unidentified"
             /mol_type="unassigned RNA"
             /db_xref="taxon:32644"

Query Match      47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731  AGGAGAAACAGA 742
Db      13  AGGAGAAACAGA 2

RESULT 85
A22593
LOCUS       A22593             16 bp    DNA             linear    PAT 24-OCT-1994
DEFINITION   Oligonucleotide.
ACCESSION    A22593
VERSION      A22593.1  GI:641563
KEYWORDS     .
SOURCE       Petunia x hybrida
ORGANISM     Petunia x hybrida

Query Match      47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731  AGGAGAAACAGA 742
Db      4  AGGAGAAACAGA 15

RESULT 86
AR096276
LOCUS       AR096276             16 bp    DNA             linear    PAT 08-SEP-2000
DEFINITION   Sequence 4 from patent US 6005167.
ACCESSION    AR096276
VERSION      AR096276.1  GI:10024937
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Van Tunen,A.Johannes., Van Der Meer,I.Maria. and
             Mol,J.Nicolaas.Maria.,
TITLE        Male-sterile plants, method for obtaining male-sterile plants and
             recombinant DNA for use therein
JOURNAL      Patent: US 6005167-A 4 21-DEC-1999;
FEATURES     Location/Qualifiers
             source          1..16
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731  AGGAGAAACAGA 742
Db      4  AGGAGAAACAGA 15

RESULT 87
AX076029/c
LOCUS       AX076029             16 bp    DNA             linear    PAT 06-FEB-2001
DEFINITION   Sequence 5 from Patent WO0104358.
ACCESSION    AX076029
VERSION      AX076029.1  GI:12710682
KEYWORDS     .
SOURCE       Hepatitis B virus
ORGANISM     Hepatitis B virus
REFERENCE    1
AUTHORS      Stuyver,L., Maertens,G. and van Geyt,C.
TITLE        Detection of anti-hepatitis b drug resistance
JOURNAL      Patent: WO 0104358-A 5 18-JAN-2001;
             INNOGENETICS N.V. (BE)
FEATURES     Location/Qualifiers
             source          1..16
             /organism="Hepatitis B virus"
             /mol_type="unassigned DNA"
             /db_xref="taxon:10407"

Query Match      47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731  AGGAGAAACAGA 742
Db      4  AGGAGAAACAGA 15

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Petunia.

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Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAC 739
DB 13 GCCATGAGAAC 2

RESULT 88
AX255620
LOCUS AX255620
DEFINITION Sequence 41 from Patent WO0170982.
ACCESSION AX255620
VERSION AX255620.1 GI:16074676
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Beger,C., Barber,J. and Wong-Staal,F.
AUTHORS Brca-1 regulators and methods of use
TITLE Patent: WO 0170982-A 41 27-SEP-2001;
JOURNAL Immusol Incorporated (US) ; Beger, Carmela (DE)
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
DB 5 AAAGAGAACACC 16

RESULT 89
AX255663
LOCUS AX255663
DEFINITION Sequence 84 from Patent WO0170982.
ACCESSION AX255663
VERSION AX255663.1 GI:16074719
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Beger,C., Barber,J. and Wong-Staal,F.
AUTHORS Brca-1 regulators and methods of use
TITLE Patent: WO 0170982-A 84 27-SEP-2001;
JOURNAL Immusol Incorporated (US) ; Beger, Carmela (DE)
FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
DB 5 AAAGAGAACACC 16

RESULT 90
AX452095/c
LOCUS AX452095/c
DEFINITION Sequence 2 from Patent EP1211326.
ACCESSION AX452095
VERSION AX452095.1 GI:21712097
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Blair,E.D., Snowden,B.W. and Ward,C.L.
AUTHORS Diagnostic method
TITLE Patent: EP 1211326-A 2 05-JUN-2002;
JOURNAL GLAXO GROUP LIMITED (GB)
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 743
DB 16 GGGGAAACAGAA 5

RESULT 91
BD208458/c
LOCUS BD208458
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD208458
VERSION BD208458.1 GI:33018228
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2048 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2048
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions
related to
CC hepatitis C virus infection.
PH Key
FT source
1..15
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
/note="Primer"

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 729 CCAGGAGAAACAGAA 743
Db 15 CCAGGAGAAAGGAAAA 1

RESULT 92
BD208459/c
LOCUS
DEFINITION
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION
BD208459
VERSION
BD208459.1 GI:33018229
KEYWORDS
JP 2002512791-A/2049.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Blatt L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
TITLE
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL
Patent: JP 2002512791-A 2049 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2049
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
hepatitis C virus infection.
FH Key
FT source
1. .15
/organism='Hepatitis virus (hepatitis C FT
virus)'
FEATURES
source
Location/Qualifiers
1. .15
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 15 GCCAGGAGAAAGGAAA 1

RESULT 93
AR123024
LOCUS
DEFINITION
Sequence 15 from patent US 6168943.
ACCESSION
AR123024
VERSION
AR123024.1 GI:14107990
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Rose, J.K.
TITLE
Methods for making modified recombinant vesiculoviruses
JOURNAL
Patent: US 6168943-A 15 02-JAN-2001;
FEATURES
source
Location/Qualifiers
1. .11

QY 729 CCAGGAGAAACAGAA 743
Db 15 CCAGGAGAAAGGAAAA 1

RESULT 92
BD208459/c
LOCUS
DEFINITION
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION
BD208459
VERSION
BD208459.1 GI:33018229
KEYWORDS
JP 2002512791-A/2049.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Blatt L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
TITLE
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL
Patent: JP 2002512791-A 2049 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2049
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
hepatitis C virus infection.
FH Key
FT source
1. .15
/organism='Hepatitis virus (hepatitis C FT
virus)'
FEATURES
source
Location/Qualifiers
1. .15
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 15 GCCAGGAGAAAGGAAA 1

RESULT 93
AR123024
LOCUS
DEFINITION
Sequence 15 from patent US 6168943.
ACCESSION
AR123024
VERSION
AR123024.1 GI:14107990
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Rose, J.K.
TITLE
Methods for making modified recombinant vesiculoviruses
JOURNAL
Patent: US 6168943-A 15 02-JAN-2001;
FEATURES
source
Location/Qualifiers
1. .11

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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 45.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 CAGGAGAAAC 739
Db 2 CAGGAGAAAC 11

RESULT 94
AX626398
LOCUS
DEFINITION
Sequence 3439 from Patent WO02053774.
ACCESSION
AX626398
VERSION
AX626398.1 GI:28454436
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Petersohn, D., Conradt, M. and Hofmann, K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 3439 11-JUN-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
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/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match 45.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
Db 1 GGAGAAACAG 10

RESULT 95
AR180388
LOCUS
DEFINITION
Sequence 456 from patent US 6333152.
ACCESSION
AR180388
VERSION
AR180388.1 GI:20222421
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W.
TITLE
Gene expression profiles in normal and cancer cells
JOURNAL
Patent: US 6333152-A 456 25-DEC-2001;
FEATURES
source
Location/Qualifiers
1. .15
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
Db 5 GGAGAAACAG 14

RESULT 96
BD208460/c

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LOCUS BD208460 15 bp RNA linear PAT 17-JUL-2003
 DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
 ACCESSION BD208460
 VERSION BD208460.1 GI:33018230
 KEYWORDS JP 2002512791-A/2050.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Blatt, L., McSwiggen, J. A., Roberts, E., Pavco, P. A., and Macejak, D.
 TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
 JOURNAL Patent: JP 2002512791-A 2050 08-MAY-2002;
 COMMENT RIBOSYME PHARMACEUTICALS INC
 OS Hepatitis virus (hepatitis C virus)
 PN JP 2002512791-A/2050
 PD 08-MAY-2002
 PF 26-APR-1999 JP 2000545991
 PR 27-APR-1998 US 60/083217, 19-SEP-1998 US 60/100942 PR
 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
 LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
 PAVCO,
 PI DENNIS MACEJAK
 PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
 PC A61K37/66,
 PC C12N15/00
 CC Enzymatic nucleic acid treatment of diseases or conditions CC
 related to
 CC hepatitis C virus infection.
 FH Key Location/Qualifiers
 FT source 1..15
 FT virus)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:32644"
 Query Match 45.5%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAA 737
 Db 13 GCCAGGAGAA 4
 RESULT 97
 A25806
 LOCUS A25806 14 bp DNA linear PAT 14-MAR-1995
 DEFINITION Polynucleotide 14CS.
 ACCESSION A25806
 VERSION A25806.1 GI:904774
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Patent: FR 2680520-A 13 26-FEB-1993;
 JOURNAL Location/Qualifiers
 FEATURES source 1..14
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 733 GAGAAACAGACA 745

Db 1 GACAAACAGACA 13
 RESULT 98
 A40589
 LOCUS A40589 14 bp DNA linear PAT 05-MAR-1997
 DEFINITION Sequence 126 from Patent WO9425578.
 ACCESSION A40589
 VERSION A40589.1 GI:2296624
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS
 TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
 JOURNAL Patent: WO 9425578-A 126 10-NOV-1994;
 COMMENT BIOGNOSTIK GES (DE)
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAAACA 740
 Db 2 GCAAGGAGAGCA 14
 RESULT 99
 A87922
 LOCUS A87922 14 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 70 from Patent WO9833904.
 ACCESSION A87922
 VERSION A87922.1 GI:6736492
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Brysch, W. and Schlingensiepen, K.
 TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 JOURNAL Patent: WO 9833904-A 70 06-AUG-1998;
 COMMENT BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
 FEATURES Location/Qualifiers
 source 1..14
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 729 CCAGGAGAAACAG 741
 Db 1 CCATGAGAGCAG 13
 RESULT 100
 A89113
 LOCUS A89113 14 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 1261 from Patent WO9833904.
 ACCESSION A89113
 VERSION A89113.1 GI:6737683
 KEYWORDS
 SOURCE unidentified

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ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingsiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1261 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 14;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACCA 740
Db 2 GCAAGGAGAACCA 14

RESULT 101
LOCUS A89889 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 70 from Patent EP0856579.
ACCESSION A89889
VERSION A89889.1 GI:6738403
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingsiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 70 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
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            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 14;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAACAG 741
Db 1 CCATGAGAGACAG 13

RESULT 102
LOCUS AR029997 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 186 from patent US 5861244.
ACCESSION AR029997
VERSION AR029997.1 GI:5943211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 186 19-JAN-1999;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 14;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAA 743
Db 13 AGGAGAGACAGCA 13

RESULT 103
LOCUS AR030009 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 198 from patent US 5861244.
ACCESSION AR030009
VERSION AR030009.1 GI:5943223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 198 19-JAN-1999;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
    source
        1..14
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            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 14;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAA 743
Db 13 AGGAGAGACAGCA 13

RESULT 104
LOCUS I26228 14 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 13 from patent US 5556955.
ACCESSION I26228
VERSION I26228.1 GI:1606098
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Vergnaud,G.
TITLE Process for detection of new polymorphic loci in a DNA sequence,
nucleotide sequences forming hybridization probes and their
applications
JOURNAL Patent: US 5556955-A 13 17-SEP-1996;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
    source
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 14;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAACAGAACCA 745
Db 1 GACAAACAGACCA 13

RESULT 105
LOCUS I52188/c 14 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5646031.
ACCESSION I52188
VERSION I52188.1 GI:2473389
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS DeYoung,M.Beth., Siwkowski,A.M. and Hampel,A.E.
TITLE SARW and scRWI hairpin ribozymes
JOURNAL Patent: US 5646031-A 11 08-JUL-1997;
FEATURES
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACCCG 748
Db 14 AACAGAACTCGG 2

RESULT 106
LOCUS 152193/c
DEFINITION Sequence 16 from patent US 5646031.
ACCESSION 152193
VERSION 152193.1 GI:2473394
KEYWORDS
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS DeYoung,M.Beth., Siwkowski,A.M. and Hampel,A.E.
TITLE SARW and scRWI hairpin ribozymes
JOURNAL Patent: US 5646031-A 16 08-JUL-1997;
FEATURES
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACCCG 748
Db 14 AACAGAACTCGG 2

RESULT 107
LOCUS AR232869
DEFINITION Sequence 126 from patent US 6455689.
ACCESSION AR232869
VERSION AR232869.1 GI:27275207
KEYWORDS
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 126 24-SEP-2002;
FEATURES
    source
        1..14
        /organism="unknown"
        /mol_type="genomic DNA"
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS DeYoung,M.Beth., Siwkowski,A.M. and Hampel,A.E.
TITLE SARW and scRWI hairpin ribozymes
JOURNAL Patent: US 5646031-A 11 08-JUL-1997;
FEATURES
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        /mol_type="unassigned DNA"
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACCCG 748
Db 14 AACAGAACTCGG 2

RESULT 108
LOCUS AX030164
DEFINITION Sequence 126 from Patent EPI008649.
ACCESSION AX030164
VERSION AX030164.1 GI:10190381
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 126 14-JUN-2000;
FEATURES
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        Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACA 740
Db 2 GCAAGGAGAGCA 14

RESULT 109
LOCUS AX316485
DEFINITION Sequence 126 from Patent EPI160319.
ACCESSION AX316485
VERSION AX316485.1 GI:17899658
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 126 05-DEC-2001;
FEATURES
    source
        1..14
        Location/Qualifiers
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="Description of unknown: unknown"
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACA 740
Db 2 GCAAGGAGAGCA 14

RESULT 110
LOCUS AX571850
DEFINITION Sequence 126 from Patent EPI160319.
ACCESSION AX316485
VERSION AX316485.1 GI:17899658
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 126 05-DEC-2001;
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="Description of unknown: unknown"
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACA 740
Db 2 GCAAGGAGAGCA 14
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LOCUS       AX571850               14 bp      DNA      linear      PAT 29-MAY-2003
DEFINITION   Sequence 9 from Patent WO02077274.
ACCESSION    AX571850
VERSION      AX571850.1  GI:26003984
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE    1
AUTHORS      Blanche,F. and Cameron,B.
TITLE        Methods for purifying and detecting double stranded dna target
              sequences by triple helix interaction
JOURNAL      Patent: WO 02077274-A 9 03-OCT-2002;
              Aventis Pharma S.A. (FR)
FEATURES     source
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              /location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db 2 AGGAGAGAGAGAA 14

RESULT 111
BD065435
LOCUS       BD065435               14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION   An antisense oligonucleotide preparation method.
ACCESSION    BD065435
VERSION      BD065435.1  GI:22611038
KEYWORDS     JP 2001511000-A/70.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Schlingensiepen,K.H. and Brysch,W.
TITLE        An antisense oligonucleotide preparation method
JOURNAL      Patent: JP 2001511000-A 70 07-AUG-2001;
              BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT      OS Unknown
              PN JP 2001511000-A/70
              PD 07-AUG-2001
              PF 30-JAN-1998 JP 1998532533
              PR 31-JAN-1997 EP 97101531.8
              PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
              PC C12N15/11,C07H21/04,A61K31/70
              CC An antisense oligonucleotide preparation method FH Key
              Location/Qualifiers
              FT source
              1..14
              /location/Qualifiers
              /organism="unknown"

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db 2 AGGAGAGAGAGAA 14

RESULT 111
BD065435
LOCUS       BD065435               14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION   An antisense oligonucleotide preparation method.
ACCESSION    BD065435
VERSION      BD065435.1  GI:22611038
KEYWORDS     JP 2001511000-A/70.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Schlingensiepen,K.H. and Brysch,W.
TITLE        An antisense oligonucleotide preparation method
JOURNAL      Patent: JP 2001511000-A 70 07-AUG-2001;
              BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT      OS Unknown
              PN JP 2001511000-A/70
              PD 07-AUG-2001
              PF 30-JAN-1998 JP 1998532533
              PR 31-JAN-1997 EP 97101531.8
              PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
              PC C12N15/11,C07H21/04,A61K31/70
              CC An antisense oligonucleotide preparation method FH Key
              Location/Qualifiers
              FT source
              1..14
              /location/Qualifiers
              /organism="unknown"

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAG 741
Db 1 CCATGAGAGAGAG 13

RESULT 112
BD066626
LOCUS       BD066626               14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION   An antisense oligonucleotide preparation method.
ACCESSION    BD066626
VERSION      BD066626.1  GI:22612229
KEYWORDS     JP 2001511000-A/1261.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Schlingensiepen,K.H. and Brysch,W.
TITLE        An antisense oligonucleotide preparation method
JOURNAL      Patent: JP 2001511000-A 1261 07-AUG-2001;
              BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT      OS Unknown
              PN JP 2001511000-A/1261
              PD 07-AUG-2001
              PF 30-JAN-1998 JP 1998532533
              PR 31-JAN-1997 EP 97101531.8
              PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
              PC C12N15/11,C07H21/04,A61K31/70
              CC An antisense oligonucleotide preparation method FH Key
              Location/Qualifiers
              FT source
              1..14
              /location/Qualifiers
              /organism="unknown"

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAGACA 740
Db 2 GCAAGGAGAGACA 14

RESULT 113
BD209300/c
LOCUS       BD209300/c             14 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION   Enzymatic nucleic acid treatment of diseases or conditions related
              to hepatitis C virus infection.
ACCESSION    BD209300
VERSION      BD209300.1  GI:33019070
KEYWORDS     JP 2002512791-A/2890.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE        Enzymatic nucleic acid treatment of diseases or conditions related
              to hepatitis C virus infection
JOURNAL      Patent: JP 2002512791-A 2890 08-MAY-2002;
              RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Hepatitis virus (hepatitis C virus)
              PN JP 2002512791-A/2890
              PD 08-MAY-2002
              PF 26-APR-1999 JP 2000545991
              PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
              25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
              LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
              PAVCO.
              PI DENNIS MACEJAK
              PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
              A61K37/66,
              PC C12N15/00
              CC Enzymatic nucleic acid treatment of diseases or conditions
              related to
              hepatitis C virus infection.
              PH Key
              FT source
              1..14

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FT          /organism='Hepatitis virus (hepatitis C FT
virus)',
Location/Qualifiers
1. .14
/organism="unidentified"
/db_type="genomic RNA"
/db_xref="taxon:32644"

Query Match      44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 744
13 GGTGAAACAGTAC 1

RESULT 114
AR130724/c
LOCUS      AR130724      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6190866.
ACCESSION  AR130724
VERSION     AR130724.1 GI:14119049
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Nielsen,P.E. and Good,L.
TITLE      Methods of bacterial gene function determination using peptide
nucleic acids
JOURNAL    Patent: US 6190866-A 11 20-FEB-2001;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="unassigned DNA"

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
15 AGGAGAAAGAGTA 3

RESULT 115
AR180392/c
LOCUS      AR180392      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 460 from patent US 6333152.
ACCESSION  AR180392
VERSION     AR180392.1 GI:20222425
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Vogelstein,B., Kinler,K.W., Zhang,L. and Zhou,W.
TITLE      Gene expression profiles in normal and cancer cells
JOURNAL    Patent: US 6333152-A 460 25-DEC-2001;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="unassigned DNA"

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACA 740
15 GCCAGCAGAAACA 3

FT          /organism='Hepatitis virus (hepatitis C FT
virus)',
Location/Qualifiers
1. .14
/organism="unidentified"
/db_type="genomic RNA"
/db_xref="taxon:32644"

Query Match      44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 744
13 GGTGAAACAGTAC 1

RESULT 114
AR130724/c
LOCUS      AR130724      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6190866.
ACCESSION  AR130724
VERSION     AR130724.1 GI:14119049
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Nielsen,P.E. and Good,L.
TITLE      Methods of bacterial gene function determination using peptide
nucleic acids
JOURNAL    Patent: US 6190866-A 11 20-FEB-2001;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="unassigned DNA"

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
15 AGGAGAAAGAGTA 3

RESULT 115
AR180392/c
LOCUS      AR180392      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 460 from patent US 6333152.
ACCESSION  AR180392
VERSION     AR180392.1 GI:20222425
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Vogelstein,B., Kinler,K.W., Zhang,L. and Zhou,W.
TITLE      Gene expression profiles in normal and cancer cells
JOURNAL    Patent: US 6333152-A 460 25-DEC-2001;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="unassigned DNA"

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACA 740
15 GCCAGCAGAAACA 3
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RESULT 116
AR235561
LOCUS      AR235561      15 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 60 from patent US 6461810.
ACCESSION  AR235561
VERSION     AR235561.1 GI:27278782
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Fresco,J.R. and Johnson,M.D.
TITLE      Triplex in-situ hybridization
JOURNAL    Patent: US 6461810-A 60 08-OCT-2002;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="genomic DNA"

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
2 AGTGAAAAGAA 14

RESULT 117
AR370348/c
LOCUS      AR370348      15 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION Sequence 11 from patent US 6300318.
ACCESSION  AR370348
VERSION     AR370348.1 GI:34606876
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Nielsen,P.E. and Good,L.
TITLE      Antibacterial and antibiotic methods using peptide nucleic acids
and pharmaceutical compositions therefor
JOURNAL    Patent: US 6300318-A 11 09-OCT-2001;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="genomic DNA"

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
15 AGGAGAAAGAGTA 3

RESULT 118
AX009449/c
LOCUS      AX009449      15 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO9961662.
ACCESSION  AX009449
VERSION     AX009449.1 GI:9996735
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS    Shchepinov,M.S. and Southern,E.M.
TITLE      Polynucleotide multimers and their use in hybridisation assays
JOURNAL    Patent: WO 961662-A 2 02-DEC-1999;
           SHCHEPINOV MIKHAIL SERGEEVICH (GB); SOUTHERN EDWIN MELLOR (GB);
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ISIS INNOVATION (GB)
FEATURES             Location/Qualifiers
     source             1..15
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Oligonucleotide"

Query Match          44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGAA 743
Db 14 AAGAGAAAGAGAA 2

RESULT 119
BD005884/c
LOCUS             15 bp DNA linear PAT 31-JAN-2002
DEFINITION       Novel probes for the detection of Mycobacteri-
ACCESSION       BD005884
VERSION         BD005884.1 GI:18634255
KEYWORDS        JP 2001501825-A/95.
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 15)
AUTHORS        Stender,H., Lund,K. and Mollerup,T.A.
TITLE          Novel probes for the detection of Mycobacteri-
JOURNAL        Patent: JP 2001501825-A 95 13-FEB-2001,
              DAKO AS

COMMENT
OS Unidentified
PN JP 2001501825-A/95
PD 13-FEB-2001
PF 03-OCT-1997 JP 1998517095
PR 04-OCT-1996 DK 1096/96,18-OCT-1996 DK 1156/96 PR
PY 05-MAY-1997 DK 0512/97
PI HENRIK STENDER,KARE LUND,TINA ANDRESEN MOLLERUP PC
C12Q1/68,C07K14/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..15
FT /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

Query Match          44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGACGACAGAA 742
Db 14 CAGGACGACAGAA 2

RESULT 120
BD208397/c
LOCUS             15 bp RNA linear PAT 17-JUL-2003
DEFINITION       Enzymatic nucleic acid treatment of diseases or conditions related
ACCESSION       BD208397
VERSION         BD208397.1 GI:33018167
KEYWORDS        JP 2002512791-A/1987.
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 15)
AUTHORS        Blatt,L., Meswigen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.

Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
Patent: JP 2002512791-A 1987 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/1987
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT /organism='Hepatitis virus (hepatitis C FT
virus)'.
FEATURES             Location/Qualifiers
     source             1..15
                        /organism="unidentified"
                        /mol_type="genomic RNA"
                        /db_xref="taxon:32644"

Query Match          44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAGAAC 744
Db 13 GGTGAACAGTAC 1

RESULT 121
AX471642/c
LOCUS             11 bp DNA linear PAT 09-AUG-2002
DEFINITION       Sequence 1219 from Patent WO02053773..
ACCESSION       AX471642
VERSION         AX471642.1 GI:22206767
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Homo sapiens
REFERENCE       1
AUTHORS        Hofmann,K., Conradt,M. and Petersohn,D.
TITLE          Method for determining skin stress or skin ageing in vitro
JOURNAL        Patent: WO 02053773-A 1219 11-JUL-2002;
              HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source             1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match          42.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 734 AGAAAACAGAAC 744
Db 11 AGAAAACAGATC 1

RESULT 122
AX627643/c
LOCUS             11 bp DNA linear PAT 21-FEB-2003
DEFINITION       Sequence 4684 from Patent WO02053774.

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<p>ACCESSION AX627643.1 GI:28455681</p> <p>VERSION Homo sapiens (human)</p> <p>KEYWORDS Homo sapiens</p> <p>SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>ORGANISM Homo sapiens</p> <p>REFERENCE Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 4684 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)</p> <p>TITLE Method for determining homeostasis of the skin</p> <p>JOURNAL JOURNAL</p> <p>FEATURES Location/Qualifiers 1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match Best Local Similarity 42.7%; Score 9.4; DB 1; Length 11; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS 734 AGAACAGAAC 744 11 AGAACAGATC 1</p> <p>LOCUS AR011923 Sequence 9 from patent US 5763175. Accession AR011923 Version AR011923.1 GI:3969913</p> <p>KEYWORDS Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 12)</p> <p>AUTHORS Brenner, S.</p> <p>TITLE Simultaneous sequencing of tagged polynucleotides</p> <p>JOURNAL Patent: US 5763175-A 9 09-JUN-1998;</p> <p>FEATURES Location/Qualifiers 1..12 /organism="unknown" /mol_type="unassigned DNA"</p> <p>Query Match Best Local Similarity 42.7%; Score 9.4; DB 1; Length 12; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS AR017794 Sequence 13 from patent US 5780231. Accession AR017794 Version AR017794.1 GI:3973397</p> <p>KEYWORDS Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 12)</p> <p>AUTHORS Brenner, S.</p> <p>TITLE DNA extension and analysis with rolling primers</p> <p>JOURNAL Patent: US 5780231-A 13 14-JUL-1998;</p> <p>FEATURES Location/Qualifiers 1..12 /organism="unknown" /mol_type="unassigned DNA"</p> <p>Query Match Best Local Similarity 42.7%; Score 9.4; DB 1; Length 12; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS AR017794 Sequence 13 from patent US 5780231. Accession AR017794 Version AR017794.1 GI:3973397</p> <p>KEYWORDS Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 12)</p> <p>AUTHORS Brenner, S.</p> <p>TITLE DNA extension and analysis with rolling primers</p> <p>JOURNAL Patent: US 5780231-A 13 14-JUL-1998;</p> <p>FEATURES Location/Qualifiers 1..12 /organism="unknown" /mol_type="unassigned DNA"</p>	<p>ACCESSION AX627643.1 GI:28455681</p> <p>VERSION Homo sapiens (human)</p> <p>KEYWORDS Homo sapiens</p> <p>SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>ORGANISM Homo sapiens</p> <p>REFERENCE Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 4684 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)</p> <p>TITLE Method for determining homeostasis of the skin</p> <p>JOURNAL JOURNAL</p> <p>FEATURES Location/Qualifiers 1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match Best Local Similarity 42.7%; Score 9.4; DB 1; Length 11; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS 734 AGAACAGAAC 744 11 AGAACAGATC 1</p> <p>LOCUS AR011923 Sequence 9 from patent US 5763175. Accession AR011923 Version AR011923.1 GI:3969913</p> <p>KEYWORDS Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 12)</p> <p>AUTHORS Brenner, S.</p> <p>TITLE Simultaneous sequencing of tagged polynucleotides</p> <p>JOURNAL Patent: US 5763175-A 9 09-JUN-1998;</p> <p>FEATURES Location/Qualifiers 1..12 /organism="unknown" /mol_type="unassigned DNA"</p> <p>Query Match Best Local Similarity 42.7%; Score 9.4; DB 1; Length 12; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS AR017794 Sequence 13 from patent US 5780231. Accession AR017794 Version AR017794.1 GI:3973397</p> <p>KEYWORDS Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 12)</p> <p>AUTHORS Brenner, S.</p> <p>TITLE DNA extension and analysis with rolling primers</p> <p>JOURNAL Patent: US 5780231-A 13 14-JUL-1998;</p> <p>FEATURES Location/Qualifiers 1..12 /organism="unknown" /mol_type="unassigned DNA"</p>	<p>ACCESSION AX627643.1 GI:28455681</p> <p>VERSION Homo sapiens (human)</p> <p>KEYWORDS Homo sapiens</p> <p>SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>ORGANISM Homo sapiens</p> <p>REFERENCE Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 4684 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)</p> <p>TITLE Method for determining homeostasis of the skin</p> <p>JOURNAL JOURNAL</p> <p>FEATURES Location/Qualifiers 1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match Best Local Similarity 42.7%; Score 9.4; DB 1; Length 11; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS 734 AGAACAGAAC 744 11 AGAACAGATC 1</p> <p>LOCUS AR011923 Sequence 9 from patent US 5763175. Accession AR011923 Version AR011923.1 GI:3969913</p> <p>KEYWORDS Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 12)</p> <p>AUTHORS Brenner, S.</p> <p>TITLE Simultaneous sequencing of tagged polynucleotides</p> <p>JOURNAL Patent: US 5763175-A 9 09-JUN-1998;</p> <p>FEATURES Location/Qualifiers 1..12 /organism="unknown" /mol_type="unassigned DNA"</p> <p>Query Match Best Local Similarity 42.7%; Score 9.4; DB 1; Length 12; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS AR017794 Sequence 13 from patent US 5780231. Accession AR017794 Version AR017794.1 GI:3973397</p> <p>KEYWORDS Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 12)</p> <p>AUTHORS Brenner, S.</p> <p>TITLE DNA extension and analysis with rolling primers</p> <p>JOURNAL Patent: US 5780231-A 13 14-JUL-1998;</p> <p>FEATURES Location/Qualifiers 1..12 /organism="unknown" /mol_type="unassigned DNA"</p>	<p>ACCESSION AX627643.1 GI:28455681</p> <p>VERSION Homo sapiens (human)</p> <p>KEYWORDS Homo sapiens</p> <p>SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>ORGANISM Homo sapiens</p> <p>REFERENCE Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 4684 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)</p> <p>TITLE Method for determining homeostasis of the skin</p> <p>JOURNAL JOURNAL</p> <p>FEATURES Location/Qualifiers 1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match Best Local Similarity 42.7%; Score 9.4; DB 1; Length 11; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS 734 AGAACAGAAC 744 11 AGAACAGATC 1</p> <p>LOCUS AR011923 Sequence 9 from patent US 5763175. Accession AR011923 Version AR011923.1 GI:3969913</p> <p>KEYWORDS Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 12)</p> <p>AUTHORS Brenner, S.</p> <p>TITLE Simultaneous sequencing of tagged polynucleotides</p> <p>JOURNAL Patent: US 5763175-A 9 09-JUN-1998;</p> <p>FEATURES Location/Qualifiers 1..12 /organism="unknown" /mol_type="unassigned DNA"</p> <p>Query Match Best Local Similarity 42.7%; Score 9.4; DB 1; Length 12; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS AR017794 Sequence 13 from patent US 5780231. Accession AR017794 Version AR017794.1 GI:3973397</p> <p>KEYWORDS Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 12)</p> <p>AUTHORS Brenner, S.</p> <p>TITLE DNA extension and analysis with rolling primers</p> <p>JOURNAL Patent: US 5780231-A 13 14-JUL-1998;</p> <p>FEATURES Location/Qualifiers 1..12 /organism="unknown" /mol_type="unassigned DNA"</p>	<p>ACCESSION AX627643.1 GI:28455681</p> <p>VERSION Homo sapiens (human)</p> <p>KEYWORDS Homo sapiens</p> <p>SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>ORGANISM Homo sapiens</p> <p>REFERENCE Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 4684 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)</p> <p>TITLE Method for determining homeostasis of the skin</p> <p>JOURNAL JOURNAL</p> <p>FEATURES Location/Qualifiers 1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:</p>
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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Inoue,T.
TITLE       Method of amplifying DNA fragment, apparatus for amplifying DNA
            fragment, method of assaying microorganisms, method of analyzing
            microorganisms and method of assaying contaminant
JOURNAL     Patent: US 6287769-A 162 11-SEP-2001;
FEATURES    Location/Qualifiers
            source
            1..12
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
        |||||
        2 AGGAGAAACG 12

RESULT 128
BD242531      12 bp      DNA      linear      PAT 17-JUL-2003
LOCUS         A system for cell based screening.
DEFINITION    BD242531
ACCESSION     BD242531
VERSION       BD242531.1 GI:33052301
KEYWORDS      JP 2002528136-A/37.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 12)
AUTHORS       Guiliano,K.A., Bright,G., Olson,K. and Tencza,S.B.
TITLE         A system for cell based screening
JOURNAL       Patent: JP 2002528136-A 37 03-SEP-2002;
COMMENT       CELLOMICS INC
OS            Artificial Sequence
PN            JP 2002528136-A/37
PD            03-SEP-2002
PF            29-OCT-1999 JP 2000579780
PR            30-OCT-1998 US 60/106308,26-MAY-1999 US 60/136078 PI
KENNETH A GUILIANO,GARY BRIGHT,KEITH OLSON,SARAH BURROUGHS PI
TENCZA
PC            C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,C12Q1/
PC            37,G01N33/15,
PC            G01N33/50,C12N15/00,C12N5/00
CC            Description of Artificial Sequence: Caspase-8 substrate CC
            recognition
            sequence
            Location/Qualifiers
            FH Key
            FT source
            1..12
            /organism="Artificial Sequence".
FEATURES      source
            1..12
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      732 GGAGAAACAGA 742
        |||||
        1 GTAGAAACAGA 11

RESULT 129
BD269489/c
LOCUS         Stable recombinant influenza virus free from helper virus.
DEFINITION    BD269489
            12 bp      RNA      linear      PAT 17-JUL-2003
SOURCE        Stable recombinant influenza virus free from helper virus.
            source
            1..12
            /organism="unclassified"
            /mol_type="RNA"
            /db_xref="taxon:32630"

ACCESSION    BD269489
VERSION      BD269489.1 GI:33079257
KEYWORDS     SYNTHETIC CONSTRUCT
SOURCE       SYNTHETIC CONSTRUCT
ORGANISM     ARTIFICIAL SEQUENCES.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Hobom,G., Flick,R., Menke,A. and AzzeH,M.
TITLE        Stable recombinant influenza virus free from helper virus
JOURNAL      Patent: JP 2002537844-A 13 12-NOV-2002;
COMMENT      ARTEMIS PHARMACEUTICALS GMBH
OS            Artificial Sequence
PN            JP 2002537844-A/13
PD            12-NOV-2002
PF            03-MAR-2000 JP 2000603407
PR            06-MAR-1999 EP 99104519.6
PI            GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEH PC
C12N15/09,A61K39/145,A61K48/00,A61P31/16,C12N7/00,C12P21/02// PC
A61K35/12,
PC            (C12N7/00,C12P1:93),C12N15/00
CC            Description of Artificial Sequence: Modified influenza A 3'
            sequence
            (pHL1104 and 1920)
            CC
            FH Key
            FT source
            1..12
            Location/Qualifiers
            /organism="Artificial Sequence".
FEATURES      source
            1..12
            /organism="synthetic construct"
            /mol_type="genomic RNA"
            /db_xref="taxon:32630"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
        |||||
        12 AGTAAACAG 2

RESULT 130
E29682
LOCUS         Method for amplifying DNA fragment, method for estimating state of
DEFINITION    microorganism existing and method for estimating state of waste
ACCESSION     E29682
VERSION       E29682.1 GI:13021185
KEYWORDS      JP 1999276176-A/162.
SOURCE        unidentified
ORGANISM      unidentified
            unclassified.
REFERENCE     1 (bases 1 to 12)
AUTHORS       Koichi,I.
TITLE         Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste
JOURNAL       Patent: JP 1999276176-A 162 12-OCT-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT       OS Unidentified
            PN JP 1999276176-A/162
            PD 12-OCT-1999
            PF 31-MAR-1998 JP 1999087652
            PR KOICHI INOUE
            PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
            Strandedness: Single;
            FH Key
            FT source
            1..12
            Location/Qualifiers
            /organism="unclassified".
FEATURES      source
            1..12
            /organism="unclassified"
            /mol_type="unclassified"
            /db_xref="taxon:32630"

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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 2 AGGAGAAACGG 12

RESULT 131
E64214/c
LOCUS          12 bp      RNA      linear      PAT 18-JUN-2001
DEFINITION     DNA elongation and analysis with the use of rolling primer.
ACCESSION      E38120
VERSION        E38120.1 GI:13027155
KEYWORDS       JP 199151092-A/15.
SOURCE         synthetic construct
ORGANISM       artificial construct
REFERENCE      1 (bases 1 to 12)
AUTHORS        Sydney,B.
TITLE          DNA elongation and analysis with the use of rolling primer
JOURNAL        LYNX THERAPEUTICS INC
COMMENT        OS Artificial Sequence
                PN JP 199151092-A/15
                PD 08-JUN-1999
                PF 24-AUG-1998 JP 1998237840
                PR 22-AUG-1997 US 08/916.120
                PC C12N15/09,C12Q1/68,C12N15/00
                CC CC
                FH Key
                FT source
                Location/Qualifiers
                1..12
                /organism="synthetic construct"
                /mol_type="genomic RNA"
                /db_xref="taxon:32630"

FEATURES
source
Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
DB 12 GCCAGGAGAGA 2

RESULT 132
E38788
LOCUS          12 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION     Method and device for amplifying DNA fragment.
ACCESSION      E38788
VERSION        E38788.1 GI:18621450
KEYWORDS       JP 2000270867-A/162.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 12)
AUTHORS        Inoue,K.
TITLE          Method and device for amplifying DNA fragment
JOURNAL        SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
COMMENT        OS Unidentified
                PN JP 2000270867-A/162
                PD 03-OCT-2000
                PF 19-MAR-1999 JP 1999076844

/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 2 AGGAGAAACGG 12

RESULT 133
E64214
LOCUS          12 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION     Method for amplifying DNA fragment, amplification apparatus of DNA
                fragment, method for assaying a group of microorganisms, method
                for analyzing a group of microorganisms, and method for assaying
                contaminating substance.
ACCESSION      E64214
VERSION        E64214.1 GI:13019618
KEYWORDS       JP 1999341989-A/162.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 12)
AUTHORS        Koichi,I.
TITLE          Method for amplifying DNA fragment, amplification apparatus of DNA
                fragment, method for assaying a group of microorganisms, method for
                analyzing a group of microorganisms, and method for assaying
                contaminating substance
JOURNAL        Patent: JP 1999341989-A 162 14-DEC-1999;
                SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
                FORESTRY AND FISHERIES
COMMENT        OS Artificial Sequence
                PN JP 1999341989-A/162
                PD 14-DEC-1999
                PF 16-MAR-1999 JP 1999069694
                PR KOICHI INOUE
                PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
                CC CC
                FH Key
                FT source
                Location/Qualifiers
                1..12
                /organism="Artificial Sequence"

FEATURES
source
Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 2 AGGAGAAACGG 12

RESULT 134
AR217456

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LOCUS       AR217456               12 bp      DNA              linear      PAT 25-SEP-2002
DEFINITION   Sequence 73 from patent US 6416959.
ACCESSION   AR217456
VERSION     AR217456.1   GI:23317149
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Giuliano,K. and Kapur,R.
TITLE       System for cell-based screening
JOURNAL     Patent: US 6416959-A 73 09-JUL-2002;
FEATURES    Location/Qualifiers
            source
            1..12
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      732 CGAGAAACAG 742
        |||||||
Db      1 GTAGAAACAG 11

RESULT 135
LOCUS       AR282763               12 bp      RNA              linear      PAT 10-APR-2003
DEFINITION   Sequence 9 from patent US 6524588.
ACCESSION   AR282763
VERSION     AR282763.1   GI:29719542
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Hobom,G., Neumann,G. and Menke,A.
TITLE       Attenuated vaccination and gene-transfer virus, a method to make
            the virus and a pharmaceutical composition comprising the virus
JOURNAL     Patent: US 6524588-A 9 25-FEB-2003;
FEATURES    Location/Qualifiers
            source
            1..12
                /organism="unknown"
                /mol_type="genomic RNA"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
        |||||||
Db      12 AGTAGAAACAG 2

RESULT 136
LOCUS       AX035438               12 bp      RNA              linear      PAT 15-NOV-2000
DEFINITION   Sequence 13 from Patent EP1035209.
ACCESSION   AX035438
VERSION     AX035438.1   GI:11191080
KEYWORDS    .
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Azzey,M., Hobom,G., Menke,A. and Flick,R.
TITLE       Stable recombinant influenza viruses free of helper viruses
JOURNAL     Patent: EP 1035209-A 13 13-SEP-2000;
            ARTEMIS PHARMACEUTICALS GMBH (DE)
FEATURES    Location/Qualifiers
            source
            1..12
                /organism="synthetic construct"

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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified Influenza A 3' sequence (pHL1104 and
1920)"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
        |||||||
Db      12 AGTAGAAACAG 2

RESULT 137
LOCUS       AX100750/c              12 bp      RNA              linear      PAT 10-APR-2001
DEFINITION   Sequence 7 from Patent WO0122083.
ACCESSION   AX100750
VERSION     AX100750.1   GI:13619696
KEYWORDS    .
SOURCE      Influenza A virus
            Influenza A virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
            A viruses; Influenzavirus A.
REFERENCE   1
AUTHORS     Bornkamm,G.W., Hobom,G., Mautner,J. and Nimmerjahn,F.
TITLE       Method for identifying mhc-restricted antigens
JOURNAL     Patent: WO 0122083-A 7 29-MAR-2001;
            GSF-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
            Pharmaceuticals GmbH (DE)
FEATURES    Location/Qualifiers
            source
            1..12
                /organism="Influenza A virus"
                /mol_type="unassigned RNA"
                /db_xref="taxon:11320"
            misc_feature
            1..12
                /note="3'-terminale Nukleotidsequenz"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
        |||||||
Db      12 AGGAGAACACG 2

RESULT 138
LOCUS       AX100751/c              12 bp      RNA              linear      PAT 10-APR-2001
DEFINITION   Sequence 8 from Patent WO0122083.
ACCESSION   AX100751
VERSION     AX100751.1   GI:13619697
KEYWORDS    .
SOURCE      Influenza A virus
            Influenza A virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
            A viruses; Influenzavirus A.
REFERENCE   1
AUTHORS     Bornkamm,G.W., Hobom,G., Mautner,J. and Nimmerjahn,F.
TITLE       Method for identifying mhc-restricted antigens
JOURNAL     Patent: WO 0122083-A 8 29-MAR-2001;
            GSF-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
            Pharmaceuticals GmbH (DE)
FEATURES    Location/Qualifiers
            source
            1..12
                /organism="Influenza A virus"
                /mol_type="unassigned RNA"
                /db_xref="taxon:11320"
            misc_feature
            1..12
                /note="3'-terminale Nukleotidsequenz"

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Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAACAG 2

RESULT 139
AX352660/c
LOCUS          AX352660          12 bp      RNA      linear      PAT 06-FEB-2002
DEFINITION     Sequence 4 from Patent EP1174514.
ACCESSION      AX352660
VERSION        AX352660.1 GI:18617790
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE         Recombinant influenza viruses with bicistronic vrnas coding for two
              Genes in tandem arrangement
JOURNAL        Patent: EP 1174514-A 4 23-JAN-2002;
              ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES       Location/Qualifiers
source         1..12
               /organism="synthetic construct"
               /mol_type="unassigned RNA"
               /db_xref="taxon:32630"
               /note="Modified influenza A 5'-sequence (pHL1104 and
               pHL1920)"

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAACAG 2

RESULT 140
AX352661/c
LOCUS          AX352661          12 bp      RNA      linear      PAT 06-FEB-2002
DEFINITION     Sequence 5 from Patent EP1174514.
ACCESSION      AX352661
VERSION        AX352661.1 GI:18617791
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE         Recombinant influenza viruses with bicistronic vrnas coding for two
              Genes in tandem arrangement
JOURNAL        Patent: EP 1174514-A 5 23-JAN-2002;
              ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES       Location/Qualifiers
source         1..12
               /organism="synthetic construct"
               /mol_type="unassigned RNA"
               /db_xref="taxon:32630"
               /note="Modified influenza A 3'-sequence (pHL1948)"

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAACAG 2

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RESULT 141
AX362218/c
LOCUS          AX362218          12 bp      RNA      linear      PAT 15-FEB-2002
DEFINITION     Sequence 4 from Patent WO208434.
ACCESSION      AX362218
VERSION        AX362218.1 GI:18694556
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE         Recombinant influenza viruses with bicistronic vrnas coding for two
              Genes in tandem arrangement
JOURNAL        Patent: WO 0208434-A 4 31-JAN-2002;
              ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES       Location/Qualifiers
source         1..12
               /organism="synthetic construct"
               /mol_type="unassigned RNA"
               /db_xref="taxon:32630"
               /note="Modified influenza A 3'-sequence (pHL1104 and
               pHL1920)"

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAACAG 2

RESULT 142
AX362219/c
LOCUS          AX362219          12 bp      RNA      linear      PAT 15-FEB-2002
DEFINITION     Sequence 5 from Patent WO208434.
ACCESSION      AX362219
VERSION        AX362219.1 GI:18694557
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE         Recombinant influenza viruses with bicistronic vrnas coding for two
              Genes in tandem arrangement
JOURNAL        Patent: WO 0208434-A 5 31-JAN-2002;
              ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES       Location/Qualifiers
source         1..12
               /organism="synthetic construct"
               /mol_type="unassigned RNA"
               /db_xref="taxon:32630"
               /note="Modified influenza A 3'-sequence (pHL1948)"

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAACAG 2

RESULT 143
AX428931/c
LOCUS          AX428931          12 bp      RNA      linear      PAT 21-JUN-2002
DEFINITION     Sequence 4 from Patent EP1201760.
ACCESSION      AX428931
VERSION        AX428931.1 GI:21540315
KEYWORDS

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SOURCE	
ORGANISM	synthetic construct artificial sequences.
REFERENCE	1
AUTHORS	Schuler,G.D., Hobom,G., Steinkasserer,A.D., Strobel,I.D. and Grassmann,R.
TITLE	Influenza virus vector for human dendritic cells
JOURNAL	Patent: EP 1201760-A 4 02-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)	
FEATURES	Location/Qualifiers
source	1..12
	/organism="synthetic construct"
	/mol_type="unassigned RNA"
	/db_xref="taxon:32630"
	/note="Modified influenza A 3'-sequence"
Query Match	42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity	90.9%; Pred.No. 1.3e+02;
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	731 AGGAGAAACAG 741
Db	12 AGTAGAACCAG 2
RESULT 144	
AX512614/c	
LOCUS	AX512615
DEFINITION	Sequence 5 from Patent EPI201760.
ACCESSION	AX512615
VERSION	AX512615.1 GI:21540316
KEYWORDS	synthetic construct
SOURCE	artificial sequences.
ORGANISM	Hobom,G. and Menke,A.
REFERENCE	1
AUTHORS	Influenza viruses with enhanced transcriptional and replicational capacities
TITLE	Patent: EP 1201760-A 5 02-MAY-2002;
JOURNAL	ARTEMIS Pharmaceuticals GmbH (DE)
ARTEMIS Pharmaceuticals GmbH (DE)	
FEATURES	Location/Qualifiers
source	1..12
	/organism="synthetic construct"
	/mol_type="unassigned RNA"
	/db_xref="taxon:32630"
	/note="Modified influenza A 3'-sequence"
Query Match	42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity	90.9%; Pred.No. 1.3e+02;
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	731 AGGAGAAACAG 741
Db	12 AGTAGAACCAG 2
RESULT 145	
AX512614/c	
LOCUS	AX512614
DEFINITION	Sequence 5 from Patent EPI201760.
ACCESSION	AX512614
VERSION	AX512614.1 GI:23503837
KEYWORDS	synthetic construct
SOURCE	artificial sequences.
ORGANISM	Hobom,G. and Menke,A.
REFERENCE	1
AUTHORS	Influenza viruses with enhanced transcriptional and replicational capacities
TITLE	Patent: EP 1233059-A 5 21-AUG-2002;
JOURNAL	ARTEMIS Pharmaceuticals GmbH (DE)
ARTEMIS Pharmaceuticals GmbH (DE)	
FEATURES	Location/Qualifiers
source	1..12
	/organism="synthetic construct"
	/mol_type="unassigned RNA"
	/db_xref="taxon:32630"
	/note="Modified influenza A 3'-sequence"
Query Match	42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity	90.9%; Pred.No. 1.3e+02;
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	731 AGGAGAAACAG 741
Db	12 AGTAGAACCAG 2
RESULT 146	
AX512615/c	
LOCUS	AX512615
DEFINITION	Sequence 6 from Patent EPI233059.
ACCESSION	AX512615
VERSION	AX512615.1 GI:23503838
KEYWORDS	synthetic construct
SOURCE	artificial sequences.
ORGANISM	Hobom,G. and Menke,A.
REFERENCE	1
AUTHORS	Influenza viruses with enhanced transcriptional and replicational capacities
TITLE	Patent: EP 1233059-A 6 21-AUG-2002;
JOURNAL	ARTEMIS Pharmaceuticals GmbH (DE)
ARTEMIS Pharmaceuticals GmbH (DE)	
FEATURES	Location/Qualifiers
source	1..12
	/organism="synthetic construct"
	/mol_type="unassigned RNA"
	/db_xref="taxon:32630"
	/note="Modified influenza A 3'-sequence"
Query Match	42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity	90.9%; Pred.No. 1.3e+02;
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	731 AGGAGAAACAG 741
Db	12 AGTAGAACCAG 2
RESULT 147	
AX522265/c	
LOCUS	AX522265
DEFINITION	Sequence 5 from Patent WO02064757.
ACCESSION	AX522265
VERSION	AX522265.1 GI:24411219
KEYWORDS	synthetic construct
SOURCE	artificial sequences.
ORGANISM	Hobom,G. and Menke,A.
REFERENCE	1
AUTHORS	Influenza viruses with enhanced transcriptional and replicational capacities
TITLE	Patent: WO 02064757-A 5 22-AUG-2002;
JOURNAL	ARTEMIS Pharmaceuticals GmbH (DE)
ARTEMIS Pharmaceuticals GmbH (DE)	
FEATURES	Location/Qualifiers
source	1..12
	/organism="synthetic construct"
	/mol_type="unassigned RNA"
	/db_xref="taxon:32630"
	/note="Modified influenza A 3'-sequence"
Query Match	42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity	90.9%; Pred.No. 1.3e+02;
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	731 AGGAGAAACAG 741
Db	12 AGTAGAACCAG 2
RESULT 148	
AX522265/c	
LOCUS	AX522265
DEFINITION	Sequence 5 from Patent WO02064757.
ACCESSION	AX522265
VERSION	AX522265.1 GI:24411219
KEYWORDS	synthetic construct
SOURCE	artificial sequences.
ORGANISM	Hobom,G. and Menke,A.
REFERENCE	1
AUTHORS	Influenza viruses with enhanced transcriptional and replicational capacities
TITLE	Patent: WO 02064757-A 5 22-AUG-2002;
JOURNAL	ARTEMIS Pharmaceuticals GmbH (DE)
ARTEMIS Pharmaceuticals GmbH (DE)	
FEATURES	Location/Qualifiers
source	1..12
	/organism="synthetic construct"
	/mol_type="unassigned RNA"
	/db_xref="taxon:32630"
	/note="Modified influenza A 3'-sequence"
Query Match	42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity	90.9%; Pred.No. 1.3e+02;
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	731 AGGAGAAACAG 741
Db	12 AGTAGAACCAG 2

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
 Db 12 AGTAGAAACAG 2

RESULT 148
 AX522266/c
 LOCUS
 DEFINITION Sequence 6 from Patent WO02064757.
 ACCESSION AX522266
 VERSION AX522266.1 GI:24411220
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Hobom, G. and Menke, A.
 TITLE Influenza viruses with enhanced transcriptional and replicational capacities
 JOURNAL Artemis Pharmaceuticals GmbH (DE)
 FEATURES
 source 1..12
 /organism="synthetic construct"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32630"
 /note="Modified influenza A 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
 Db 12 AGGAGAACACG 2

RESULT 149
 AX766784
 LOCUS
 DEFINITION Sequence 73 from Patent EP1314980.
 ACCESSION AX766784
 VERSION AX766784.1 GI:32260536
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Giuliano, K.A. and Kapur, R.
 TITLE A system for cell-based screening
 JOURNAL Patent: EP 1314980-A 73 28-MAY-2003;
 Cellomics, Inc. (US)

FEATURES
 source 1..12
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Capase-8 substrate recognition sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 742
 Db 1 GTAGAAACAG 11

RESULT 150
 AR282758/c
 LOCUS

DEFINITION Sequence 4 from patent US 6524588.
 ACCESSION AR282758
 VERSION AR282758.1 GI:29719537
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 13)
 AUTHORS Hobom, G., Neumann, G. and Menke, A.
 TITLE Attenuated vaccination and gene-transfer virus, a method to make the virus and a pharmaceutical composition comprising the virus
 JOURNAL Patent: US 6524588-A 4 25-FEB-2003;
 FEATURES
 source 1..13
 /organism="unknown"
 /mol_type="genomic RNA"

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 1.4e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
 Db 13 AGTAGAAACAG 3

RESULT 151
 AR407966/c
 LOCUS
 DEFINITION Sequence 59 from patent US 6632057.
 ACCESSION AR407966
 VERSION AR407966.1 GI:40157953
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 13)
 AUTHORS Fauchet, C.R.J.
 TITLE Fixing unit with an end imprint in a threaded terminal portion
 JOURNAL Patent: US 6632057-A 59 14-OCT-2003;
 FEATURES
 source 1..13
 /organism="unknown"
 /mol_type="unassigned RNA"

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 1.4e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
 Db 11 AGCAGAAACAG 1

RESULT 152
 BD237463
 LOCUS
 DEFINITION Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof.
 ACCESSION BD237463
 VERSION BD237463.1 GI:33047233
 KEYWORDS JP 2002534434-A/1.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 14)
 AUTHORS Dale, R.M.K., Gattton, S.L. and Arrow, A.
 TITLE Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof
 JOURNAL Patent: JP 2002534434-A 1 15-OCT-2002;
 ChigOS ETC INC
 COMMENT OS Artificial Sequence
 PN JP 2002534434-A/1

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PD 15-OCT-2002
PF 16-DEC-1999 JP 2000592300
PR 30-DEC-1998 US 09/223498,19-JUL-1999 US 09/356069 PI
RODERIC M K DALE,STEVEN L GATTON,AMY ARROW
PC C07H21/00,A61K9/127,A61K31/7088,A61K47/44,A61K48/00,
PC A61P3/00,
PC A61P17/02,A61P29/00,A61P31/04,A61P31/10,A61P31/12,A61P35/00,
PC C12N5/10,
PC C12N15/09,C12N15/00,C12N5/00
CC Nucleic acid having blocked terminals modified with an acid-
CC stable
CC skeleton and therapeutic method thereof
FH Key Location/Qualifiers
FT source 1..14
/organism='Artificial Sequence'
FEATURES
source
Location/Qualifiers
1..14
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
DB 3 TGTCCAGGAGAA 13

RESULT 153
BD263138
LOCUS
DEFINITION Phosphodiesterase inhibitors for therapeutic use.
ACCESSION BD263138
VERSION BD263138.1 GI:33072906
KEYWORDS JP 2002534086-A/32.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Dale,R.M.K., Arrow,A. and Thompson,T.
TITLE Phosphodiesterase inhibitors for therapeutic use
JOURNAL Patent: JP 2002534086-A 32 15-OCT-2002;
COMMENT OLIGOS ETC INC
OS Artificial Sequence
PN JP 2002534086-A/32
PD 15-OCT-2002
PF 15-DEC-1999 JP 2000592411
PR 30-DEC-1998 US 09/223586,29-JUL-1999 US 09/364626 PI
RODERIC M K DALE,AMY ARROW,TERRY THOMPSON
PC C12N15/09,A61K31/7088,A61K48/00,A61P1/00,A61P3/10,PC
A61P9/00,
PC A61P9/10,A61P11/00,A61P11/06,A61P13/00,A61P17/04,PC
A61P17/06,
PC A61P19/02,A61P25/00,A61P25/24,A61P25/28,A61P27/14,A61P27/16,
PC A61P29/00,
PC A61P31/18,A61P33/06,A61P35/00,A61P37/06,A61P43/00,C12N15/00 CC
Synthesized oligonucleotide
FH Key Location/Qualifiers
FT source 1..14
/organism='Artificial Sequence'
FEATURES
source
Location/Qualifiers
1..14
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737

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DB 3 TGTCCAGGAGAA 13

RESULT 154
BD269502/c
LOCUS
DEFINITION Stable recombinant influenza virus free from helper virus.
ACCESSION BD269502
VERSION BD269502.1 GI:33079270
KEYWORDS JP 2002537844-A/26.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Hobom,G., Flick,R., Menke,A. and Azzezh,M.
TITLE Stable recombinant influenza virus free from helper virus
JOURNAL Patent: JP 2002537844-A 26 12-NOV-2002;
COMMENT ARTEMIS PHARMACEUTICALS GMBH
OS Artificial Sequence
PN JP 2002537844-A/26
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603407
PR 06-MAR-1999 EP 99104519,6
PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEZH PC
C12N15/09,A61K39/145,A61K48/00,A61P1/16,C12N7/00,C12P21/02// PC
A61K35/12,
PC (C12N7/00,C12P1:93),C12N15/00
CC Description of Artificial Sequence: Modified influenza C 3'
CC sequence
FH Key Location/Qualifiers
FT source 1..14
/organism='Artificial Sequence'
FEATURES
source
Location/Qualifiers
1..14
/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
DB 14 AGTAGAACAG 4

RESULT 155
AX035451/c
LOCUS
DEFINITION Sequence 26 from Patent EP1035209.
ACCESSION AX035451
VERSION AX035451.1 GI:11191093
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Azzezh,M., Hobom,G., Menke,A. and Flick,R.
TITLE Stable recombinant influenza viruses free of helper viruses
JOURNAL Patent: EP 1035209-A 26 13-SEP-2000;
COMMENT ARTEMIS PHARMACEUTICALS GMBH (DE)
OS Artificial Sequence
PN JP 2002537844-A/26
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603407
PR 06-MAR-1999 EP 99104519,6
PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEZH PC
C12N15/09,A61K39/145,A61K48/00,A61P1/16,C12N7/00,C12P21/02// PC
A61K35/12,
PC (C12N7/00,C12P1:93),C12N15/00
CC Description of Artificial Sequence: Modified influenza C 3'
CC sequence
FH Key Location/Qualifiers
FT source 1..14
/organism='Artificial Sequence'
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source
Location/Qualifiers
1..14
/organism='synthetic construct'
/mol_type='unassigned RNA'
/db_xref='taxon:32630'
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737

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QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 156
AX352673/c
LOCUS 14 bp RNA linear PAT 06-FEB-2002
DEFINITION Sequence 17 from Patent EP1174514.
ACCESSION AX352673
VERSION AX352673.1 GI:18617803
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE Recombinant influenza viruses with bicistronic vrnas coding for two
JOURNAL genes in tandem arrangement
PATENT: EP 1174514-A 17 23-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza C 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 157
AX362231/c
LOCUS 14 bp RNA linear PAT 15-FEB-2002
DEFINITION Sequence 17 from Patent WO0208434.
ACCESSION AX362231
VERSION AX362231.1 GI:18694569
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE Recombinant influenza viruses with bicistronic vrnas coding for two
JOURNAL genes in tandem arrangement
PATENT: WO 0208434-A 17 31-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza C 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 160
AX522279/c
LOCUS 14 bp RNA linear PAT 24-OCT-2002
DEFINITION Sequence 19 from Patent WO02064757.
ACCESSION AX522279
VERSION AX522279.1 GI:24411233
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hobom,G. and Menke,A.

```

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DEFINITION Sequence 17 from Patent EP1201760.
ACCESSION AX428944
VERSION AX428944.1 GI:21540328
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schuler,G.D., Hobom,G., Steinkasserer,A.D., Strobel,I.D. and
Grassmann,R.
TITLE Influenza virus vector for human dendritic cells
JOURNAL Patent: EP 1201760-A 17 02-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza C 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 159
AX512628/c
LOCUS 14 bp RNA linear PAT 03-OCT-2002
DEFINITION Sequence 19 from Patent EP1233059.
ACCESSION AX512628
VERSION AX512628.1 GI:23503851
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hobom,G. and Menke,A.
TITLE Influenza viruses with enhanced transcriptional and replicational
capacities
JOURNAL Patent: EP 1233059-A 19 21-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza C 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 160
AX522279/c
LOCUS 14 bp RNA linear PAT 24-OCT-2002
DEFINITION Sequence 19 from Patent WO02064757.
ACCESSION AX522279
VERSION AX522279.1 GI:24411233
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hobom,G. and Menke,A.

```

```

TITLE      Influenza viruses with enhanced transcriptional and replicational
JOURNAL    Patent: WO 02064757-A 19 22-AUG-2002;
FEATURES   ARTEMIS Pharmaceuticals GmbH (DE)
           Location/Qualifiers
           1..14
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Modified influenza C 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAACAG 741
Db      14 AGTAGAACAG 4

RESULT 161
LOCUS    A40498                14 bp    DNA        linear    PAT 05-MAR-1997
DEFINITION Sequence 35 from Patent WO9425578.
ACCESSION A40498
VERSION   A40498.1 GI:2296533
KEYWORDS .
SOURCE   unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS .
TITLE    ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL  EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES Patent: WO 9425578-A 35 10-NOV-1994;
           BIOGNOSTIK GES (DE)
           Location/Qualifiers
           1..14
           /organism="unidentified"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32644"

Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      730 CAGGAGAACAGAA 743
Db      1 CATGAGAGCAGGA 14

RESULT 162
LOCUS    A89025                14 bp    DNA        linear    PAT 22-JAN-2000
DEFINITION Sequence 1173 from Patent WO9833904.
ACCESSION A89025
VERSION   A89025.1 GI:6737595
KEYWORDS .
SOURCE   unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE    AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL  Patent: WO 9833904-A 1173 06-AUG-1998;
FEATURES BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Query Match 41.8%; Score 9.2; DB 1; Length 14;

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Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      730 CAGGAGAACAGAA 743
Db      1 CATGAGAGCAGGA 14

RESULT 163
LOCUS    AR232778                14 bp    DNA        linear    PAT 20-DEC-2002
DEFINITION Sequence 35 from patent US 6455689.
ACCESSION AR232778
VERSION   AR232778.1 GI:27275116
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
           Schlingensiepen,R. and Bogdahn,U.
TITLE    Antisense-oligonucleotides for transforming growth factor-.beta.
JOURNAL  (TGF-.beta.)
FEATURES Patent: US 6455689-A 35 24-SEP-2002;
           Location/Qualifiers
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Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      730 CAGGAGAACAGAA 743
Db      1 CATGAGAGCAGGA 14

RESULT 164
LOCUS    AX316394                14 bp    DNA        linear    PAT 14-DEC-2001
DEFINITION Sequence 35 from Patent EPI160319.
ACCESSION AX316394
VERSION   AX316394.1 GI:17899567
KEYWORDS .
SOURCE   unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
           Schlingensiepen,R. and Bogdahn,U.
TITLE    Antisense-oligonucleotides for the treatment of immunosuppressive
JOURNAL  effects of transforming growth factor-beta (tgf-beta)
FEATURES Patent: EP 1160319-A 35 05-DEC-2001;
           BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
           Location/Qualifiers
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Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      730 CAGGAGAACAGAA 743
Db      1 CATGAGAGCAGGA 14

RESULT 165
BD066538

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LOCUS BD066538 14 bp DNA linear PAT 27-AUG-2002
 DEFINITION An antisense oligonucleotide preparation method.
 ACCESSION BD066538
 VERSION BD066538.1 GI:22612141
 KEYWORDS JP 2001511000-A/1173.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Schlingensiepen,K.H. and Brysch,W.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: JP 2001511000-A 1173 07-AUG-2001;
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
 COMMENT OS Unknown.
 PN JP 2001511000-A/1173
 PD 07-AUG-2001
 PE 30-JAN-1998 JP 1998532533
 PR 31-JAN-1997 EP 97101531.8
 PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
 PC C12N15/11.C07H21/04.A61K31/70
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 Best Local Similarity 78.6%; Pred. No. 1.6e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 730 CAGGAGAACAGAA 743
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 Db 1 CATGAGAGCAGGA 14
 RESULT 166
 BD199355/C
 LOCUS BD199355 14 bp RNA linear PAT 17-JUL-2003
 DEFINITION Method and reagent for treating diseases or conditions concerning
 molecule participating in vasculogenic response.
 ACCESSION BD199355
 VERSION BD199355.1 GI:33009125
 KEYWORDS JP 2002509721-A/2381.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
 TITLE Method and reagent for treating diseases or conditions concerning
 molecule participating in vasculogenic response
 JOURNAL Patent: JP 2002509721-A 2381 02-APR-2002;
 RIBOZYNE PHARMACEUTICALS INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002509721-A/2381
 PD 02-APR-2002
 PE 24-MAR-1999 JP 2000541291
 PR 27-MAR-1998 US 60/079678
 PI FAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
 PI JAMES A MCSWIGGEN
 PC C12N15/09.A61K31/7088.A61K31/7125.A61K48/00.A61P3/10.A61P17/06. PC
 A61P29/00.
 CC A61P35/00.A61P43/00.C12N5/10.C12N9/00//A61K35/76.C12N15/00. PC
 C12N5/00
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 concerning molecule
 CC participating in vasculogenic response
 FH Key Location/Qualifiers

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 /mol_type='genomic RNA'
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 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 731 AGGAGAACAGAAC 744
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 Db 14 AGAGGAGACAGCAC 1
 RESULT 167
 S59977S1/c
 LOCUS S59977S1 14 bp mRNA linear ROD 11-OCT-2002
 DEFINITION GM-CSF-granulocyte-macrophage colony-stimulating factor [mice,
 WEHI-231 cell line, mRNA Partial, 14 nt, segment 1 of 2].
 ACCESSION S59977
 VERSION S59977.1 GI:237044
 KEYWORDS 1 of 2
 SEGMENT Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Leslie,K.B., Lee,F. and Schrader,J.W.
 TITLE Intracisternal A-type particle-mediated activations of cytokine
 genes in a murine myelomonocytic leukemia: generation of functional
 cytokine mRNAs by retroviral splicing events
 JOURNAL Mol. Cell. Biol. 11 (11), 5562-5570 (1991)
 MEDLINE 92017836
 PUBMED 1922064
 REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI gibbsg 59977] from the original journal article.
 COMMENT This sequence comes from fig6b.
 spliced transcript.
 Location/Qualifiers
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 /mol_type='mRNA'
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 /cell_line='WEHI-274'
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 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 733 GAGAAACAGAACAC 746
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 Db 14 GAGAGAGAGAAAC 1
 RESULT 168
 BD240369
 LOCUS BD240369 10 bp DNA linear PAT 17-JUL-2003
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD240369
 VERSION BD240369.1 GI:33050139
 KEYWORDS JP 2002534056-A/1787.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Roberts,B.L. and Shankara,S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 1787 15-OCT-2002;

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COMMENT
  GENZYME CORP
  OS Homo sapiens (human)
  PN JP 2002534056-A/1787
  PD 15-OCT-2002
  PF 18-JUN-1999 JP 2000554749
  PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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  19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
  08-DEC-1998 US 60/111715
  PI BRUCE L ROBERTS,SRINIVAS SHANKARA
  PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
  C12N1/19,
  PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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  Query Match 40.9%; Score 9; DB 1; Length 10;
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  QY 734 AGAAGACAGA 742
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  RESULT 169
  LOCUS BD240503 10 bp DNA linear PAT 17-JUL-2003
  DEFINITION Preparation and use of superior vaccines.
  ACCESSION BD240503
  VERSION BD240503.1 GI:33050273
  KEYWORDS JP 2002534056-A/1921.
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 10)
  TITLE Roberts,B.L. and Shankara,S.
  AUTHORS Preparation and use of superior vaccines
  JOURNAL Patent: JP 2002534056-A 1921 15-OCT-2002;
  GENZYME CORP
  OS Homo sapiens (human)
  PN JP 2002534056-A/1921
  PD 15-OCT-2002
  PF 18-JUN-1999 JP 2000554749
  PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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  19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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  PI BRUCE L ROBERTS,SRINIVAS SHANKARA
  PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
  C12N1/19,
  PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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  CC Preparation and use of superior vaccines
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  QY 730 CAGGAGAAA 738
  Db 9 CAGGAGAAA 1
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  RESULT 171
  LOCUS AR303305 10 bp DNA linear PAT 12-JUN-2003
  DEFINITION Sequence 30 from patent US 6544736.
  ACCESSION AR303305
  VERSION AR303305.1 GI:31692081
  KEYWORDS Unknown.
  SOURCE Unknown.
  ORGANISM Unknown.
  1 (bases 1 to 10)
  TITLE Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
  AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
  JOURNAL Watahiki,M.
  JOURNAL Patent: US 6544736-A 21 08-APR-2003;
  GENZYME CORP
  OS Homo sapiens (human)
  PN JP 2002534056-A/1921
  PD 15-OCT-2002
  PF 18-JUN-1999 JP 2000554749
  PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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  08-DEC-1998 US 60/111715
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  PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
  C12N1/19,
  PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
  G01N37/00,
  PC C12N15/00,C12N5/00,C12N15/00
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  QY 738 ACAGAACAC 746
  Db 9 ACAGAACAC 1
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  RESULT 170
  LOCUS AR303296/c 10 bp DNA linear PAT 12-JUN-2003
  DEFINITION Sequence 21 from patent US 6544736.
  ACCESSION AR303296
  VERSION AR303296.1 GI:31692072
  KEYWORDS Unknown.
  SOURCE Unknown.
  ORGANISM Unknown.
  1 (bases 1 to 10)
  TITLE Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
  AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
  JOURNAL Watahiki,M.
  JOURNAL Patent: US 6544736-A 21 08-APR-2003;
  GENZYME CORP
  OS Homo sapiens (human)
  PN JP 2002534056-A/1921
  PD 15-OCT-2002
  PF 18-JUN-1999 JP 2000554749
  PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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  PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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  PC C12N15/00,C12N5/00,C12N15/00
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  QY 730 CAGGAGAAA 738
  Db 9 CAGGAGAAA 1
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  RESULT 171
  LOCUS AR303305 10 bp DNA linear PAT 12-JUN-2003
  DEFINITION Sequence 30 from patent US 6544736.
  ACCESSION AR303305
  VERSION AR303305.1 GI:31692081
  KEYWORDS Unknown.
  SOURCE Unknown.
  ORGANISM Unknown.
  1 (bases 1 to 10)
  TITLE Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
  AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and

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Watahiki,M.
Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 30 08-APR-2003;
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Query Match      40.9%; Score 9; DB 1; Length 10;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 733 GAGAAACAG 741
Db 1 GAGAAACAG 9

RESULT 172
AR303339/c
LOCUS          AR303339          10 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION     Sequence 64 from patent US 6544736.
ACCESSION      AR303339
VERSION        AR303339.1 GI:31692115
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
                Watahiki,M.
TITLE          Method for synthesizing cDNA from mRNA sample
JOURNAL        Patent: US 6544736-A 64 08-APR-2003;
FEATURES       Location/Qualifiers
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                /mol_type="genomic DNA"
Query Match      40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 733 GAGAAACAG 741
Db 10 GAGAAACAG 2

RESULT 173
BD161312/c
LOCUS          BD161312          10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION     Human activated Th1 and Th2 cell expression genes.
ACCESSION      BD161312
VERSION        BD161312.1 GI:27867070
KEYWORDS       JP 2002186482-A/134.
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE          Human activated Th1 and Th2 cell expression genes
JOURNAL        Patent: JP 2002186482-A 134 02-JUL-2002;
                JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT        OS Homo sapiens (human)
                PN JP 2002186482-A/134
                PD 02-JUL-2002
                PF 19-DEC-2000 JP 2000385816
                PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
                C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
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Watahiki,M.
Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 30 08-APR-2003;
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 AGAACACCG 748
Db 10 AGAACACCG 2

RESULT 174
AX470590
LOCUS          AX470590          11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION     Sequence 167 from Patent WO02053773.
ACCESSION      AX470590
VERSION        AX470590.1 GI:22205715
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Hofmann,K., Conradt,M. and Petersohn,D.
TITLE          Method for determining skin stress or skin ageing in vitro
JOURNAL        Patent: WO 02053773-A 167 11-JUL-2002;
                HENKEL KGAA (DE)
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 729 CCAGGAGAA 737
Db 3 CCAGGAGAA 11

RESULT 175
AX623138/c
LOCUS          AX623138          11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION     Sequence 179 from Patent WO02053774.
ACCESSION      AX623138
VERSION        AX623138.1 GI:28451079
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 179 11-JUL-2002;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 744
Db 1 AAACAGAAC 11

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Db          9 AACAGAAC 1

RESULT 176
AX624843/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 1884 from Patent WO02053774.
ACCESSION  AX624843
VERSION     AX624843.1  GI:28452784
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1884 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      738 ACAGAACAC 746
      |||||
Db      9 ACAGAACAC 1

RESULT 177
AX625131
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2172 from Patent WO02053774.
ACCESSION  AX625131
VERSION     AX625131.1  GI:28453072
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 2172 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      729 CCAGAGAAC 737
      |||||
Db      3 CCAGAGAAC 11

RESULT 178
AX626407/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3448 from Patent WO02053774.
ACCESSION  AX626407
VERSION     AX626407.1  GI:28454445
KEYWORDS
SOURCE      Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 3448 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      739 CAGAACACC 747
      |||||
Db      3 CAGAACACC 11

RESULT 180
AX630559/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7600 from Patent WO02053774.
ACCESSION  AX630559
VERSION     AX630559.1  GI:28458597
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 7600 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"

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RESULT 183		BD242525		BD242525		12 bp		DNA		linear		PAT 17-JUL-2003	
LOCUS		A system for cell based screening.		A system for cell based screening.									
DEFINITION		BD242525		BD242525									
ACCESSION		BD242525		BD242525									
VERSION		1		1		GI:33052295							
KEYWORDS		JP 2002528136-A/31.		JP 2002528136-A/31.									
SOURCE		synthetic construct		synthetic construct									
ORGANISM		artificial sequences.		artificial sequences.									
REFERENCE		1 (bases 1 to 12)		1 (bases 1 to 12)									
AUTHORS		Guiliano,K.A., Bright,G., Olson,K. and Tencza,S.B.		Guiliano,K.A., Bright,G., Olson,K. and Tencza,S.B.									
TITLE		A system for cell based screening		A system for cell based screening									
JOURNAL		Patent: JP 2002528136-A 31 03-SEP-2002;		Patent: JP 2002528136-A 31 03-SEP-2002;									
COMMENT		CELLOMICS INC		CELLOMICS INC									
		OS Artificial Sequence		OS Artificial Sequence									
		PN JP 2002528136-A/31		PN JP 2002528136-A/31									
		PD 03-SEP-2002		PD 03-SEP-2002									
		PF 29-OCT-1999 JP 2000579780		PF 29-OCT-1999 JP 2000579780									
		PR 30-OCT-1998 US 60/106308,26-MAY-1999 US 60/136078 PI		PR 30-OCT-1998 US 60/106308,26-MAY-1999 US 60/136078 PI									
		KENNETH A GULLIANO,GARY BRIGHT,KEITH OLSON,SARAH BURROUGHS PI		KENNETH A GULLIANO,GARY BRIGHT,KEITH OLSON,SARAH BURROUGHS PI									
		TENCZA		TENCZA									
		PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,C12Q1/02		PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,C12Q1/02									
		PC 37,G01N33/15,		PC 37,G01N33/15,									
		PC G01N33/50,C12N15/00,C12N5/00		PC G01N33/50,C12N15/00,C12N5/00									
		CC Description of Artificial Sequence: proCaspase-3 substrate		CC Description of Artificial Sequence: proCaspase-3 substrate									
		CC recognition		CC recognition									
		CC sequence		CC sequence									
		FH Key		FH Key									
		FT source		FT source									
		1. .12		1. .12									
		Location/Qualifiers		Location/Qualifiers									
		/organism="synthetic construct"		/organism="synthetic construct"									
		/mol_type="genomic DNA"		/mol_type="genomic DNA"									
		/db_xref="taxon:32630"		/db_xref="taxon:32630"									
FEATURES		source		source									
		1. .12		1. .12									
		Location/Qualifiers		Location/Qualifiers									
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		/mol_type="genomic DNA"		/mol_type="genomic DNA"									
		/db_xref="taxon:32630"		/db_xref="taxon:32630"									
Query Match		40.9%; Score 9; DB 1; Length 12;		40.9%; Score 9; DB 1; Length 12;									
Best Local Similarity		100.0%; Pred. No. 1.6e+02;		100.0%; Pred. No. 1.6e+02;									
Matches		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY		734 AGAAGACAG 742		734 AGAAGACAG 742									
DB		3 AGAAGACAG 11		3 AGAAGACAG 11									
RESULT 184		BD242532		BD242532		12 bp		DNA		linear		PAT 17-JUL-2003	
LOCUS		A system for cell based screening.		A system for cell based screening.									
DEFINITION		BD242532		BD242532									
ACCESSION		BD242532		BD242532									
VERSION		1		1		GI:33052302							
KEYWORDS		JP 2002528136-A/38.		JP 2002528136-A/38.									
SOURCE		synthetic construct		synthetic construct									
ORGANISM		artificial sequences.		artificial									

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CC sequence recognition
FH Key Location/Qualifiers
FT source 1..12 /organism='Artificial Sequence'

FEATURES
    source
        Location/Qualifiers
            1..12 /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 185
LOCUS AR217450 12 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 61 from patent US 6416959.
ACCESSION AR217450
VERSION AR217450.1 GI:23317143
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Giuliano,K. and Kapur,R.
TITLE System for cell-based screening
JOURNAL Patent: US 6416959-A 61 09-JUL-2002;
FEATURES
    source
        Location/Qualifiers
            1..12 /organism="unknown"
            /mol_type="genomic DNA"

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 186
LOCUS AR217457 12 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 75 from patent US 6416959.
ACCESSION AR217457
VERSION AR217457.1 GI:23317150
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Giuliano,K. and Kapur,R.
TITLE System for cell-based screening
JOURNAL Patent: US 6416959-A 75 09-JUL-2002;
FEATURES
    source
        Location/Qualifiers
            1..12 /organism="unknown"
            /mol_type="genomic DNA"

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 187
LOCUS AX766772 12 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 61 from Patent EP1314980.
ACCESSION AX766772
VERSION AX766772.1 GI:32260530
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Giuliano,K.A. and Kapur,R.
TITLE A system for cell-based screening
JOURNAL Patent: EP 1314980-A 61 28-MAY-2003;
CELLONICS, Inc. (US)
FEATURES
    source
        Location/Qualifiers
            1..12 /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="proCaspase-3 substrate recognition sequence"

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 188
LOCUS AX766786 12 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 75 from Patent EP1314980.
ACCESSION AX766786
VERSION AX766786.1 GI:32260537
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Giuliano,K.A. and Kapur,R.
TITLE A system for cell-based screening
JOURNAL Patent: EP 1314980-A 75 28-MAY-2003;
CELLONICS, Inc. (US)
FEATURES
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            /note="proCaspase-8 substrate recognition sequence"

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 189
LOCUS AR364664 13 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 3 from patent US 5395927.
ACCESSION AR364664
VERSION AR364664.1 GI:34427588
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Bock, A., Binder, F., and Muller, F.
TITLE DNA-fragment having the cyclodextrin glycosyltransferase gene
JOURNAL Patent: US 5395927-A 3 07-MAR-1995;
FEATURES Location/Qualifiers
source
1. .13
/organism="unknown"
/mol_type="genomic DNA"

Query Match 40.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAAACAGAA 743
Db 3 GAAACAGAA 11
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RESULT 190
ARI23872/c
LOCUS ARI23872 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6171821.
ACCESSION ARI23872
VERSION ARI23872.1 GI:14109233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Korneluk, R.G., Holcik, M., and Liston, P.
TITLE XIAP IRES and uses thereof
JOURNAL Patent: US 6171821-A 5 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAACAGAA 745
Db 12 AGAACAGAA 1
|||||

RESULT 191
ARI23873
LOCUS ARI23873 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 6 from patent US 6171821.
ACCESSION ARI23873
VERSION ARI23873.1 GI:14109234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Korneluk, R.G., Holcik, M., and Liston, P.
TITLE XIAP IRES and uses thereof
JOURNAL Patent: US 6171821-A 6 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAACAGAA 745
Db 12 AGAACAGAA 1
|||||

Db 1 AAAAAAGAGACA 12
|||||

RESULT 192
ARI23877/c
LOCUS ARI23877 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6171821.
ACCESSION ARI23877
VERSION ARI23877.1 GI:14109238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Korneluk, R.G., Holcik, M., and Liston, P.
TITLE XIAP IRES and uses thereof
JOURNAL Patent: US 6171821-A 10 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .12
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/mol_type="unassigned DNA"

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAACAGAGACA 745
Db 12 AGAACAGAGACA 1
|||||

RESULT 193
ARI78311/c
LOCUS ARI78311 12 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 28 from patent US 6319672.
ACCESSION ARI78311
VERSION ARI78311.1 GI:20219449
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Crouzet, J., Scherman, D., Wils, P., Blanche, F., and Cameron, B.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: US 6319672-A 28 20-NOV-2001;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAACAGACA 742
Db 12 AGGAGAACAGACA 1
|||||

RESULT 194
AX323393/c
LOCUS AX323393 12 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 28 from Patent WO0192511.
ACCESSION AX323393
VERSION AX323393.1 GI:18094155
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Crouzet, J., Scherman, D., Wils, P., Blanche, F., and Cameron, B.
TITLE Purification of a triple helix formation with an immobilized

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oligonucleotide
Patent: WO 0192511-A 28 06-DEC-2001;
Aventis Pharma (FR)
FEATURES
    source
        1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="caxon:32630"
            /note="synthetic oligonucleotide"
Query Match
    Best Local Similarity 40.0%; Score 8.8; DB 1; Length 12;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGA 742
    ||||| |||||
Db 12 AGGAAAAAAGA 1

RESULT 195
LOCUS AR021478 13 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 8 from patent US 5789651.
ACCESSION AR021478
VERSION AR021478.1 GI:3976093
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Woychik,R.P.
TITLE Isolation and characterization of Agouti: a diabetes/obesity
related gene
JOURNAL Patent: US 5789651-A 8 04-AUG-1998;
FEATURES
    source
        1..13
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            /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 40.0%; Score 8.8; DB 1; Length 13;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAACCA 745
    ||||| |||||
Db 13 AGAAGCAGCACCA 2

RESULT 196
LOCUS AR061316 13 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5843652.
ACCESSION AR061316
VERSION AR061316.1 GI:5989007
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Woychik,R.P.
TITLE Isolation and characterization of Agouti: a diabetes/obesity
related gene
JOURNAL Patent: US 5843652-A 8 01-DEC-1998;
FEATURES
    source
        1..13
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 40.0%; Score 8.8; DB 1; Length 13;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAACCA 745
    ||||| |||||
Db 13 AGAAGCAGCACCA 2

RESULT 197
LOCUS AR100114 13 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6080550.
ACCESSION AR100114
VERSION AR100114.1 GI:12810562
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Woychik,R.P.
TITLE Isolation and characterization of Agouti: a diabetes/obesity
related gene
JOURNAL Patent: US 6080550-A 9 27-JUN-2000;
FEATURES
    source
        1..13
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 40.0%; Score 8.8; DB 1; Length 13;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAACCA 745
    ||||| |||||
Db 13 AGAAGCAGCACCA 2

RESULT 198
LOCUS AR100119 13 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 6080550.
ACCESSION AR100119
VERSION AR100119.1 GI:12810567
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Woychik,R.P.
TITLE Isolation and characterization of Agouti: a diabetes/obesity
related gene
JOURNAL Patent: US 6080550-A 14 27-JUN-2000;
FEATURES
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            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 40.0%; Score 8.8; DB 1; Length 13;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAACCA 745
    ||||| |||||
Db 13 AGAAGCAGCACCA 2

RESULT 199
LOCUS AR175971 13 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 23 from patent US 6310034.
ACCESSION AR175971
VERSION AR175971.1 GI:17917270
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)

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AUTHORS      Woychik,R.P., Bultman,S.J. and Michaud,E.J.
TITLE        Agouti polypeptide compositions
JOURNAL      Patent: US 6310034-A 23 30-OCT-2001;
FEATURES     Location/Qualifiers
source       1..13
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGACACA 745
Db 13 AGAAGCAGACACA 2

RESULT 200
LOCUS      BD269493                13 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Stable recombinant influenza virus free from helper virus.
ACCESSION  BD269493
VERSION     BD269493.1 GI:33079261
KEYWORDS    JP 2002537844-A/17.
SOURCE      Influenza B virus
ORGANISM    Influenza B virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus B.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Hobom,G., Flick,R., Menke,A. and AzzeH,M.
TITLE       Stable recombinant influenza virus free from helper virus
JOURNAL     Patent: JP 2002537844-A 17 12-NOV-2002;
            ARTEMIS PHARMACEUTICALS GMBH
COMMENT     OS Influenza B virus
            PN JP 2002537844-A/17
            PD 12-NOV-2002
            PF 03-MAR-2000 JP 2000603407
            PR 06-MAR-1999 EP 99104519.6
            PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEH PC
            C12N15/09,A61K39/145,A61K48/00,A61P31/16,C12N7/00,C12P21/02// PC
            A61K35/12
            PC (C12N7/00,C12N15/09),C12N15/00
            CC Stable recombinant influenza virus free from helper virus FH
            Key Location/Qualifiers
            FT source 1..13
            FT /organism='Influenza B virus'.
            FT Location/Qualifiers
FEATURES     source
             1..13
             /organism="Influenza B virus"
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Query Match      39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 201
LOCUS      AX035442                13 bp      RNA      linear      PAT 15-NOV-2000
DEFINITION Sequence 17 from Patent EP1035209.
ACCESSION  AX035442
VERSION     AX035442.1 GI:11191084
KEYWORDS    Influenza B virus
SOURCE      Influenza B virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus B.
REFERENCE   1
AUTHORS     Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE       Recombinant influenza viruses with bicistronic vrnas coding for two
            genes in tandem arrangement
JOURNAL     Patent: EP 1174514-A 7 23-JAN-2002;
            ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES     source
             1..13
             /organism="Influenza B virus"

AUTHORS      AzzeH,M., Hobom,G., Menke,A. and Flick,R.
TITLE        Stable recombinant influenza viruses free of helper viruses
JOURNAL      Patent: EP 1035209-A 17 13-SEP-2000;
            ARTEMIS PHARMACEUTICALS GMBH (DE)
FEATURES     Location/Qualifiers
source       1..13
             /organism="Influenza B virus"
             /mol_type="unassigned RNA"
             /db_xref="taxon:11520"

Query Match      39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 202
LOCUS      AX100748                13 bp      RNA      linear      PAT 10-APR-2001
DEFINITION Sequence 5 from Patent WO0122083.
ACCESSION  AX100748
VERSION     AX100748.1 GI:13619694
KEYWORDS    Influenza B virus
SOURCE      Influenza B virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus B.
REFERENCE   1
AUTHORS     Bornkamm,G.W., Hobom,G., Mautner,J. and Nimmerjahn,F.
TITLE       Method for identifying mhc-restricted antigens
JOURNAL     Patent: WO 0122083-A 5 29-MAR-2001;
            GSF-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
            Pharmaceuticals GmbH (DE)
FEATURES     Location/Qualifiers
source       1..13
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             /db_xref="taxon:11520"
             misc_feature 1..13
             /note="5'-Konservierte Region des Wildtyp-Influenzavirus"

Query Match      39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 203
LOCUS      AX352663                13 bp      RNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 7 from Patent EP1174514.
ACCESSION  AX352663
VERSION     AX352663.1 GI:18617793
KEYWORDS    Influenza B virus
SOURCE      Influenza B virus
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus B.
REFERENCE   1
AUTHORS     Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE       Recombinant influenza viruses with bicistronic vrnas coding for two
            genes in tandem arrangement
JOURNAL     Patent: EP 1174514-A 7 23-JAN-2002;
            ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES     source
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/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
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Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 204
AX362221
LOCUS AX362221 13 bp RNA linear PAT 15-FEB-2002
DEFINITION Sequence 7 from Patent WO208434.
ACCESSION AX362221
VERSION AX362221.1 GI:18694559
KEYWORDS
SOURCE
ORGANISM
Influenza B virus
Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
REFERENCE
1.
AUTHORS Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE Recombinant Influenza viruses with bicistronic vrnas coding for two
genes in tandem arrangement
JOURNAL Patent: WO 0208434-A 7 31-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1. .13
/organism="Influenza B virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
Best Local Similarity 39.1%; Score 8.6; DB 1; Length 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 205
AX428934
LOCUS AX428934 13 bp RNA linear PAT 21-JUN-2002
DEFINITION Sequence 7 from Patent EP1201760.
ACCESSION AX428934
VERSION AX428934.1 GI:21540318
KEYWORDS
SOURCE
ORGANISM
Influenza B virus
Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
REFERENCE
1.
AUTHORS Schuler,G.D., Hobom,G., Steinkasserer,A.D., Strobel,I.D. and
Grassmann,R.
TITLE Influenza virus vector for human dendritic cells
JOURNAL Patent: EP 1201760-A 7 02-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1. .13
/organism="Influenza B virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
Best Local Similarity 39.1%; Score 8.6; DB 1; Length 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 206
AX512617
LOCUS AX512617 13 bp RNA linear PAT 03-OCT-2002
DEFINITION Sequence 8 from Patent EP1233059.
ACCESSION AX512617
VERSION AX512617.1 GI:23503840
KEYWORDS
SOURCE
ORGANISM
Influenza B virus
Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
REFERENCE
1.
AUTHORS Hobom,G. and Menke,A.
TITLE Influenza viruses with enhanced transcriptional and replicational
capacities
JOURNAL Patent: EP 1233059-A 8 21-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1. .13
/organism="Influenza B virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
Best Local Similarity 39.1%; Score 8.6; DB 1; Length 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 207
AX522268
LOCUS AX522268 13 bp RNA linear PAT 24-OCT-2002
DEFINITION Sequence 8 from Patent WO2064757.
ACCESSION AX522268
VERSION AX522268.1 GI:24411222
KEYWORDS
SOURCE
ORGANISM
Influenza B virus
Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
REFERENCE
1.
AUTHORS Hobom,G. and Menke,A.
TITLE Influenza viruses with enhanced transcriptional and replicational
capacities
JOURNAL Patent: WO 02064757-A 8 22-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1. .13
/organism="Influenza B virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
Best Local Similarity 39.1%; Score 8.6; DB 1; Length 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 208
AR026539
LOCUS AR026539 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5856103.
ACCESSION AR026539
VERSION AR026539.1 GI:5937379

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KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Gray,D.M. and Clark,C.L.
TITLE          Method for selectively ranking sequences for antisense targeting
JOURNAL        Patent: US 5856103-A 2 05-JAN-1999;
FEATURES       Location/Qualifiers
               1..10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match    38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches        9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY             731 AGGAGAACCA 740
Db             |||||
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RESULT 210
LOCUS          BD239757
DEFINITION     Preparation and use of superior vaccines.
ACCESSION      BD239757
VERSION        BD239757.1 GI:33049527
KEYWORDS       JP 2002534056-A/1175.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE      1 (bases 1 to 10)
AUTHORS        Roberts,B.L. and Shankara,S.
TITLE           Preparation and use of superior vaccines
JOURNAL         Patent: JP 2002534056-A 1175 15-OCT-2002;
                GENZYME CORP
COMMENT         OS Homo sapiens (human)
                PN JP 2002534056-A/1175
                PD 15-OCT-2002
                PF 18-JUN-1999 JP 2000554749
                PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090040 PR
                19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
                19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
                19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
                19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
                19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
                19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
                19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
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                19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
                19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
                19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
                19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
                19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

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Query Match    38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches        9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY             727 TGCAGGAGGA 736
Db             |||||
              1 TGCAGGAGGA 10

RESULT 209
LOCUS          BD238913/c
DEFINITION     Preparation and use of superior vaccines.
ACCESSION      BD238913
VERSION        BD238913.1 GI:33048683
KEYWORDS       JP 2002534056-A/331.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE      1 (bases 1 to 10)
AUTHORS        Roberts,B.L. and Shankara,S.
TITLE           Preparation and use of superior vaccines
JOURNAL         Patent: JP 2002534056-A 331 15-OCT-2002;
                GENZYME CORP
COMMENT         OS Homo sapiens (human)
                PN JP 2002534056-A/331
                PD 15-OCT-2002
                PF 18-JUN-1999 JP 2000554749
                PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
                19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
                19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
                19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
                19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
                19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
                19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
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                19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
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                19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
                19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
                19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

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Query Match    38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches        9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY             727 TGCAGGAGGA 736
Db             |||||
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RESULT 211
LOCUS          BD239797
DEFINITION     Preparation and use of superior vaccines.

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ACCESSION BD239797
 VERSION BD239797.1 GI:33049567
 KEYWORDS JP 2002534056-A/1215
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 10)
 REFERENCE Roberts,B.L. and Shankar,S.
 AUTHORS Preparation and use of superior vaccines
 TITLE Patent: JP 2002534056-A 1215 15-OCT-2002;
 JOURNAL GENZYME CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002534056-A/1215
 PD 15-OCT-2002
 PF 18-JUN-1999 JP 2000554749
 PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
 19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
 19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
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 19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
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 19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
 08-DEC-1998 US 60/111715
 PI BRUCE L ROBERTS,SRINIVAS SHANKARA
 PC C12N15/09,C12N15/09,A61K39/00,A61P37/04,C12N1/15, PC
 C12N1/19
 PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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 Db 1 CCAGGAGAAA 10
 RESULT 212
 E39660/c
 LOCUS AR303316/c
 DEFINITION Sequence 41 from patent US 6544736.
 ACCESSION AR303316
 VERSION AR303316.1 GI:18621751
 KEYWORDS JP 2000279181-A/193.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 10)
 REFERENCE Hashimoto,S., Matsushima,X. and Suzuki,T.
 AUTHORS Genes with human dendritic cell expression
 TITLE Patent: JP 2000279181-A 193 10-OCT-2000;
 JOURNAL SCIENCE & TECH AGENCY
 COMMENT OS Homo sapiens (human)

PN JP 2000279181-A/193
 PD 10-OCT-2000
 PF 01-APR-1999 JP 1999095481
 PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
 C12N15/09,C07K14/475,C07K16/18,C12N15/00
 CC
 FH Key Location/Qualifiers
 FT source 1..10 /organism='Homo sapiens (human)'.
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 /mol_type='genomic DNA'
 /db_xref='taxon:9606'
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 Best Local Similarity 90.0%; Pred.No.1.7e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 731 AGGAGAAACA 740
 Db 10 AGGAGAAACA 1
 RESULT 213
 AR303294
 LOCUS AR303294
 DEFINITION Sequence 19 from patent US 6544736.
 ACCESSION AR303294
 VERSION AR303294.1 GI:31692070
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
 TITLE Method for synthesizing cDNA from mRNA sample
 JOURNAL Patent: US 6544736-A 19 08-APR-2003;
 FEATURES source
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 QY 730 CAGGAGAAAC 739
 Db 1 CTGAGAGAAAC 10
 RESULT 214
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 LOCUS AR303316/c
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 ACCESSION AR303316
 VERSION AR303316.1 GI:31692092
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
 TITLE Method for synthesizing cDNA from mRNA sample
 JOURNAL Patent: US 6544736-A 41 08-APR-2003;
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DEFINITION	Sequence 1293 from Patent WO0138577.				
ACCESSION	AXI53378				
VERSION	AXI53378.1 GI:14535029				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W. Human transcriptomes Patent: WO 0138577-A 834 31-MAY-2001;				
AUTHORS	The Johns Hopkins University (US) Location/Qualifiers				
TITLE	1..10				
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Db	10	AGGATAAACA	1		
LOCUS	AXI53448/c			DNA	linear
DEFINITION	Sequence 1363 from Patent WO0138577.				
ACCESSION	AXI53448				
VERSION	AXI53448.1 GI:14535099				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W. Human transcriptomes Patent: WO 0138577-A 1363 31-MAY-2001;				
AUTHORS	The Johns Hopkins University (US) Location/Qualifiers				
TITLE	1..10				
JOURNAL	/organism="Homo sapiens" /mol_type="unassigned DNA"				
FEATURES	/db_xref="taxon:9606"				
source					
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Best Local Similarity	90.0%; Pred. No. 1.7e+02;				
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DEFINITION	Sequence 1364 from Patent WO0138577.				
ACCESSION	AXI53449				
VERSION	AXI53449.1 GI:14535100				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W. Human transcriptomes Patent: WO 0138577-A 1364 31-MAY-2001;				
AUTHORS	The Johns Hopkins University (US) Location/Qualifiers				
TITLE	1..10				
JOURNAL	/organism="Homo sapiens" /mol_type="unassigned DNA"				
FEATURES	/db_xref="taxon:9606"				
source					
Query Match	38.2%; Score 8.4; DB 1; Length 10;				
Best Local Similarity	90.0%; Pred. No. 1.7e+02;				
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				

PF	19-JAN-2001 JP 2001012328
PI	KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO,TARO PI YAMASHITA
PC	C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC	C12P21/08,
PC	C12N15/00,
CC	Human liver disease-expressing genes
FH	Key Location/Qualifiers
FT	source 1..10
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Best Local Similarity	90.0%; Pred.No.1.7e+02;
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	735 GAACAGAAC 744
Db	1 GAACTGAAC 10
RESULT 224	
BD156874	
LOCUS	BD166874 10 bp DNA linear PAT 17-JAN-2003
DEFINITION	Human liver disease-expressing genes.
ACCESSION	BD166874
VERSION	BD166874.1 GI:27872686
KEYWORDS	JP 2002209591-A/419.
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 10)
AUTHORS	Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE	Human liver disease-expressing genes
JOURNAL	Patent: JP 2002209591-A 419 30-JUL-2002;
COMMENT	JAPAN SCIENCE AND TECHNOLOGY CORP
	OS Homo sapiens (human)
	PN JP 2002209591-A/419
	PD 30-JUL-2002
PF	19-JAN-2001 JP 2001012328
PI	KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO,TARO PI YAMASHITA
PC	C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC	C12P21/08,
PC	C12N15/00,
CC	Human liver disease-expressing genes
FH	Key Location/Qualifiers
FT	source 1..10
FEATURES	Location/Qualifiers
source	1..10
	/organism="unidentified"
	/mol_type="genomic DNA"
	/db_xref="taxon:32644"
Query Match	38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity	90.0%; Pred.No.1.7e+02;
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	735 GAACAGAAC 744
Db	1 GAACTGAAC 10
RESULT 225	
AX470470/c	
LOCUS	AX470470 11 bp DNA linear PAT 09-AUG-2002
DEFINITION	Sequence 47 from Patent WO02053773.
ACCESSION	AX470470

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FEATURES             Location/Qualifiers
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    1..11
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACCG 748
Db 1 CGGAACACCG 10

RESULT 228
AX471036/c
LOCUS AX471036 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 613 from Patent WO02053773.
ACCESSION AX471036
VERSION AX471036.1 GI:22206161
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE Method for determining skin stress or skin ageing in vitro
  JOURNAL PATENT: WO 02053773-A 613 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
  source
    1..11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
Db 10 AGAAACAGAA 1

RESULT 229
AX471164
LOCUS AX471164 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 741 from Patent WO02053773.
ACCESSION AX471164
VERSION AX471164.1 GI:22206289
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE Method for determining skin stress or skin ageing in vitro
  JOURNAL PATENT: WO 02053773-A 741 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
  source
    1..11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAAA 738
Db 10 CCAGGAGAAA 1

RESULT 230
AX623587/c
LOCUS AX623587 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 628 from Patent WO02053774.
ACCESSION AX623587
VERSION AX623587.1 GI:28451528
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE Method for determining homeostasis of the skin
  JOURNAL PATENT: WO 02053774-A 628 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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    1..11
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAAACA 745
Db 10 AATCAGAAACA 1

RESULT 231
AX623632
LOCUS AX623632 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 673 from Patent WO02053774.
ACCESSION AX623632
VERSION AX623632.1 GI:28451573
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE Method for determining homeostasis of the skin
  JOURNAL PATENT: WO 02053774-A 673 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACAC 746
Db 2 AACAGAACAC 11

RESULT 232
AX624664/c
LOCUS AX624664 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1705 from Patent WO02053774.
ACCESSION AX624664
VERSION AX624664.1 GI:28452605
KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 1705 11-JUL-2002; (DE)
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      734 AGAACAGAA 743
Db      10 AGAAAGAA 1

RESULT 233
LOCUS      AX624971      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2012 from Patent WO02053774.
ACCESSION  AX624971
VERSION     AX624971.1 GI:28452912
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2012 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      736 AAACAGAA 745
Db      2 AAACAGAA 11

RESULT 234
LOCUS      AX626122      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3163 from Patent WO02053774.
ACCESSION  AX626122
VERSION     AX626122.1 GI:28454160
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3163 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11

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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      739 CAGAACACG 748
Db      1 CGAACACG 10

RESULT 235
LOCUS      AX627227      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4268 from Patent WO02053774.
ACCESSION  AX627227
VERSION     AX627227.1 GI:28455265
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4268 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      729 CCAGGAGAA 738
Db      2 CCAGGAGAA 11

RESULT 236
LOCUS      AX627341      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4382 from Patent WO02053774.
ACCESSION  AX627341
VERSION     AX627341.1 GI:28455379
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4382 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      728 GCACGAGAA 737
Db      1 GTCAGAGAA 10

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RESULT 237
AX627766/c
LOCUS AX627766 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4807 from Patent WO02053774.
ACCESSION AX627766
VERSION AX627766.1 GI:28455804
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 4807 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAAA 738
Db 11 CCAGGAGAAA 2

RESULT 238
AX628298
LOCUS AX628298 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5339 from Patent WO02053774.
ACCESSION AX628298
VERSION AX628298.1 GI:28456336
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5339 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
Db 1 GGAGAAACAG 10

RESULT 239
AX628930/c
LOCUS AX628930 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5971 from Patent WO02053774.
ACCESSION AX628930
VERSION AX628930.1 GI:28456968
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5971 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGA 742
Db 10 GATAAACAGA 1

RESULT 240
AX629191/c
LOCUS AX629191 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6232 from Patent WO02053774.
ACCESSION AX629191
VERSION AX629191.1 GI:28457229
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 6232 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
Db 11 AAAAAACAGAA 2

RESULT 241
AX630040/c
LOCUS AX630040 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7081 from Patent WO02053774.
ACCESSION AX630040
VERSION AX630040.1 GI:28458078
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 7081 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"

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/db_xref="taxon:9606"
Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAAA 738
Db 11 CCAGCAGAAA 2

RESULT 242
AX630299
LOCUS AX630299 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7340 from Patent WO02053774.
ACCESSION AX630299
VERSION AX630299.1 GI:28458337
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7340 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAAA 738
Db 1 CCAGGAGAAA 10

RESULT 243
AX631008/c
LOCUS AX631008 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8049 from Patent WO02053774.
ACCESSION AX631008
VERSION AX631008.1 GI:28459050
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8049 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACACAGAAC 745
Db 10 AATCAGAAC 1

RESULT 244
AX631053
LOCUS AX631053 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8094 from Patent WO02053774.
ACCESSION AX631053
VERSION AX631053.1 GI:28459095
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8094 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGACAC 746
Db 2 AACAGACGC 11

RESULT 245
AX632085/c
LOCUS AX632085 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9127 from Patent WO02053774.
ACCESSION AX632085
VERSION AX632085.1 GI:28467700
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9127 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAGAGAA 743
Db 10 AGAAGAGAA 1

RESULT 246
AX632392
LOCUS AX632392 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9434 from Patent WO02053774.
ACCESSION AX632392
VERSION AX632392.1 GI:28468007
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
1
AUTHORS Peterschn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9434 11-JUN-2002;
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAGACA 745
Db 2 AACAGAGACA 11

RESULT 247
AR123885/c
LOCUS AR123885 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 18 from patent US 6171821.
ACCESSION AR123885
VERSION AR123885.1 GI:14109246
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
1
AUTHORS Korneluk,R.G., Holcik,M. and Liston,P.
TITLE XIAP IRES and uses thereof
JOURNAL Patent: US 6171821-A 18 09-JAN-2001;
FEATURES Location/Qualifiers
1. .12
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAGACA 745
Db 10 AACAGAGACA 1

RESULT 248
AX328584
LOCUS AX328584 12 bp DNA linear PAT 08-JAN-2002
DEFINITION Sequence 81 from Patent EP1164203.
ACCESSION AX328584
VERSION AX328584.1 GI:18101783
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1
AUTHORS Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
TITLE Dna diagnostics based on mass spectrometry
JOURNAL Patent: EP 1164203-A 81 19-DEC-2001;
FEATURES Location/Qualifiers
1. .12
source /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
Db 2 GCCAGGAGAA 11

RESULT 249
AX328589
LOCUS AX328589 12 bp DNA linear PAT 08-JAN-2002
DEFINITION Sequence 86 from Patent EP1164203.
ACCESSION AX328589
VERSION AX328589.1 GI:18101788
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1
AUTHORS Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
TITLE Dna diagnostics based on mass spectrometry
JOURNAL Patent: EP 1164203-A 86 19-DEC-2001;
FEATURES Location/Qualifiers
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source /organism="unidentified"
/mol_type="unassigned DNA"
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Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
Db 2 GCCAGGAGAA 11

RESULT 250
BD132149
LOCUS BD132149 12 bp DNA linear PAT 18-SEP-2002
DEFINITION Dna diagnosis method based on mass spectrometry.
ACCESSION BD132149
VERSION BD132149.1 GI:23227094
KEYWORDS JP 2002507883-A/81.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 12)
AUTHORS Koester,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jurinke,C. and Rupert,A.
TITLE Dna diagnosis method based on mass spectrometry
JOURNAL Patent: JP 2002507883-A 81 12-MAR-2002;
COMMENT SEQUENOM INC
PN JP 2002507883-A/81
PD 12-MAR-2002
PF 06-NOV-1997 JP 1998521832
PR 06-NOV-1996 US 08/744481, 06-NOV-1996 US 08/746036 PR
06-NOV-1996 US 08/746055, 06-NOV-1996 US 08/744590 PR
23-JAN-1997 US 08/786988, 23-JAN-1997 US 08/787639 PR
19-SEP-1997 US 08/933792, 08-OCT-1997 US 08/947801 FI
KOSTER,DANIEL P LITTLE,ANDREAS BRAUN,DAVID M LOUGH, PI GUOBIING
XIANG,
PI DIRK VAN DEN BOOM,CHRISTIAN JURINKE,ANDREAS RUPERT PC
C12Q1/68,C07H21/00,C07F9/24
CC Strandedness: Single;
CC Topology: Unknown;
FH Key Location/Qualifiers
1. .12
source /organism="synthetic construct"
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/db_xref="taxon:32630"

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Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
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Db 2 GCCAGGAGAA 11

RESULT 251
BD132154
LOCUS
DEFINITION DNA diagnosis method based on mass spectrometry.
ACCESSION BD132154
VERSION BD132154.1 GI:23227059
KEYWORDS JP 2002507883-A/86.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jurinke,C. and Rupert,A.
TITLE DNA diagnosis method based on mass spectrometry
JOURNAL Patent: JP 2002507883-A 86 12-MAR-2002;
SEQUENCE INC
COMMENT PN JP 2002507883-A/86
PD 12-MAR-2002
PR 06-NOV-1997 JP 1998521832
PR 06-NOV-1996 US 08/744481, 06-NOV-1996 US 08/746036 PR
08-NOV-1996 US 08/746055, 06-NOV-1996 US 08/744590 PR
23-JAN-1997 US 08/786988, 23-JAN-1997 US 08/787639 PR
19-SEP-1997 US 08/933792, 08-OCT-1997 US 08/947801 PI HUBERT
KOSTER, DANIEL P LITTLE, ANDREAS BRAUN, DAVID M LOUGH, PI GUOBING
XIANG.
PI DIRK VAN DEN BOOM, CHRISTIAN JURINKE, ANDREAS RUPERT PC
C12Q1/68, C07H21/00, C07F9/24
CC Strandedness: Single;
CC Topology: Unknown;
FH Key Location/Qualifiers.

FEATURES
source
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
|||||
Db 2 GCCAGGAGAA 11

RESULT 252
S73118S1
LOCUS
DEFINITION dystrophin {intragenic deletion} [human, Genomic Mutant, 12 nt,
segment 1 of 2].
ACCESSION S73118
VERSION S73118
KEYWORDS S73118.1 GI:241100
SEGMENT
SOURCE i of 2
Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 12)
AUTHORS Love,D.R., Flint,T.J., Genet,S.A., Middleton-Price,H.R. and
Davies,K.E.
TITLE Becker muscular dystrophy patient with a large intragenic
dystrophin deletion: implications for functional minigenes and gene
therapy

J. Med. Genet. 28 (12), 860-864 (1991)
92099269
MEDLINE
1757963
PUBMED
GenBank staff at the National Library of Medicine created this
entry [NCBI gibseq 73118] from the original journal article.
This sequence comes from 2.
Location/Qualifiers
1..12
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACAC 746
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Db 2 AACAGATCAC 11

RESULT 253
BD239119
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239119
VERSION BD239119.1 GI:33048889
KEYWORDS JP 2002534056-A/537.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.I. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 537 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/537
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992, 19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878, 19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090006, 19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999, 19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042, 19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044, 19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080, 19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994, 19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078, 19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19, C12N5/10, C01N33/53, C01N33/50, C01N33/53, C01N33/566, PC
GOIN37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 36.4%; Score 8; DB 1; Length 10;

[illegible]


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AUTHORS      van der Kuyl, A.C. and Cornelissen, M.
TITLE        Means and methods for treatment evaluation
JOURNAL      Patent: EP 1225233-A 27 24-JUL-2002;
             Amsterdam Support Diagnostics B.V. (NL)
FEATURES     Location/Qualifiers
             source
               1..11
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="TAG sequence Hs23579"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 268
AX623051
LOCUS      AX623051
DEFINITION Sequence 92 from Patent WO02053774.
ACCESSION  AX623051
VERSION     AX623051.1 GI:28450992
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conrad, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 92 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 269
AX623051
LOCUS      AX623051
DEFINITION Sequence 92 from Patent WO02053774.
ACCESSION  AX623051
VERSION     AX623051.1 GI:28450992
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conrad, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 92 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

AUTHORS      van der Kuyl, A.C. and Cornelissen, M.
TITLE        Means and methods for treatment evaluation
JOURNAL      Patent: WO 02059558-A 27 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES     Location/Qualifiers
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               1..11
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 268
AX511289
LOCUS      AX511289
DEFINITION Sequence 27 from Patent WO02059558.
ACCESSION  AX511289
VERSION     AX511289.1 GI:23392166
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE    1
AUTHORS      van der Kuyl, A.C. and Cornelissen, M.
TITLE        Means and methods for treatment evaluation
JOURNAL      Patent: WO 02059558-A 27 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES     Location/Qualifiers
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 269
AX623051
LOCUS      AX623051
DEFINITION Sequence 92 from Patent WO02053774.
ACCESSION  AX623051
VERSION     AX623051.1 GI:28450992
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conrad, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 92 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source
               1..11
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               /db_xref="taxon:9606"

AUTHORS      van der Kuyl, A.C. and Cornelissen, M.
TITLE        Means and methods for treatment evaluation
JOURNAL      Patent: EP 1225233-A 27 24-JUL-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES     Location/Qualifiers
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               /note="TAG sequence Hs23579"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 270
AX623196/c
LOCUS      AX623196/c
DEFINITION Sequence 237 from Patent WO02053774.
ACCESSION  AX623196
VERSION     AX623196.1 GI:28451137
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conrad, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 237 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
Db      11 GCCAGGAG 4

RESULT 271
AX623555/c
LOCUS      AX623555/c
DEFINITION Sequence 596 from Patent WO02053774.
ACCESSION  AX623555
VERSION     AX623555.1 GI:28451496
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conrad, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 596 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      729 CCAGGAGA 736
Db      8 CCAGGAGA 1

RESULT 272
AX624933

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LOCUS       AX624933               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 1974 from Patent WO02053774.
ACCESSION    AX624933
VERSION      AX624933.1  GI:28452874
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 1974 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AACACAGAA 743
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Db 3 AACACAGAA 10

RESULT 273
AX624958/c
LOCUS       AX624958               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 1999 from Patent WO02053774.
ACCESSION    AX624958
VERSION      AX624958.1  GI:28452899
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 1999 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
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             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AACACAGAA 743
|||||
Db 11 AACACAGAA 4

RESULT 274
AX624999/c
LOCUS       AX624999               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 2040 from Patent WO02053774.
ACCESSION    AX624999
VERSION      AX624999.1  GI:28452940
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.

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TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2040 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAG 735
|||||
Db 8 GCCAGGAG 1

RESULT 275
AX625252
LOCUS       AX625252               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 2293 from Patent WO02053774.
ACCESSION    AX625252
VERSION      AX625252.1  GI:28453193
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2293 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAG 735
|||||
Db 1 GCCAGGAG 8

RESULT 276
AX625448
LOCUS       AX625448               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 2489 from Patent WO02053774.
ACCESSION    AX625448
VERSION      AX625448.1  GI:28453389
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2489 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAG 735
|||||
Db 1 GCCAGGAG 8

RESULT 277
AX625448
LOCUS       AX625448               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 2489 from Patent WO02053774.
ACCESSION    AX625448
VERSION      AX625448.1  GI:28453389
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2489 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
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             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAG 735
|||||
Db 1 GCCAGGAG 8

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Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      741  GAACACCG 748
Db      1  GAACACCG 8

RESULT 277
AX625885/c
LOCUS      AX625885      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2926 from Patent WO02053774.
ACCESSION  AX625885
VERSION     AX625885.1  GI:28453923
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2926 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
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Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      728  GCCAGGAG 735
Db      3  GCCAGGAG 10

RESULT 280
AX626990/c
LOCUS      AX626990      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4031 from Patent WO02053774.
ACCESSION  AX626990
VERSION     AX626990.1  GI:28455028
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4031 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      732  GGAGAAAC 739
Db      10 GGAGAAAC 3

RESULT 281
AX627679
LOCUS      AX627679      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4720 from Patent WO02053774.
ACCESSION  AX627679
VERSION     AX627679.1  GI:28455717
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4720 11-JUL-2002;

Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      741  GAACACCG 748
Db      1  GAACACCG 8

RESULT 277
AX625885/c
LOCUS      AX625885      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2926 from Patent WO02053774.
ACCESSION  AX625885
VERSION     AX625885.1  GI:28453923
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2926 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      728  GCCAGGAG 735
Db      3  GCCAGGAG 10

RESULT 280
AX626990/c
LOCUS      AX626990      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4031 from Patent WO02053774.
ACCESSION  AX626990
VERSION     AX626990.1  GI:28455028
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4031 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      732  GGAGAAAC 739
Db      10 GGAGAAAC 3

RESULT 281
AX627679
LOCUS      AX627679      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4720 from Patent WO02053774.
ACCESSION  AX627679
VERSION     AX627679.1  GI:28455717
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4720 11-JUL-2002;

Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      741  GAACACCG 748
Db      1  GAACACCG 8

RESULT 277
AX625885/c
LOCUS      AX625885      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2926 from Patent WO02053774.
ACCESSION  AX625885
VERSION     AX625885.1  GI:28453923
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2926 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      728  GCCAGGAG 735
Db      3  GCCAGGAG 10

RESULT 280
AX626990/c
LOCUS      AX626990      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4031 from Patent WO02053774.
ACCESSION  AX626990
VERSION     AX626990.1  GI:28455028
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4031 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      732  GGAGAAAC 739
Db      10 GGAGAAAC 3

RESULT 281
AX627679
LOCUS      AX627679      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4720 from Patent WO02053774.
ACCESSION  AX627679
VERSION     AX627679.1  GI:28455717
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4720 11-JUL-2002;

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FEATURES             Henkel Kommanditgesellschaft auf Aktien (DE)
source
  1. .11
  Location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 CAGGAGAA 737
Db 1 CAGGAGAA 8

RESULT 282
AX627723
LOCUS             AX627723
DEFINITION       Sequence 4764 from Patent WO02053774.
ACCESSION        AX627723
VERSION          AX627723.1 GI:28455761
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 4764 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
  1. .11
  Location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACAC 746
Db 3 CAGAACAC 10

RESULT 283
AX628113
LOCUS             AX628113
DEFINITION       Sequence 5154 from Patent WO02053774.
ACCESSION        AX628113
VERSION          AX628113.1 GI:28456151
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 5154 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
  1. .11
  Location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 CAGAAACA 740
Db 1 CAGAAACA 8

RESULT 284
AX628247/c
LOCUS             AX628247/c
DEFINITION       Sequence 5288 from Patent WO02053774.
ACCESSION        AX628247
VERSION          AX628247.1 GI:28456285
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 5288 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
  1. .11
  Location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACAC 746
Db 8 CAGAACAC 1

RESULT 285
AX628626/c
LOCUS             AX628626/c
DEFINITION       Sequence 5667 from Patent WO02053774.
ACCESSION        AX628626
VERSION          AX628626.1 GI:28456664
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 5667 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
  1. .11
  Location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGAA 743
Db 9 AAACAGAA 2

RESULT 286
AX628755/c
LOCUS             AX628755/c
DEFINITION       Sequence 5796 from Patent WO02053774.
ACCESSION        AX628755
VERSION          AX628755.1 GI:28456793

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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 5796 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches       8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           732 GGAGAAAC 739
Db           11 GGAGAAAC 4

RESULT 287
LOCUS        AX629350/c              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION   Sequence 6391 from Patent WO02053774.
ACCESSION    AX629350
VERSION      AX629350.1 GI:28457388
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6391 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches       8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           728 GCCAGGAG 735
Db           10 GCCAGGAG 3

RESULT 288
LOCUS        AX629616/c              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION   Sequence 6657 from Patent WO02053774.
ACCESSION    AX629616
VERSION      AX629616.1 GI:28457654
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6657 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches       8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           728 GCCAGGAG 735
Db           10 GCCAGGAG 3

RESULT 289
LOCUS        AX630472              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION   Sequence 7513 from Patent WO02053774.
ACCESSION    AX630472
VERSION      AX630472.1 GI:28458510
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7513 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches       8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           730 CAGGAGAA 737
Db           4 CAGGAGAA 11

RESULT 290
LOCUS        AX630617/c              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION   Sequence 7658 from Patent WO02053774.
ACCESSION    AX630617
VERSION      AX630617.1 GI:28458655
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7658 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches       8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           730 CAGGAGAA 737
Db           4 CAGGAGAA 11

RESULT 291
LOCUS        AX630617/c              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION   Sequence 7658 from Patent WO02053774.
ACCESSION    AX630617
VERSION      AX630617.1 GI:28458655
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7658 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches       8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           728 GCCAGGAG 735
Db           10 GCCAGGAG 3

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	VERSION	AR029900.1	GI:5943114	
KEYWORDS	SOURCE	Unknown.		
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 11)			
AUTHORS	Wang,C.-G. and Hepburn,A.G.			
TITLE	Genetic sequence assay using DNA triple strand formation			
JOURNAL	Patent: US 5861244-A 89 19-JAN-1999;			
FEATURES	Location/Qualifiers			
	source			
	1..11			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	35.5%; Score 7.8; DB 1; Length 11;			
Best Local Similarity	81.8%; Pred. No. 2.3e+02;			
Matches	9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	731 AGGAGAAACAG 741			
Db	1 AGGAGAGAAG 11			
RESULT 299				
LOCUS	AR070933			
DEFINITION	Sequence 14 from patent US 5908972.			
ACCESSION	AR070933			
VERSION	AR070933.1			
KEYWORDS	GI:7221821			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 11)			
AUTHORS	Houtz,R.L.			
TITLE	Isolated spinach ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit sup. epsilon. N-methyltransferase and method of inactivating ribulose-1,5-bisphosphatase carboxylase/oxygenase large subunit sup. epsilon. N-methyltransferase activity			
JOURNAL	Patent: US 5908972-A 14 01-JUN-1999;			
FEATURES	Location/Qualifiers			
	source			
	1..11			
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	/mol_type="unassigned DNA"			
Query Match	35.5%; Score 7.8; DB 1; Length 11;			
Best Local Similarity	81.8%; Pred. No. 2.3e+02;			
Matches	9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	733 GAGAAACAGAA 743			
Db	11 GAGAAAAAAA 1			
RESULT 300				
LOCUS	AR157632			
DEFINITION	Sequence 14 from patent US 6245541.			
ACCESSION	AR157632			
VERSION	AR157632.1			
KEYWORDS	GI:16218594			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 11)			
AUTHORS	Houtz,R.L.			
TITLE	Isolated spinach ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit epsilon. n-methyltransferase and method of inactivating ribulose-1,5-bisphosphatase .epsilon.silicon. n-methyltransferase activity			
JOURNAL	Patent: US 6245541-A 14 12-JUN-2001;			
FEATURES	Location/Qualifiers			
	source			
	1..11			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	36.4%; Score 8; DB 1; Length 11;			
Best Local Similarity	100.0%; Pred. No. 2.1e+02;			
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	728 GCCAGAG 735			
Db	1 GCCAGAG 8			
RESULT 296				
LOCUS	AR029821/c			
DEFINITION	Sequence 10 from patent US 5861244.			
ACCESSION	AR029821			
VERSION	AR029821.1			
KEYWORDS	GI:5943035			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 12)			
AUTHORS	Wang,C.-G. and Hepburn,A.G.			
TITLE	Genetic sequence assay using DNA triple strand formation			
JOURNAL	Patent: US 5861244-A 10 19-JAN-1999;			
FEATURES	Location/Qualifiers			
	source			
	1..12			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	36.4%; Score 8; DB 1; Length 12;			
Best Local Similarity	100.0%; Pred. No. 2.3e+02;			
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	731 AGGAGAAA 738			
Db	8 AGGAGAAA 1			
RESULT 297				
LOCUS	I43337			
DEFINITION	Sequence 5 from patent US 5631148.			
ACCESSION	I43337			
VERSION	I43337.1			
KEYWORDS	GI:2468581			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 12)			
AUTHORS	Urdea,M.S.			
TITLE	Ribozymes with product ejection by strand displacement			
JOURNAL	Patent: US 5631148-A 5 20-MAY-1997;			
FEATURES	Location/Qualifiers			
	source			
	1..12			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	36.4%; Score 8; DB 1; Length 12;			
Best Local Similarity	88.9%; Pred. No. 2.3e+02;			
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	731 AGGAGAAC 739			
Db	4 ANGAGAAC 12			
RESULT 298			</	

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AX393119.1 GI:19701169					
VERSION KEYWORDS Homo sapiens (human) SOURCE ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B. TITLE Endothelial cell expression patterns JOURNAL Patent: WO 0210217-A 49 07-FEB-2002; The Johns Hopkins University (US)					
FEATURES source Location/Qualifiers 1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"					
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QY 727 TGCCAGGAGAA 737 Db 1 TGCCAGGTGCA 11					
RESULT 304 AX470720/c LOCUS AX470720 11 bp DNA linear PAT 09-AUG-2002 DEFINITION Sequence 297 from Patent WO02053773. ACCESSION AX470720 VERSION AX470720.1 GI:22205845 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE AUTHORS Hofmann,K., Conradt,M. and Petersohn,D. TITLE Method for determining skin stress or skin ageing in vitro JOURNAL Patent: WO 02053773-A 297 11-JUL-2002; HENKEL KGAA (DE)					
FEATURES source Location/Qualifiers 1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"					
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QY 727 TGCCAGGAGAA 737 Db 11 TGCCAAGAGTA 1					
RESULT 305 AX471467/c LOCUS AX471467 11 bp DNA linear PAT 09-AUG-2002 DEFINITION Sequence 1044 from Patent WO02053773. ACCESSION AX471467 VERSION AX471467.1 GI:22206592 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE AUTHORS Hofmann,K., Conradt,M. and Petersohn,D. TITLE Method for determining skin stress or skin ageing in vitro JOURNAL Patent: WO 02053773-A 1044 11-JUL-2002; HENKEL KGAA (DE)					
/organism="unknown" /mol_type="unassigned DNA"					
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RESULT 301 AR164474 LOCUS AR164474 11 bp DNA linear PAT 17-OCT-2001 DEFINITION Sequence 8 from patent US 6274134. ACCESSION AR164474 VERSION AR164474.1 GI:16237515 KEYWORDS SOURCE Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 11) AUTHORS Beckner,M.E., Krutzsch,H.C. and Liotta,L.A. TITLE Human cell adhesion protein AAMP-1 and uses thereof JOURNAL Patent: US 6274134-A 8 14-AUG-2001; Location/Qualifiers 1..11 /organism="unknown" /mol_type="unassigned DNA"					
Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 2.3e+02; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY 731 AGGAGAACAG 741 Db 1 AGGAGGAAG 11					
RESULT 302 AR301492/c LOCUS AR301492 11 bp DNA linear PAT 12-JUN-2003 DEFINITION Sequence 73 from patent US 6538173. ACCESSION AR301492 VERSION AR301492.1 GI:31689294 KEYWORDS SOURCE Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 11) AUTHORS Heber-Katz,E. TITLE Compositions and methods for wound healing JOURNAL Patent: US 6538173-A 73 25-MAR-2003; Location/Qualifiers 1..11 /organism="unknown" /mol_type="genomic DNA"					
Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 2.3e+02; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY 732 GGAGAAACAGA 742 Db 11 GCAGAAACCGA 1					
RESULT 303 AX393119 LOCUS AX393119 11 bp DNA linear PAT 23-MAR-2002 DEFINITION Sequence 49 from Patent W00210217. ACCESSION AX393119					

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KEYWORDS Homo sapiens (human)					
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE 1 St Croix,B., Kinzler,K.W. and Vogelstein,B. Endothelial cell expression patterns Patent: WO 0210217-A 49 07-FEB-2002; The Johns Hopkins University (US) FEATURES Location/Qualifiers					
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;					
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY 727 TGCCAGGAGAA 737					
Db 1 TGCCAGGTGCA 11					
RESULT 304					
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LOCUS AX470720 11 bp DNA linear PAT 09-AUG-2002					
DEFINITION Sequence 297 from Patent WO02053773.					
ACCESSION AR301492					
VERSION AR301492.1 GI:22205845					
KEYWORDS Homo sapiens (human)					
SOURCE Homo sapiens					
ORGANISM Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE 1 Hofmann,K., Conradt,M. and Petersohn,D. Method for determining skin stress or skin ageing in vitro Patent: WO 02053773-A 297 11-JUL-2002; HENKEL KGAA (DE) FEATURES Location/Qualifiers					
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QY 727 TGCCAGGAGAA 737					
Db 11 TGCCAAGAGTA 1					
RESULT 305					
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LOCUS AX471467 11 bp DNA linear PAT 09-AUG-2002					
DEFINITION Sequence 1044 from Patent WO02053773.					
ACCESSION AR471467					
VERSION AR471467.1 GI:22206592					
KEYWORDS Homo sapiens (human)					
SOURCE Homo sapiens					
ORGANISM Homo sapiens					
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REFERENCE 1 Hofmann,K., Conradt,M. and Petersohn,D. Method for determining skin stress or skin ageing in vitro Patent: WO 02053773-A 1044 11-JUL-2002; HENKEL KGAA (DE)					
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;					
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QY 733 GAGAAAACAGA 743					
Db 11 GAGAAAAA 1					
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LOCUS AR164474 11 bp DNA linear PAT 17-OCT-2001					
DEFINITION Sequence 8 from patent US 6274134.					
ACCESSION AR164474					
VERSION AR164474.1 GI:16237515					
KEYWORDS Unknown.					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 11) Beckner,M.E., Krutzsch,H.C. and Liotta,L.A. Human cell adhesion protein AAMP-1 and uses thereof Patent: US 6274134-A 8 14-AUG-2001; FEATURES Location/Qualifiers					
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Db 1 AGGAGGAAGC 11					
RESULT 302					
AR301492/c					
LOCUS AR301492 11 bp DNA linear PAT 12-JUN-2003					
DEFINITION Sequence 73 from patent US 6538173.					
ACCESSION AR301492					
VERSION AR301492.1 GI:31689294					
KEYWORDS Unknown.					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 11) Heber-Katz,E. Compositions and methods for wound healing Patent: US 6538173-A 73 25-MAR-2003; FEATURES Location/Qualifiers					
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;					
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QY 732 GGAGAAAACAGA 742					
Db 11 GCAGAAACCGA 1					
RESULT 303					
AX393119					
LOCUS AX393119 11 bp DNA linear PAT 23-MAR-2002					
DEFINITION Sequence 49 from Patent W00210217.					
ACCESSION AX393119					

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Location/Qualifiers
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Query Match
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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAACACAGA 742
Db 11 GGGGATACAGA 1

RESULT 306
AX623210
LOCUS AX623210 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 251 from Patent WO02053774.
ACCESSION AX623210
VERSION AX623210.1 GI:28451151
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 251 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
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/db_xref="taxon:9606"

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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
Db 1 TGCCAGGTGCA 11

RESULT 307
AX623389
LOCUS AX623389 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 430 from Patent WO02053774.
ACCESSION AX623389
VERSION AX623389.1 GI:28451330
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 430 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 738 ACAGAACACCG 748
Db 11 GGGGATACAGA 1

RESULT 308
AX623815
LOCUS AX623815 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 856 from Patent WO02053774.
ACCESSION AX623815
VERSION AX623815.1 GI:28451756
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 856 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11;
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QY 735 GAACAGAACAA 745
Db 1 GAACAGGAAA 11

RESULT 309
AX623866/C
LOCUS AX623866 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 907 from Patent WO02053774.
ACCESSION AX623866
VERSION AX623866.1 GI:28451807
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 907 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Query Match
Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAACACAGAA 743
Db 11 GAGAACACAAA 1

RESULT 310
AX624241/C
LOCUS AX624241 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1282 from Patent WO02053774.
ACCESSION AX624241
VERSION AX624241.1 GI:28452182
KEYWORDS
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1282 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGACAGAAC 744
DB      11 AAAAGAGAGAAC 1

RESULT 311
LOCUS      AX624366                      11 bp      DNA
DEFINITION Sequence 1407 from Patent WO02053774.
ACCESSION  AX624366
VERSION     AX624366.1 GI:28452307
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1407 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      733 GAGAAACAGAA 743
DB      1 GAGAGAGAGAA 11

RESULT 312
LOCUS      AX625243                      11 bp      DNA
DEFINITION Sequence 2284 from Patent WO02053774.
ACCESSION  AX625243
VERSION     AX625243.1 GI:28453184
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 2284 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGACAGAAC 744
DB      1 AGCACCAGAAC 11

RESULT 313
LOCUS      AX625333                      11 bp      DNA
DEFINITION Sequence 2374 from Patent WO02053774.
ACCESSION  AX625333
VERSION     AX625333.1 GI:28453274
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 2374 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 GGAGAAACAGAA 742
DB      11 GGTGTACAGAA 1

RESULT 314
LOCUS      AX626135                      11 bp      DNA
DEFINITION Sequence 3176 from Patent WO02053774.
ACCESSION  AX626135
VERSION     AX626135.1 GI:28454173
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 3176 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match      35.5%; Score 7.8; DB 1; Length 11;
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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGACAGAAC 744
DB      11 AGAACCAGAGC 1

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RESULT 315
AX626314
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3355 from Patent WO02053774.
ACCESSION  AX626314
VERSION     AX626314.1 GI:28454352
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3355 11-JUL-2002; (DE)
           Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      738 ACAGAACACCG 748
Db      1 ACAGAGCACAG 11

RESULT 316
AX626528
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3569 from Patent WO02053774.
ACCESSION  AX626528
VERSION     AX626528.1 GI:28454566
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3569 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      736 AACACAGAACAC 746
Db      1 AACACATACAC 11

RESULT 317
AX626853/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3894 from Patent WO02053774.
ACCESSION  AX626853
VERSION     AX626853.1 GI:28454891
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 4522 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      735 GAAACAGACACA 745
Db      1 GAAACAGAAAAA 11

RESULT 319
AX627481
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4522 from Patent WO02053774.
ACCESSION  AX627481
VERSION     AX627481.1 GI:28455519
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 4522 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      1 GAAACAGAAAAA 11
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REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3894 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      734 AGAACAGACAC 744
Db      11 AGAATCAGCAC 11

RESULT 318
AX627269
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4310 from Patent WO02053774.
ACCESSION  AX627269
VERSION     AX627269.1 GI:28455307
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 4310 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      735 GAAACAGACACA 745
Db      1 GAAACAGAAAAA 11

RESULT 319
AX627481
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4522 from Patent WO02053774.
ACCESSION  AX627481
VERSION     AX627481.1 GI:28455519
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 4522 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      735 GAAACAGACACA 745
Db      1 GAAACAGAAAAA 11
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/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
Db 1 GCCAGGAGAAA 11

RESULT 320
AX628291/c
LOCUS
DEFINITION
Sequence 5332 from Patent WO02053774.
ACCESSION
AX628291
VERSION
AX628291.1 GI:28456329
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5332 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAA 737
Db 11 TGCCAAGAGTA 1

RESULT 321
AX628354/c
LOCUS
DEFINITION
Sequence 5395 from Patent WO02053774.
ACCESSION
AX628354
VERSION
AX628354.1 GI:28456392
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5395 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACCAACA 745
Db 11 GAAACCAACA 1

/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACA 740
Db 1 CAGGAGAAACA 11

RESULT 324
AX628943/c
LOCUS
DEFINITION
Sequence 5984 from Patent WO02053774.
ACCESSION
AX628943
VERSION
AX628943.1 GI:28456981
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5888 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
Db 11 GGGATACAGA 1

RESULT 323
AX628847
LOCUS
DEFINITION
Sequence 5988 from Patent WO02053774.
ACCESSION
AX628847
VERSION
AX628847.1 GI:28456885
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5888 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GGAGAAACAGA 742
Db 11 GGGATACAGA 1

RESULT 324
AX628943/c
LOCUS
DEFINITION
Sequence 5984 from Patent WO02053774.
ACCESSION
AX628943
VERSION
AX628943.1 GI:28456981
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5888 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACCAACA 745
Db 11 GAAACCAACA 1

```



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REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5984 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGAGAAC 744
Db 11 ACAAGAGAAC 1

RESULT 325
AX629425
LOCUS AX629425 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6466 from Patent WO02053774.
ACCESSION AX629425
VERSION AX629425.1 GI:28457463
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6466 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
Db 1 AAACAAATCAC 11

RESULT 326
AX629695/c
LOCUS AX629695 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6736 from Patent WO02053774.
ACCESSION AX629695
VERSION AX629695.1 GI:28457733
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6736 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 737 AACAGAACAC 747
Db 11 AAAAAACAGC 1

RESULT 327
AX629821/c
LOCUS AX629821 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6862 from Patent WO02053774.
ACCESSION AX629821
VERSION AX629821.1 GI:28457859
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6862 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
Db 11 AGGAGGACCAG 1

RESULT 328
AX629849
LOCUS AX629849 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6890 from Patent WO02053774.
ACCESSION AX629849
VERSION AX629849.1 GI:28457887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6890 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 738
Db 1 GCCAGGTGAA 11

RESULT 329
AX630158/c

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LOCUS      AX630158                      11 bp      DNA          linear          PAT 21-FEB-2003
DEFINITION Sequence 7199 from Patent WO02053774.
ACCESSION  AX630158
VERSION     AX630158.1  GI:28458196
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7199 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      735  GAACAGAACCA 745
Db      11  GAACAGAGACA 1

RESULT 330
LOCUS      AX630160/c
DEFINITION Sequence 7201 from Patent WO02053774.
ACCESSION  AX630160
VERSION     AX630160.1  GI:28458198
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7201 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      733  GAGACAGACAA 743
Db      11  GTGACAGACAA 1

RESULT 331
LOCUS      AX630631                      11 bp      DNA          linear          PAT 21-FEB-2003
DEFINITION Sequence 7672 from Patent WO02053774.
ACCESSION  AX630631
VERSION     AX630631.1  GI:28458669
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7672 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      733  GAGACAGACAA 743
Db      11  GTGACAGACAA 1

RESULT 332
LOCUS      AX630810                      11 bp      DNA          linear          PAT 21-FEB-2003
DEFINITION Sequence 7851 from Patent WO02053774.
ACCESSION  AX630810
VERSION     AX630810.1  GI:28458850
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7851 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source
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               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      727  TGCAGAGAGAA 737
Db      11  TGCAGAGTGCA 11

RESULT 333
LOCUS      AX631236                      11 bp      DNA          linear          PAT 21-FEB-2003
DEFINITION Sequence 8278 from Patent WO02053774.
ACCESSION  AX631236
VERSION     AX631236.1  GI:28459282
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8278 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      738  ACAGAACACCG 748
Db      11  ACAAACACCG 11

RESULT 333
LOCUS      AX631236                      11 bp      DNA          linear          PAT 21-FEB-2003
DEFINITION Sequence 8278 from Patent WO02053774.
ACCESSION  AX631236
VERSION     AX631236.1  GI:28459282
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8278 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      738  ACAGAACACCG 748
Db      11  ACAAACACCG 11

```


Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 742

Db 11 GGTGTAACAG 1

RESULT 339

AX772229/c

LOCUS AX772229 11 bp DNA linear PAT 02-JUL-2003

DEFINITION Sequence 19 from Patent WO03042407.

ACCESSION AX772229

VERSION AX772229.1 GI:32438802

KEYWORDS

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS Dickson,B., Berger,J., Suzuki,T. and Knoblich,J.

TITLE Method for identifying therapeutic targets by use of genetic

JOURNAL screens in drosophila melanogaster

PATENT: WO 03042407-A 19 22-MAY-2003;

BOEHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents (DE)

FEATURES

source
Location/Qualifiers
1. .11
/organism="Drosophila melanogaster"
/mol_type="unassigned DNA"
/db_xref="taxon:7227"

Query Match

Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746

Db 11 AAACAAAAAC 1

RESULT 340

BD124242/c

LOCUS BD124242 11 bp DNA linear PAT 18-SEP-2002

DEFINITION Compositions and method for healing wound.

ACCESSION BD124242

VERSION BD124242.1 GI:23219187

KEYWORDS JP 2002503460-A/73.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 11)

REFERENCE

AUTHORS Katzi,E.H.

TITLE Compositions and method for healing wound

JOURNAL Patent: JP 2002503460-A 73 05-FEB-2002;

THE WISTAR INSTITUTE

COMMENT OS Mus musculus (mouse)

PN JP 2002503460-A/73

PD 05-FEB-2002

PF 12-FEB-1999 JP 2000331545

PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR

28-SEP-1998 US 60/102051

PI ELLEN HEBER KATZ

PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC

C12N5/00

CC Compositions and method for healing wound

Location/Qualifiers

FT Key 1. .11

FT source /organism="Mus musculus (mouse)"

Location/Qualifiers

1. .11

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

Query Match 35.5%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 2.3e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 742

Db 11 GCAGAAACCGA 1

RESULT 341

BD174612

LOCUS BD174612 11 bp DNA linear PAT 18-MAR-2003

DEFINITION Modified promoter.

ACCESSION BD174612

VERSION BD174612.1 GI:29120302

KEYWORDS JP 200272466-A/1.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 11)

AUTHORS Mizubuchi,H., Fushimi,N. and Miyoshi,S.

TITLE Modified promoter

JOURNAL Patent: JP 200272466-A 1 24-SEP-2002;

SHOWA SANGYO CO LTD DIRECTOR GENERAL OF NATIONAL INSTITUTE OF

ADVANCED INDUSTRIAL SCIENCE AND

COMMENT OS Artificial Sequence

PN JP 200272466-A/1

PD 24-SEP-2002

PF 15-MAR-2001 JP 2001074780

PI HIROYUKI MIZUBUCHI, NAOYA FUSHIMI, SHINSUKE MIYOSHI PC

C12N15/09,C12N1/21,C12P21/02// (C12N1/21,C12R1/07), (C12N1/21, PC

C12R1/01)

PC (C12N1/21,C12R1/19), C12N15/00

CC Modified promoter

FT Key 1. .11

FT source Location/Qualifiers

Location/Qualifiers

1. .11

/organism="Artificial Sequence".

FEATURES

source

Location/Qualifiers

1. .11

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match

Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741

Db 1 AGGAGTACCG 11

RESULT 342

BD174617

LOCUS BD174617 11 bp DNA linear PAT 18-MAR-2003

DEFINITION Modified promoter.

ACCESSION BD174617

VERSION BD174617.1 GI:29120307

KEYWORDS JP 200272466-A/6.

SOURCE synthetic construct

ORGANISM artificial sequences.

```

REFERENCE 1 (bases 1 to 11)
AUTHORS Mizubuchi,H., Fushimi,N. and Miyoshi,S.
TITLE Modified promoter
JOURNAL Patent: JP 200272466-A 6 24-SEP-2002;
COMMENT SHOWA SANGYO CO LTD
OS Artificial Sequence
PN JP 200272466-A/6
PD 24-SEP-2002
PF 15-MAR-2001 JP 2001074780
PI HIROYUKI MIZUBUCHI,NAOYA FUSHIMI,SHINSUKE MIYOSHI PC
C12N15/09,C12N1/21,C12P21/02/(C12N1/21,C12R1:07), (C12N1/21, PC
C12R1:01),
PC (C12N1/21,C12R1:19),C12N15/00
CC Modified promoter
FH Key Location/Qualifiers
FT source 1..11
FT /organism='Artificial Sequence'.
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/db_xref="taxon:32630"
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
|||||
DB 1 AGGAGGAGCAG 11
|||||
RESULT 343
A06060 12 bp DNA linear PAT 25-MAY-1993
LOCUS
DEFINITION Synthetic primer 579-590.
ACCESSION A06060
VERSION A06060.1 GI:411192
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Hudson,P.J., Haley,J.D., Niall,H.D. and Shine,J.
TITLE Molecular cloning and characterization of the gene sequence coding
for porcine relaxin
JOURNAL Patent: EP 0086649-A 10 24-AUG-1993;
HOWARD FLOREY INSTITUTE OF EXPERIMENTAL PHYSIOLOGY AND MEDICINE
FEATURES
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 735 GAAACAGAACCA 745
|||||
DB 2 GAAGCAGAGA 12
|||||
RESULT 344
A06061/c 12 bp DNA linear PAT 25-MAY-1993
LOCUS
DEFINITION Synthetic primer 579-590 (Reverse complement).
ACCESSION A06061
VERSION A06061.1 GI:411193
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 11)
AUTHORS Hudson,P.J., Haley,J.D., Niall,H.D. and Shine,J.
TITLE Molecular cloning and characterization of the gene sequence coding
for porcine relaxin
JOURNAL Patent: EP 0086649-A 10 24-AUG-1993;
HOWARD FLOREY INSTITUTE OF EXPERIMENTAL PHYSIOLOGY AND MEDICINE
FEATURES
source
1..11
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 735 GAAACAGAACCA 745
|||||
DB 2 GAAGCAGAGA 12
|||||
RESULT 345
A16603 12 bp DNA linear PAT 29-SEP-1994
LOCUS
DEFINITION Nucleotide sequence 11 from patent number AU562012.
ACCESSION A16603
VERSION A16603.1 GI:641064
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS
JOURNAL Patent: AU 562012-B 11 28-MAY-1987;
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Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 735 GAAACAGAACCA 745
|||||
DB 2 GAAGCAGAGA 12
|||||
RESULT 346
A16604/c 12 bp DNA linear PAT 29-SEP-1994
LOCUS
DEFINITION Nucleotide sequence 12 from patent number AU562012.
ACCESSION A16604
VERSION A16604.1 GI:641065
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS
JOURNAL Patent: AU 562012-B 12 28-MAY-1987;
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1..12
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 735 GAAACAGAACCA 745
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DB 2 GAAGCAGAGA 12
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Db      11 GAAGCAGAGA 1
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RESULT 347
A47643
LOCUS      A47643      12 bp      DNA      linear      PAT 07-MAR-1997
DEFINITION Sequence 3 from Patent EP0692535.
ACCESSION  A47643
VERSION    A47643.1  GI:2301584
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 12)
AUTHORS    Colote,S. and Pirotzky,E.
TITLE      Oligonucleotides to inhibit the role of isoprenyl protein
           transferases
JOURNAL    Patent: EP 0692535-A 3 17-JAN-1996;
           SOD CONSEILS RECH APPLIC (FR)
COMMENT    Other publication CN 1124142 960612
           Other publication CZ 9501688 960515
           Other publication BR 9503015 960504
           Other publication NZ 272398 960426
           Other publication HU 72133 960328
           Other publication JP 8051985 960227
           Other publication FR 2721930 960105
           Other publication FR 2721827 960105
           Other publication FI 9531170 951230
           Other publication SE 9502259 951230
           Other publication PL 309384 960108
           Other publication NO 952601 960102
           Other publication AU 2329995 960111
           Other publication CA 2152233 951230
           Other publication GB 2290791 960110.
FEATURES   source
           1..12
           /organism="unidentified"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32644"

Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGAACAG 741
|||||
Db      2 AGGAGTAGCAG 12

RESULT 348
A61481/c
LOCUS      A61481      12 bp      DNA      linear      PAT 09-MAR-1998
DEFINITION Sequence 50 from Patent WO9710332.
ACCESSION  A61481
VERSION    A61481.1  GI:3715876
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS    Schmidt,G.
TITLE      CHIMAERIC OLIGONUCLEOTIDES AND USES THEREOF IN THE IDENTIFICATION
           OF ANTISENSE BINDING SITES
JOURNAL    Patent: WO 9710332-A 50 20-MAR-1997;
           BRAX GENOMICS LTD (GB)
FEATURES   Location/Qualifiers
           source
           1..12
           /organism="unidentified"
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           /db_xref="taxon:32644"

Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGAACAG 741
|||||
Db      2 AGGAGTAGCAG 12

RESULT 349
A47643
LOCUS      A47643      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5856461.
ACCESSION  A47643
VERSION    A47643.1  GI:5938681
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 12)
AUTHORS    Colote,S. and Pirotzky,E.
TITLE      Oligonucleotides to inhibit the expression of isoprenyl protein
           transferases
JOURNAL    Patent: US 5856461-A 3 05-JAN-1999;
           Location/Qualifiers
           source
           1..12
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           /mol_type="unassigned DNA"

Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGAACAG 741
|||||
Db      2 AGGAGTAGCAG 12

RESULT 350
A47643
LOCUS      A47643      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 215 from patent US 5861244.
ACCESSION  A47643
VERSION    A47643.1  GI:5943240
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 12)
AUTHORS    Wang,C.-G. and Hepburn,A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 215 19-JAN-1999;
           Location/Qualifiers
           source
           1..12
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Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      733 GAGGAGAACAG 743
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Db      1 GAGGAGAACAG 11

RESULT 351
A47643
LOCUS      A47643      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 229 from patent US 5861244.
ACCESSION  A47643
VERSION    A47643.1  GI:5943254
KEYWORDS   unidentified
SOURCE     unidentified

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Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGCAGAAC 744
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Db      12 AGGAGTAGCAG 2

RESULT 349
A47643
LOCUS      A47643      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5856461.
ACCESSION  A47643
VERSION    A47643.1  GI:5938681
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 12)
AUTHORS    Colote,S. and Pirotzky,E.
TITLE      Oligonucleotides to inhibit the expression of isoprenyl protein
           transferases
JOURNAL    Patent: US 5856461-A 3 05-JAN-1999;
           Location/Qualifiers
           source
           1..12
           /organism="unassigned DNA"
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Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGAACAG 741
|||||
Db      2 AGGAGTAGCAG 12

RESULT 350
A47643
LOCUS      A47643      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 215 from patent US 5861244.
ACCESSION  A47643
VERSION    A47643.1  GI:5943240
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 12)
AUTHORS    Wang,C.-G. and Hepburn,A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 215 19-JAN-1999;
           Location/Qualifiers
           source
           1..12
           /organism="unassigned DNA"
           /mol_type="unassigned DNA"

Query Match      35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      733 GAGGAGAACAG 743
|||||
Db      1 GAGGAGAACAG 11

RESULT 351
A47643
LOCUS      A47643      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 229 from patent US 5861244.
ACCESSION  A47643
VERSION    A47643.1  GI:5943254
KEYWORDS   unidentified
SOURCE     unidentified

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ORGANISM      Unknown.
Unclassified.
REFERENCE      1 (bases 1 to 12)
AUTHORS        Wang, C.-G. and Hepburn, A.G.
TITLE          Genetic sequence assay using DNA triple strand formation
JOURNAL        Patent: US 5861244-A 229 19-JAN-1999;
FEATURES       1. .12
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Query Match    35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
Db 1 GAGATAGAGAA 11

RESULT 352
LOCUS          AR030162
DEFINITION     Sequence 351 from patent US 5861244.
ACCESSION      AR030162
VERSION        AR030162.1 GI:5943376
KEYWORDS       .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE      1 (bases 1 to 12)
AUTHORS        Wang, C.-G. and Hepburn, A.G.
TITLE          Genetic sequence assay using DNA triple strand formation
JOURNAL        Patent: US 5861244-A 351 19-JAN-1999;
FEATURES       1. .12
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Query Match    35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
Db 2 GAGGAGAGAA 12

RESULT 353
LOCUS          AR058694/c
DEFINITION     Sequence 271 from patent US 5837832.
ACCESSION      AR058694
VERSION        AR058694.1 GI:5984271
KEYWORDS       .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE      1 (bases 1 to 12)
AUTHORS        Chee, M., Cronin, M.T., Fodor, S.P.A., Huang, X.X., Hubbell, E.A.,
               Lipshutz, R.J., Lobban, P.E., Morris, M.S. and Sheldon, E.L.
TITLE          Arrays of nucleic acid probes on biological chips
JOURNAL        Patent: US 5837832-A 271 17-NOV-1998;
FEATURES       1. .12
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               /mol_type="unassigned DNA"

Query Match    35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 742
Db 1 GTAGAAATAGA 11

RESULT 354
LOCUS          BD242527
DEFINITION     A system for cell based screening.
ACCESSION      BD242527
VERSION        BD242527.1 GI:33052297
KEYWORDS       JP 2002528136-A/33.
SOURCE          synthetic construct
               ORGANISM      artificial sequences.
               1 (bases 1 to 12)
REFERENCE      Guiliano, K.A., Bright, G., Olson, K. and Tencza, S.B.
AUTHORS        A system for cell based screening
TITLE          Patent: JP 2002528136-A 33 03-SEP-2002;
JOURNAL        CELLOMICS INC
COMMENT         OS Artificial Sequence
               PN JP 2002528136-A/33
               PD 03-SEP-2002
               PF 23-OCT-1999 JP 2000579780
               PR 30-OCT-1998 US 60/106308, 26-MAY-1999 US 60/136078 PI
               KENNETH A GUILIANO, GARY BRIGHT, KEITH OLSON, SARAH BURROUGHS PI
               TENCZA
               PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/02, C12Q1/
               PC 37, G01N33/15,
               PC G01N33/50, C12N15/00, C12N5/00
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Query Match    35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 742
Db 1 GTAGAAATAGA 11

RESULT 355
LOCUS          BD248202
DEFINITION     Short-chain oligonucleotide for inhibiting VEGF expression.
ACCESSION      BD248202
VERSION        BD248202.1 GI:33057972
KEYWORDS       JP 2002524038-A/21.
SOURCE          synthetic construct
               ORGANISM      artificial sequences.
               1 (bases 1 to 12)
REFERENCE      Uhlmann, E., Peyman, A., Bitonti, A. and Woessner, R.
AUTHORS        Short-chain oligonucleotide for inhibiting VEGF expression
TITLE          Patent: JP 2002524038-A 21 06-AUG-2002;
JOURNAL        AVENTIS PHARMA DEUTSCHLAND GMBH
FEATURES       1. .12
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               /mol_type="unassigned DNA"

Query Match    35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 742
Db 1 GTAGAAATAGA 11

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Db 12 GGGAAGCAGA 2

RESULT 354
LOCUS          BD242527
DEFINITION     A system for cell based screening.
ACCESSION      BD242527
VERSION        BD242527.1 GI:33052297
KEYWORDS       JP 2002528136-A/33.
SOURCE          synthetic construct
               ORGANISM      artificial sequences.
               1 (bases 1 to 12)
REFERENCE      Guiliano, K.A., Bright, G., Olson, K. and Tencza, S.B.
AUTHORS        A system for cell based screening
TITLE          Patent: JP 2002528136-A 33 03-SEP-2002;
JOURNAL        CELLOMICS INC
COMMENT         OS Artificial Sequence
               PN JP 2002528136-A/33
               PD 03-SEP-2002
               PF 23-OCT-1999 JP 2000579780
               PR 30-OCT-1998 US 60/106308, 26-MAY-1999 US 60/136078 PI
               KENNETH A GUILIANO, GARY BRIGHT, KEITH OLSON, SARAH BURROUGHS PI
               TENCZA
               PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/02, C12Q1/
               PC 37, G01N33/15,
               PC G01N33/50, C12N15/00, C12N5/00
               CC Description of Artificial Sequence: Caspase-6 substrate CC
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               CC sequence
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               FT source
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Query Match    35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGGAAGCAGA 742
Db 1 GTAGAAATAGA 11

RESULT 355
LOCUS          BD248202
DEFINITION     Short-chain oligonucleotide for inhibiting VEGF expression.
ACCESSION      BD248202
VERSION        BD248202.1 GI:33057972
KEYWORDS       JP 2002524038-A/21.
SOURCE          synthetic construct
               ORGANISM      artificial sequences.
               1 (bases 1 to 12)
REFERENCE      Uhlmann, E., Peyman, A., Bitonti, A. and Woessner, R.
AUTHORS        Short-chain oligonucleotide for inhibiting VEGF expression
TITLE          Patent: JP 2002524038-A 21 06-AUG-2002;
JOURNAL        AVENTIS PHARMA DEUTSCHLAND GMBH
FEATURES       1. .12
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Query Match    35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGGAAGCAGA 742
Db 1 GTAGAAATAGA 11

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PC A61P13/12,A61P17/16,A61P27/02,A61P29/00,A61P35/00,A61P43/00,
PC C12N15/00
CC Description of Artificial Sequence: Antisense FH Key
FT Location/Qualifiers
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FT Location/Qualifiers
FT /organism='Artificial Sequence'.
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
DB 1 GACAGCAGAAA 11

RESULT 356
BD263213/c
LOCUS
DEFINITION
ACCESSION BD263213
VERSION BD263213.1 GI:33072981
KEYWORDS JP 2002536346-A/26.
SOURCE synthetic construct
ORGANISM artificial sequences
REFERENCE 1 (bases 1 to 12)
AUTHORS Pasternack,G.R. and Bai,J.
TITLE Method of treating cancer by restoration of pp32 function
JOURNAL Patent: JP 2002536346-A 26 29-OCT-2002;
COMMENT THE JOHNS HOPKINS UNIVERSITY
OS Artificial Sequence
PN JP 2002536346-A/26
PD 29-OCT-2002
PF 03-FEB-2000 JP 2000596971
PR 03-FEB-1999 US 60/118667
PI GARY R PASTERNAK,JINING BAI
PC A61K48/00,A61K31/115,A61K45/00,A61P35/00,C12Q1/42,G01N33/15,
PC G01N33/50//
PC C12N15/09,C12N15/00
CC recognition sequence
FH Key Location/Qualifiers
FT source 1..12
FT /organism='Artificial Sequence'.
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/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAAA 745
DB 12 GAAAAAGAAA 2

RESULT 357
BD269488/c
LOCUS
DEFINITION
ACCESSION BD269488
VERSION BD269488.1 GI:33079256
KEYWORDS JP 2002537844-A/12.
SOURCE Influenza C virus
ORGANISM Influenza C virus

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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
REFERENCE 1 (bases 1 to 12)
AUTHORS Hobom,G., Flick,R., Menke,A. and Azzezh,M.
TITLE Stable recombinant influenza virus free from helper virus
JOURNAL Patent: JP 2002537844-A 12 12-NOV-2002;
COMMENT ARTEMIS PHARMACEUTICALS GMBH
OS Influenza C virus
PN JP 2002537844-A/12
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603407
PR 06-MAR-1999 EP 99104519.6
PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEZH PC
C12N15/09,A61K39/145,A61K48/00,A61P31/16,C12N7/00,C12P21/02// PC
A61K35/12,
PC (C12N7/00,C12R1:93),C12N15/00
CC Stable recombinant influenza virus free from helper virus FH
Key Location/Qualifiers
FT source 1..12
FT /organism='Influenza C virus'.
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Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 12 AGCAGAGCAG 2

RESULT 358
BD269490/c
LOCUS
DEFINITION
ACCESSION BD269490
VERSION BD269490.1 GI:33079258
KEYWORDS JP 2002537844-A/14.
SOURCE synthetic construct
ORGANISM artificial sequences
REFERENCE 1 (bases 1 to 12)
AUTHORS Hobom,G., Flick,R., Menke,A. and Azzezh,M.
TITLE Stable recombinant influenza virus free from helper virus
JOURNAL Patent: JP 2002537844-A 14 12-NOV-2002;
COMMENT ARTEMIS PHARMACEUTICALS GMBH
OS Artificial Sequence
PN JP 2002537844-A/14
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603407
PR 06-MAR-1999 EP 99104519.6
PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEZH PC
C12N15/09,A61K39/145,A61K48/00,A61P31/16,C12N7/00,C12P21/02// PC
A61K35/12,
PC (C12N7/00,C12R1:93),C12N15/00
CC Description of Artificial Sequence: Modified influenza A 3'
sequence
FH Key Location/Qualifiers
FT source 1..12
FT /organism='Artificial Sequence'.
FEATURES
source
1..12
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;

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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
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 12 AGGAGAACAG 2

Db

RESULT 359
 E04220/c
 LOCUS 5'-region of satellite RNA. 12 bp RNA linear PAT 29-SEP-1997
 DEFINITION
 ACCESSION E04220
 VERSION E04220.1 GI:5708497
 KEYWORDS JP 1993003789-A/1.
 SOURCE Cucurbit mosaic virus (cucumber mosaic cucumovirus)
 ORGANISM Cucurbit mosaic virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae; Cucumovirus.

REFERENCE 1 (bases 1 to 12)
 AUTHORS Kominato,M., Sato,S. and Sayama,H.
 TITLE WEAK TOXIC VIRUS OF CUCUMBER MOSAIC VIRUS USING CLONED SATELLITE RNA

JOURNAL Patent: JP 1993003789-A 1 14-JAN-1993;
 NIPPON DERUMONTE KK

COMMENT OS Cucurbit mosaic virus
 PN JP 1993003789-A/1
 PD 14-JAN-1993
 PF 30-SEP-1991 JP 1991252204
 PR 11-OCT-1990 JP 90P 274465
 PI KOMINATO MASAYUKI, SATO SADAICHI, SAYAMA HARUKI PC
 C12N15/33,A01N63/00,C12N1/21,C12N7/04,C12N15/10,C12N1/21, PC
 C12R1:19;

CC strandedness: Single;
 CC topology: Linear;
 PH Key Location/Qualifiers
 FT misc_RNA 1..12
 FT /note='5'-region of satellite RNA'.

FEATURES
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 1..12
 /organism="Cucurbit mosaic virus"
 /mol_type="genomic RNA"
 /db_xref="taxon:12305"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAAGAAC 744
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 11 ACAACAAGAAC 1

Db

RESULT 360
 E32720
 LOCUS Small triple strand-forming PNA oligo. 12 bp DNA linear PAT 18-JUN-2001
 DEFINITION
 ACCESSION E32720
 VERSION E32720.1 GI:13026825
 KEYWORDS JP 1999127876-A/1.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Naesubi,M.
 TITLE Small triple strand-forming PNA oligo
 JOURNAL Patent: JP 1999127876-A 1 18-MAY-1999;
 BOEHRINGER MANNHEIM GMBH

COMMENT OS Artificial Sequence
 PN JP 1999127876-A/1
 PD 18-MAY-1999
 PF 21-AUG-1998 JP 1998235065
 PR 22-AUG-1997 DE 97 114 512:3

PI NAESUBI MICHAEL
 PC C12N15/09,C07K9/00,C12Q1/68,C12N15/00
 CC
 FH Key Location/Qualifiers
 FT source 1..12
 FT /organism='Artificial Sequence'.

FEATURES
 source
 1..12
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGAGAAAC 739
 |||||
 2 CCAGAGATAC 12

Db

RESULT 361
 I04321
 LOCUS Sequence 6 from Patent EP 0147819. 12 bp DNA linear PAT 02-DEC-1994
 DEFINITION
 ACCESSION I04321
 VERSION I04321.1 GI:591773
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Kung H.-F. and Yamazaki, S.
 TITLE Purification of recombinant interleukin-2
 JOURNAL Patent: EP 0147819-A2 6 10-JUL-1985;
 FEATURES
 source
 1..12
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 737 AACAGAACAC 747
 |||||
 1 AACAGTGACC 11

Db

RESULT 362
 I07920/c
 LOCUS Sequence 32 from Patent EP 0159123. 12 bp DNA linear PAT 02-DEC-1994
 DEFINITION
 ACCESSION I07920
 VERSION I07920.1 GI:589373
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Hsiung,H.M., Schoner,R.G. and Schoner,B.E.
 TITLE Vectors for expressing bovine growth hormone derivatives
 JOURNAL Patent: EP 0159123-A2 32 23-OCT-1985;
 FEATURES
 source
 1..12
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741

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Db      11 AGGAGAGAG 1
|||||
RESULT 363
LOCUS   AR199085          12 bp  DNA          linear  PAT 20-APR-2002
DEFINITION Sequence 33 from patent US 6355418.
ACCESSION AR199085
VERSION   AR199085.1 GI:20249159
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Schmidt,G.
TITLE    Chimeric oligonucleotides and uses thereof in the identification of
JOURNAL antisense binding sites
FEATURES Patent: US 6355418-A 33 12-MAR-2002;
SOURCE   Location/Qualifiers
1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGAGAGAC 744
|||||
Db      12 AGGAGAGAGAC 2

RESULT 364
LOCUS   AR217452          12 bp  DNA          linear  PAT 25-SEP-2002
DEFINITION Sequence 65 from patent US 6416959.
ACCESSION AR217452
VERSION   AR217452.1 GI:23317145
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Giuliano,K. and Kapur,R.
TITLE    System for cell-based screening
JOURNAL Patent: US 6416959-A 65 09-JUL-2002;
FEATURES Location/Qualifiers
1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 GGAGAGAGACAG 742
|||||
Db      1 GTAGAGAGATAG 11

RESULT 365
LOCUS   AR241771          12 bp  DNA          linear  PAT 20-DEC-2002
DEFINITION Sequence 59 from patent US 6472154.
ACCESSION AR241771
VERSION   AR241771.1 GI:27287583
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.

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TITLE    Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 59 29-OCT-2002;
FEATURES Location/Qualifiers
1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      730 CAGAGAGAGAC 740
|||||
Db      1 CAGAGAGACAC 11

RESULT 366
LOCUS   AR242041          12 bp  DNA          linear  PAT 20-DEC-2002
DEFINITION Sequence 329 from patent US 6472154.
ACCESSION AR242041
VERSION   AR242041.1 GI:27287853
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE    Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 329 29-OCT-2002;
FEATURES Location/Qualifiers
1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 GGAGAGAGACAG 742
|||||
Db      12 GGAGAGAGACAG 2

RESULT 367
LOCUS   AX000276          12 bp  DNA          linear  PAT 10-MAR-2000
DEFINITION Sequence 1 from Patent EP0897991.
ACCESSION AX000276
VERSION   AX000276.1 GI:7240702
KEYWORDS
SOURCE   unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 12)
AUTHORS Naesby,M.D.
TITLE    Small Triplex Forming PNA Oligos
JOURNAL Patent: EP 0897991-A 1 24-FEB-1999;
FEATURES BOEHRINGER MANNHEIM GMBH (DE)
SOURCE   Location/Qualifiers
1..12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      729 CCAGAGAGAGAC 739
|||||
Db      2 CCAGAGAGATAC 12

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RESULT 368
AX035437/c
LOCUS AX035437 12 bp RNA linear PAT 15-NOV-2000
DEFINITION Sequence 12 from Patent EP1035209.
ACCESSION AX035437
VERSION AX035437.1 GI:11191079
FEATURES
    source
        Influenza C virus
    ORGANISM
        Influenza C virus
        Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
        Influenzavirus C.
REFERENCE
1
AUTHORS Azzey,M., Hobom,G., Menke,A. and Flick,R.
TITLE Stable recombinant influenza viruses free of helper viruses
JOURNAL Patent: EP 1035209-A 12 13-SEP-2000;
ARTEMIS PHARMACEUTICALS GMBH (DE)
FEATURES
    source
        1. .12
        /organism="Influenza C virus"
        /mol_type="unassigned RNA"
        /db_xref="taxon:11552"
        /note="3'-konservierte Region des Wildtyp-Influenzavirus"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 369
AX035439/c
LOCUS AX035439 12 bp RNA linear PAT 15-NOV-2000
DEFINITION Sequence 14 from Patent EP1035209.
ACCESSION AX035439
VERSION AX035439.1 GI:11191081
KEYWORDS
    synthetic construct
    synthetic construct
    artificial sequences.
ORGANISM
1
REFERENCE
1
AUTHORS Azzey,M., Hobom,G., Menke,A. and Flick,R.
TITLE Stable recombinant influenza viruses free of helper viruses
JOURNAL Patent: EP 1035209-A 14 13-SEP-2000;
ARTEMIS PHARMACEUTICALS GMBH (DE)
FEATURES
    source
        1. .12
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        /db_xref="taxon:32630"
        /note="Modified influenza A 3' sequence (pH1948)"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 370
AX100746/c
LOCUS AX100746 12 bp RNA linear PAT 10-APR-2001
DEFINITION Sequence 3 from Patent WO0122083.
ACCESSION AX100746
VERSION AX100746.1 GI:13619692
KEYWORDS
    Influenza C virus
    Influenza C virus
    Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

```

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Influenzavirus C.
REFERENCE
1
AUTHORS Bornkamm,G.W., Hobom,G., Mautner,J. and Nimmerjahn,F.
TITLE Method for identifying mhc-restricted antigens
JOURNAL Patent: WO 0122083-A 3 29-MAR-2001;
GSP-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
Pharmaceuticals GmbH (DE)
FEATURES
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        1. .12
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        /note="3'-konservierte Region des Wildtyp-Influenzavirus"
misc_feature
    1. .12
    35.5%; Score 7.8; DB 1; Length 12;
Query Match 81.8%; Pred. No. 2.5e+02;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 371
AX352659/c
LOCUS AX352659 12 bp RNA linear PAT 06-FEB-2002
DEFINITION Sequence 3 from Patent EP1174514.
ACCESSION AX352659
VERSION AX352659.1 GI:18617789
KEYWORDS
    Influenza C virus
    Influenza C virus
    Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
    Influenzavirus C.
ORGANISM
1
REFERENCE
1
AUTHORS Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE Recombinant influenza viruses with bicistronic vrnas coding for two
    genes in tandem arrangement
JOURNAL Patent: EP 1174514-A 3 23-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
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        1. .12
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        /mol_type="unassigned RNA"
        /db_xref="taxon:11552"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 372
AX362217/c
LOCUS AX362217 12 bp RNA linear PAT 15-FEB-2002
DEFINITION Sequence 3 from Patent WO0208434.
ACCESSION AX362217
VERSION AX362217.1 GI:18694555
KEYWORDS
    Influenza C virus
    Influenza C virus
    Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
    Influenzavirus C.
ORGANISM
1
REFERENCE
1
AUTHORS Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE Recombinant influenza viruses with bicistronic vrnas coding for two
    genes in tandem arrangement
JOURNAL Patent: WO 0208434-A 3 31-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)

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FEATURES
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      /mol_type="unassigned RNA"
      /db_xref="taxon:11552"

Query Match
  Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 373
AX428930/c
LOCUS AX428930 12 bp RNA linear PAT 21-JUN-2002
DEFINITION Sequence 3 from Patent EP1201760.
ACCESSION AX428930
VERSION AX428930.1 GI:21540314
KEYWORDS
SOURCE Influenza C virus
ORGANISM Influenza C virus
          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
          Influenzavirus C.
REFERENCE
  1
  AUTHORS Schuler,G.D., Hobom,G., Steinkasserer,A.D., Strobel,I.D. and
           Grassmann,R.
  TITLE Influenza virus vector for human dendritic cells
  JOURNAL Patent: EP 1201760-A 3 02-MAY-2002;
          ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..12
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      /mol_type="unassigned RNA"
      /db_xref="taxon:11552"

Query Match
  Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 374
AX428953/c
LOCUS AX428953 12 bp RNA linear PAT 21-JUN-2002
DEFINITION Sequence 26 from Patent EP1201760.
ACCESSION AX428953
VERSION AX428953.1 GI:21540337
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1
  AUTHORS Schuler,G.D., Hobom,G., Steinkasserer,A.D., Strobel,I.D. and
           Grassmann,R.
  TITLE Influenza virus vector for human dendritic cells
  JOURNAL Patent: EP 1201760-A 26 02-MAY-2002;
          ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..12
      /organism="synthetic construct"
      /mol_type="unassigned RNA"
      /db_xref="taxon:32630"
      /note="Modified influenza A 3'-sequence"

Query Match
  Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAAACAG 2

RESULT 375
AX512612/c
LOCUS AX512612 12 bp RNA linear PAT 03-OCT-2002
DEFINITION Sequence 3 from Patent EP1233059.
ACCESSION AX512612
VERSION AX512612.1 GI:23503835
KEYWORDS
SOURCE Influenza C virus
ORGANISM Influenza C virus
          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
          Influenzavirus C.
REFERENCE
  1
  AUTHORS Hobom,G. and Menke,A.
  TITLE Influenza viruses with enhanced transcriptional and replicational
          capacities
  JOURNAL Patent: EP 1233059-A 3 21-AUG-2002;
          ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
  source
    Location/Qualifiers
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      /mol_type="unassigned RNA"
      /db_xref="taxon:11552"

Query Match
  Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 376
AX512613/c
LOCUS AX512613 12 bp RNA linear PAT 03-OCT-2002
DEFINITION Sequence 4 from Patent EP1233059.
ACCESSION AX512613
VERSION AX512613.1 GI:23503836
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1
  AUTHORS Hobom,G. and Menke,A.
  TITLE Influenza viruses with enhanced transcriptional and replicational
          capacities
  JOURNAL Patent: EP 1233059-A 4 21-AUG-2002;
          ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
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    Location/Qualifiers
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      /db_xref="taxon:32630"
      /note="Modified influenza A 3'-sequence"

Query Match
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  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAAACAG 2

RESULT 377
AX522263/c
LOCUS AX522263 12 bp RNA linear PAT 24-OCT-2002

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DEFINITION Sequence 3 from Patent WO02064757.
ACCESSION AX522263
VERSION AX522263.1 GI:24411217
KEYWORDS Influenza C virus
SOURCE Influenza C virus
ORGANISM Viruses; sRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus C.
REFERENCE 1
AUTHORS Hobom, G. and Menke, A.
TITLE Influenza viruses with enhanced transcriptional and replicational capacities
JOURNAL Patent: WO 02064757-A 3 22-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES source
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/organism="Influenza C virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11552"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2
RESULT 378
LOCUS AX522264/C
DEFINITION Sequence 4 from Patent WO02064757.
ACCESSION AX522264
VERSION AX522264.1 GI:24411218
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Hobom, G. and Menke, A.
TITLE Influenza viruses with enhanced transcriptional and replicational capacities
JOURNAL Patent: WO 02064757-A 4 22-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES source
1. .12
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Modified influenza A 3'-sequence"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
Db 12 AGTAAACACAG 2
RESULT 379
LOCUS AX711980
DEFINITION Sequence 1 from Patent WO0208381.
ACCESSION AX711980
VERSION AX711980.1 GI:29787762
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Tcherkassov, D.

TITLE Method for determining gene expression
JOURNAL Patent: WO 0208381-A 1 07-NOV-2002;
Genovoxx GmbH (DE)
FEATURES source
1. .12
Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="ermittelte Sequenz (Beispiel 4)"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 737 AACAGAACACC 747
Db 1 ACCAAACACC 11
RESULT 380
LOCUS AX742026
DEFINITION Sequence 6 from Patent WO03020968.
ACCESSION AX742026
VERSION AX742026.1 GI:30524538
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Tcherkassov, D.
TITLE Method for analyzing nucleic acid sequences and gene expression
JOURNAL Patent: WO 03020968-A 6 13-MAR-2003;
Genovoxx GmbH (DE)
FEATURES source
1. .12
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequenz aus Beispiel 2"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 737 AACAGAACACC 747
Db 1 ACCAAACACC 11
RESULT 381
LOCUS AX766776
DEFINITION Sequence 65 from Patent EPI314980.
ACCESSION AX766776
VERSION AX766776.1 GI:32260532
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Giuliano, K.A. and Kapur, R.
TITLE A system for cell-based screening
JOURNAL Patent: EP 1314980-A 65 28-MAY-2003;
Cellomics, Inc. (US)
FEATURES source
1. .12
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Caspase-6 substrate recognition sequence"
Query Match 35.5%; Score 7.8; DB 1; Length 12;

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Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAACAGCA 742
Db 1 GTAGAAATAGA 11

RESULT 392
BD139745/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BD139745
Gene family with transformation modulating activity.
PAT 18-SEP-2002
BD139745
BD139745.1 GI:23234690
JP 2002508154-A/26.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 12)
Pasternack,G.R., Kochevar,G.J., Brody,J.R. and Kadkol,S.S.
Gene family with transformation modulating activity
Patent: JP 2002508154-A 26 19-MAR-2002;
THE JOHNS HOPKINS UNIVERSITY
OS Artificial Sequence
PN JP 2002508154-A/26
PD 19-MAR-2002
PF 11-DEC-1998 JP 2000524477
PR 12-DEC-1997 US 60/069677
PI GARY R PASTERNAK,GERALD J KOCHAVAR,JONATHAN R BRODY,SHRIHARI

PC C12N15/09,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
,C12Q/68,G01N33/15,
PC G01N33/50,G01N33/50,G01N33/53//C12P21/08,C12N15/00,C12N5/00 CC
recognition sequence
FH Key
FT source
FT Location/Qualifiers
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QY 735 GAAACAGAACCA 745
Db 12 GAAAAAGAAAA 2

RESULT 383
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VERSION
KEYWORDS
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AUTHORS
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EMBO Rep. 3 (12), 1152-1157 (2002)

ATH528392
Arabidopsis thaliana 12 bp DNA linear PLN 29-MAR-2003
162G09.
AJ528392
AJ528392.1 GI:2679652
left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepoint,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL

Best Local Similarity 81.8%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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ORGANISM
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AUTHORS
TITLE
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)

ATH528392
Arabidopsis thaliana 12 bp DNA linear PLN 29-MAR-2003
162G09.
AJ528392
AJ528392.1 GI:2679652
left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepoint,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL

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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Joyce, G.F. and Breaker, R.R.
TITLE Enzymatic DNA molecules
JOURNAL Patent: US 6326174-A 41 04-DEC-2001;
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RESULT 391
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238657
VERSION BD238657.1 GI:33048427
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts, B.L. and Shankara, S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 75 15-OCT-2002;
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/75
PF 18-JUN-1999 JP 2000554749
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PC C12N1/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
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RESULT 393
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LOCUS 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238818
VERSION BD238818.1 GI:33048588

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KEYWORDS      JP 2002534056-A/236.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE     1 (bases 1 to 10)
AUTHORS      Roberts,B.L. and Shankara,S.
TITLE        Preparation and use of superior vaccines
JOURNAL      Patent: JP 2002534056-A 236 15-OCT-2002;
              GENZYME CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002534056-A/236
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Db 10 CCAGCAGAA 2
RESULT 395
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DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD238955
VERSION     BD238955.1 GI:330486725
KEYWORDS   JP 2002534056-A/373.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1 (bases 1 to 10)
AUTHORS     Roberts,B.L. and Shankara,S.
TITLE       Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 373 15-OCT-2002;
              GENZYME CORP
COMMENT     OS Homo sapiens (human)
              PN JP 2002534056-A/373
              PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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Db 10 AACACAGAAC 2
RESULT 394
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LOCUS      10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD238921
VERSION     BD238921.1 GI:33048691
KEYWORDS   JP 2002534056-A/339.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Roberts,B.L. and Shankara,S.
TITLE       Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 339 15-OCT-2002;
              GENZYME CORP
COMMENT     OS Homo sapiens (human)
              PN JP 2002534056-A/339
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QY 735 GAGACAGAA 743
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RESULT 396
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LOCUS BD239177 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239177.1 GI:33048947
VERSION JP 2002534056-A/595.
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 595 15-OCT-2002;
GENZYME CORP
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RESULT 397
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LOCUS BD239362 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239362
VERSION BD239362.1 GI:33049132
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 780 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/780
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Best Local Similarity 88.9%; Pred. No. 2.5e+02;
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QY 727 TGCACGAG 735
Db 9 TGCACGAG 1

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PI BRUCE L ROBERTS,SRINIVAS SHANKARA

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RESULT 401

BD239924/c

LOCUS

DEFINITION

BD239924

ACCESSION

BD239924

VERSION

BD239924.1 GI:33049694

KEYWORDS

JP 2002534056-A/1342.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 10)

Authors, B.L. and Shankara, S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 1342 15-OCT-2002;

GENZYME CORP

COMMENT

OS Homo sapiens (human)

PN JP 2002534056-A/1342

PD 15-OCT-2002

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PI BRUCE L ROBERTS,SRINIVAS SHANKARA

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QY 735 GAACAGAA 743

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RESULT 402

BD239978

LOCUS

DEFINITION

BD239978

ACCESSION

BD239978.1 GI:33049748

KEYWORDS

JP 2002534056-A/1396.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 10)

Authors, B.L. and Shankara, S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 1396 15-OCT-2002;

GENZYME CORP

COMMENT

OS Homo sapiens (human)

PN JP 2002534056-A/1396

PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR

19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR

19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR

19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR

19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR

19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR

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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR

19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR

19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR

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19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR

19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC

C12N1/19, C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC

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CC Preparation and use of superior vaccines

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	ORGANISM	Homo sapiens
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	OS	Homo sapiens (human)
	PN	JP 2002534056-A/1496
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	PX	19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
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	QB	19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089834 PR
	QC	19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
	QD	19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
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	QF	DEC-1998 US 60/111715
	QG	PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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	QJ	PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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	ACCESSION	BD240001
	VERSION	BD240001.1 GI:33049771
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	PN	JP 2002534056-A/1419
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	PU	19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
	PV	19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
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	QI	PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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PD 15-OCT-2002
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PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240581
VERSION BD240581.1 GI:33050351
KEYWORDS JP 2002534056-A/1999.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1999 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1999
PD 15-OCT-2002
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G01N37/00,
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Db 2 GAGAAACAG 10

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DEFINITION DNA sequence required for efficient protein transcription in
Breivibacterium flavum.
ACCESSION E16893
VERSION E16893.1 GI:5711576
KEYWORDS JP 1998229881-A/34.
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 10)
AUTHORS Kobayashi,M., Man,T. and Yugawa,H.
TITLE DNA HAVING SEQUENCE CAPABLE OF EFFICIENTLY TRANSLATING PROTEIN IN
CORYNEFORM BACTERIA
JOURNAL Patent: JP 1998229881-A 34 02-SEP-1998;
MITSUBISHI CHEM CORP
COMMENT OS Breivibacterium flavum
PN JP 1998229881-A/34
PD 02-SEP-1998
PF 19-FEB-1997 JP 1997035338
PI KOBAYASHI MIKI, MAN TOMOKO, YUGAWA HIDEAKI
PC C12N15/09, C07H21/04, C12N1/21, C12N9/38, C12Q1/68, (C12N15/09, PC
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
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RESULT 407
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LOCUS E16893
DEFINITION DNA sequence required for efficient protein transcription in
Breivibacterium flavum.
ACCESSION E16893
VERSION E16893.1 GI:5711576
KEYWORDS JP 1998229881-A/34.
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 10)
AUTHORS Kobayashi,M., Man,T. and Yugawa,H.
TITLE DNA HAVING SEQUENCE CAPABLE OF EFFICIENTLY TRANSLATING PROTEIN IN
CORYNEFORM BACTERIA
JOURNAL Patent: JP 1998229881-A 34 02-SEP-1998;
MITSUBISHI CHEM CORP
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PN JP 1998229881-A/34
PD 02-SEP-1998
PF 19-FEB-1997 JP 1997035338
PI KOBAYASHI MIKI, MAN TOMOKO, YUGAWA HIDEAKI
PC C12N15/09, C07H21/04, C12N1/21, C12N9/38, C12Q1/68, (C12N15/09, PC
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CC hypothetical: No;
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Matches 8; Conservative 0;

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Db 1 CGAGGAGAA 9

RESULT 408
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DEFINITION Fusarium sp. - specific sequence in 18S rRNA gene. PAT 28-JUL-1999
ACCESSION E17077
VERSION E17077.1 GI:57111760
KEYWORDS JP 1998234380-A/6.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 10)
AUTHORS Shibata,Y., Takashina,T., Shindo,Y. and Takahashi,I.
TITLE NUCLEIC ACID SEQUENCE FOR DETECTING FUNGUS OF GENUS FUSARIUM
JOURNAL Patent: JP 1998234380-A 6 08-SEP-1998;
SHINKINRUI KINOU KAIHATSU KENKYUSHO:KK

OS None
COMMENT OS Artificial sequences.
PN JP 1998234380-A/6
PD 08-SEP-1998
PF 28-FEB-1997 JP 1997062104
PI SHIBATA YOSHIKAZU, TAKASHINA TOMONORI, SHINDO YOSHIO, PI
TAKAHASHI ISAMU
PC C12N15/09,C07H21/04,C12Q1/68/(C12N1/14,(C12N15/09,C12R1/77),
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Qy 740 AGAACACCG 748
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Db 10 ATAAACCG 2

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DEFINITION Genes with human dendritic cell expression. PAT 31-JAN-2002
ACCESSION E39629
VERSION E39629.1 GI:18621720
KEYWORDS JP 2000279181-A/162.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 162 10-OCT-2000;
SCIENCE & TECH AGENCY
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PN JP 2000279181-A/162
PD 10-OCT-2000

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Qy 727 TGCCAGGAG 735
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Db 2 TGGCAGGAG 10

RESULT 410
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LOCUS
DEFINITION Genes with human dendritic cell expression. PAT 31-JAN-2002
ACCESSION E39712
VERSION E39712.1 GI:18621803
KEYWORDS JP 2000279181-A/245.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 245 10-OCT-2000;
SCIENCE & TECH AGENCY
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PN JP 2000279181-A/245
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
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Qy 733 GAGAAACAG 741
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RESULT 411
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LOCUS
DEFINITION Sequence 135 from patent US 6472154. PAT 20-DEC-2002
ACCESSION AR241847
VERSION AR241847.1 GI:27287659
KEYWORDS Unknown.
SOURCE

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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 135 29-OCT-2002;
FEATURES
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    source
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    /mol_type="genomic DNA"

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGACA 745
Db 1 AACAGATA 9

RESULT 412
LOCUS AR303311/c 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 36 from patent US 6544736.
ACCESSION AR303311
VERSION AR303311.1 GI:31692087
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuchi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 36 08-APR-2003;
FEATURES
    Location/Qualifiers
    source
    1..10
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAA 743
Db 9 GAACAGAA 1

RESULT 413
LOCUS AX080422 10 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 34 from Patent WO0105974.
ACCESSION AX080422
VERSION AX080422.1 GI:13159864
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nicklin,M. and Barton,J.
TITLE The il-11 gene and polypeptide products
JOURNAL Patent: WO 0105974-A 34 25-JAN-2001;
INTERLEUKIN Genetics, Inc. (US)
FEATURES
    Location/Qualifiers
    source
    1..10
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;

QY 727 TCCAGGAG 735
Db 9 TCCAGGAG 1

RESULT 416
LOCUS AX119668/c 10 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 61 from Patent WO0129213.
ACCESSION AX119668
VERSION AX119668.1 GI:14036562
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Todd,J.A., Twells,R.C., Hess,J.W., Hey,P., Hey,P., Caskey,C.T., Hammond,H. and Metzker,M.L.
TITLE Human sit4 associated proteins like (sap1) proteins and encoding genes; uses thereof
JOURNAL Patent: WO 0129213-A 61 26-APR-2001;
The Wellcome Trust Limited as Trustee to the Wellcome Trust (GB);
Merck & Co., Inc. (US)
FEATURES
    Location/Qualifiers
    source
    1..10
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    /mol_type="unassigned DNA"
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Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAA 743
Db 10 GAACAGAA 2

RESULT 415
LOCUS AX152323/c 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 238 from Patent WO0138577.
ACCESSION AX152323
VERSION AX152323.1 GI:14533974
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 238 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
    Location/Qualifiers
    source
    1..10
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGAG 735
Db 9 TCCAGGAG 1

RESULT 416

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AX152484/c
LOCUS      AX152484      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 399 from Patent WO0138577.
ACCESSION  AX152484
VERSION     AX152484.1  GI:14534135
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE       Human transcriptomes
JOURNAL     Patent: WO 0138577-A 399 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES    Location/Qualifiers
            source
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAA 738
Db 10 CAGCAGAAA 2

RESULT 417
LOCUS      AX301498      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 212 from Patent WO0185941.
ACCESSION  AX301498
VERSION     AX301498.1  GI:17382581
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Versteeg,R. and Caron,H.N.
TITLE       MYC targets
JOURNAL     Patent: WO 0185941-A 212 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES    Location/Qualifiers
            source
              1..10
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAAC 739
Db 2 AGGGGAAAC 10

RESULT 418
LOCUS      AX687134/c    10 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 55 from Patent WO03008638.
ACCESSION  AX687134
VERSION     AX687134.1  GI:29409629
KEYWORDS    synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Schweitzer,M., Anderson,R., Fiechtner,M., Mueller-Ibel,J.,
            Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
            Pignot,M. and Kienle,S.
TITLE       Sorting and immobilization system for nucleic acids using synthetic
            binding systems
JOURNAL     Patent: WO 03008638-A 55 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
FEATURES    Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic binding system"

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Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
Pignot,M. and Kienle,S.
TITLE       Sorting and immobilization system for nucleic acids using synthetic
            binding systems
JOURNAL     Patent: WO 03008638-A 55 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
FEATURES    Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
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              /db_xref="taxon:32630"
              /note="Synthetic binding system"
            misc_feature
              1..10
              /note="pyranosyl RNA"
Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 9 GATACAGAA 1

RESULT 419
LOCUS      AX687135      10 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 56 from Patent WO03008638.
ACCESSION  AX687135
VERSION     AX687135.1  GI:29409630
KEYWORDS    synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Schweitzer,M., Anderson,R., Fiechtner,M., Mueller-Ibel,J.,
            Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
            Pignot,M. and Kienle,S.
TITLE       Sorting and immobilization system for nucleic acids using synthetic
            binding systems
JOURNAL     Patent: WO 03008638-A 56 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
FEATURES    Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic binding system"
            misc_feature
              1..10
              /note="pyranosyl RNA"
Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 2 GATACAGAA 10

RESULT 420
LOCUS      BD007909      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007909
VERSION     BD007909.1  GI:18636282
KEYWORDS    JP 2001069993-A/185.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.

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TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 200106993-A 185 21-MAR-2001;

COMMENT OS Homo sapiens (human)
PN JP 200106993-A/185
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079

PR KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
A61P23/00,
CC A61P31/00, C12P21/08, C12N15/00

PF Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'

FEATURES
source Location/Qualifiers
1..10
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/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
| | | | |
Db 1 GGGAAACAG 9

RESULT 421

BD065085 10 bp DNA linear PAT 27-AUG-2002
LOCUS Characterization of the yeast transcriptome.
DEFINITION
ACCESSION BD065085
VERSION BD065085.1 GI:22610688

KEYWORDS JP 2001050917-A/21.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae

REFERENCE 1 (bases 1 to 10);
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.

AUTHORS Characterization of the yeast transcriptome
TITLE Patent: JP 2001050917-A 21 10-JUL-2001;
JOURNAL THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001050917-A/21
PD 10-JUL-2001

PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917

PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC

Characterization of the yeast transcriptome
PF Key Location/Qualifiers
FT source 1..10
/organism='Saccharomyces cerevisiae (yeast)'

FEATURES
source Location/Qualifiers
1..10
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/mol_type='genomic DNA'
/db_xref='taxon:4932'

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAAC 745
| | | | |
Db 1 AACAGACCA 9

RESULT 422

BD065354 10 bp DNA linear PAT 27-AUG-2002
LOCUS Characterization of the yeast transcriptome.
DEFINITION
ACCESSION BD065354
VERSION BD065354.1 GI:22610957

KEYWORDS JP 2001050917-A/290.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae

REFERENCE 1 (bases 1 to 10);
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.

AUTHORS Characterization of the yeast transcriptome
TITLE Patent: JP 2001050917-A 290 10-JUL-2001;
JOURNAL THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001050917-A/290
PD 10-JUL-2001

PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917

PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC

Characterization of the yeast transcriptome
PF Key Location/Qualifiers
FT source 1..10
/organism='Saccharomyces cerevisiae (yeast)'

FEATURES
source Location/Qualifiers
1..10
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/mol_type='genomic DNA'
/db_xref='taxon:4932'

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAC 739
| | | | |
Db 2 AGGAGACAC 10

RESULT 423

BD073423/c 10 bp DNA linear PAT 27-AUG-2002
LOCUS Utilization of transcription factor Brn-3a.
DEFINITION
ACCESSION BD073423
VERSION BD073423.1 GI:22619026

KEYWORDS JP 2001511344-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 10);
Damien, S.M. and Seymar, L.D.

AUTHORS Utilization of transcription factor Brn-3a
TITLE Patent: JP 2001511344-A 5 14-AUG-2001;
JOURNAL NEUROVEX LTD

COMMENT OS Artificial Sequence
PN JP 2001511344-A/5
PD 14-AUG-2001

PF 27-JUL-1998 JP 2000504246
PR 25-JUL-1997 GB 9715823.2, 10-DEC-1997 US 08/988476 P1

SMITH MARTIN DAMIEN, LATCHMAN DAVID SEYMAR
PC C12N15/09, A61K38/17, A61K39/245, A61K48/00, A61P25/00, C07K14/47,

PC C12N7/00,
PC C12N15/00, A61K37/12

CC Description of Artificial Sequence: primer
PF Key Location/Qualifiers
FT source 1..10
/organism='Artificial Sequence'

FEATURES
source Location/Qualifiers
1..10
/organism='synthetic construct'

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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAA 743
DB 10 GAACAGAA 2

RESULT 424
BD161340
LOCUS BD083320 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083320
VERSION BD083320.1 GI:22628930
KEYWORDS JP 2001327293-A/241.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001327293-A/241
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC NAGAI

FH Key Location/Qualifiers
source 1..10
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/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 AGACACCG 748
DB 1 AGACACCG 9

RESULT 425
BD161340
LOCUS BD161340 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161340
VERSION BD161340.1 GI:27867098
KEYWORDS JP 2002186482-A/162.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/162
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC

/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAA 743
DB 9 GAATAGAA 1

RESULT 427
BD161433/c
LOCUS BD161433 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161433
VERSION BD161433.1 GI:27867191
KEYWORDS JP 2002186482-A/255.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGAG 735
DB 1 TGCTAGGAG 9

RESULT 426
BD161418/c
LOCUS BD161418 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161418
VERSION BD161418.1 GI:27867176
KEYWORDS JP 2002186482-A/240.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/240
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC

/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAA 743
DB 9 GAATAGAA 1

RESULT 427
BD161433/c
LOCUS BD161433 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161433
VERSION BD161433.1 GI:27867191
KEYWORDS JP 2002186482-A/255.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
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AUTHORS Nagai, S., Matsushima, K. and Hashimoto, S.
 TITLE Human activated Th1 and Th2 cell expression genes
 JOURNAL Patent: JP 2002186482-A 255 02-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002186482-A/255
 PD 02-JUL-2002

PF 19-DEC-2000 JP 2000385816
 PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TARO
 C12N15/09, C07K14/47, C07K16/18, C12P21/08, C12N15/00 CC Human
 activated Th1 and Th2 cell expression genes FH Key.
 Location/Qualifiers
 FT source 1..10
 /organism='Homo sapiens (human)'.
 FT

FEATURES
 source

1..10
 Location/Qualifiers
 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 739 CAGAACACC 747
 |||||
 Db 10 CAGAACACG 2

RESULT 428

BD166608
 LOCUS Human liver disease-expressing genes.
 DEFINITION Human liver disease-expressing genes.
 ACCESSION BD166608
 VERSION BD166608.1 GI:27872420
 KEYWORDS JP 2002209591-A/153.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 153 30-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002209591-A/153
 PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
 YAMASHITA
 C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
 C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key Location/Qualifiers
 FT source 1..10
 /organism='Homo sapiens (human)'.
 FT

FEATURES
 source

1..10
 Location/Qualifiers
 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 735 GAACACAGAA 743
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 Db 1 GAACACAAA 9

RESULT 429

BD166767

LOCUS Human liver disease-expressing genes.
 DEFINITION Human liver disease-expressing genes.
 ACCESSION BD166767
 VERSION BD166767.1 GI:27872579
 KEYWORDS JP 2002209591-A/312.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 312 30-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002209591-A/312
 PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
 YAMASHITA
 C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
 C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key Location/Qualifiers
 FT source 1..10
 /organism='Homo sapiens (human)'.
 FT

FEATURES
 source

1..10
 Location/Qualifiers
 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAACG 741
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 Db 1 GAGAACG 9

RESULT 430

BD166844/c
 LOCUS Human liver disease-expressing genes.
 DEFINITION Human liver disease-expressing genes.
 ACCESSION BD166844
 VERSION BD166844.1 GI:27872656
 KEYWORDS JP 2002209591-A/389.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 389 30-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002209591-A/389
 PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
 YAMASHITA
 C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
 C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key Location/Qualifiers
 FT source 1..10
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FEATURES
 source

1..10
 Location/Qualifiers
 /organism='unidentified'


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Qy      734 AGAACAACA 742
Db      11 AGAACAACA 3

RESULT 435
LOCUS   AR106012                11 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION   Sequence 8 from patent US 6103491.
ACCESSION   AR106012
VERSION     AR106012.1 GI:12820077
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Sampath,K.T.
TITLE      Methods and compositions for identifying morphogen analogs
JOURNAL    Patent: US 6103491-A 8 15-AUG-2000;
FEATURES    Location/Qualifiers
            source
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      736 AACACAGAAC 744
Db      3 AACACATAAC 11

RESULT 436
LOCUS   I11798/c                11 bp      DNA      linear      PAT 26-JUL-1995
DEFINITION   Sequence 3 from Patent US 5414077.
ACCESSION   I11798
VERSION     I11798.1 GI:909742
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Lin,K.-Y. and Matteucci,M.
TITLE      Non-nucleoside linkers for convenient attachment of labels to
            oligonucleotides using standard synthetic methods
JOURNAL    Patent: US 5414077-A 3 09-MAY-1995;
FEATURES    Location/Qualifiers
            source
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            /mol_type="unassigned DNA"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      732 GGAGAAACA 740
Db      9 GGAGAAAAA 1

RESULT 437
LOCUS   I35006                11 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION   Sequence 92 from patent US 5599704.
ACCESSION   I35006
VERSION     I35006.1 GI:2087974
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)

AUTHORS    Thompson,J.D. and Draper,K.G.
TITLE      ErbB2/neu targeted ribozymes
JOURNAL    Patent: US 5599704-A 92 04-FEB-1997;
FEATURES    Location/Qualifiers
            source
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      727 TCCACGAGAG 735
Db      1 TACCAGGAG 9

RESULT 438
LOCUS   AR207570                11 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION   Sequence 4 from patent US 6379881.
ACCESSION   AR207570
VERSION     AR207570.1 GI:21507358
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Fouchier,R.Adrianus. and Schuitemaker,J.
TITLE      Nucleic acids and methods for the discrimination between syncytium
            inducing and non syncytium inducing variants of the human
            immunodeficiency virus
JOURNAL    Patent: US 6379881-A 4 30-APR-2002;
FEATURES    Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      734 AGAAACACA 742
Db      3 AGAAACACA 11

RESULT 439
LOCUS   AR301505                11 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION   Sequence 86 from patent US 6538173.
ACCESSION   AR301505
VERSION     AR301505.1 GI:31689307
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Heber-Katz,E.
TITLE      Compositions and methods for wound healing
JOURNAL    Patent: US 6538173-A 86 25-MAR-2003;
FEATURES    Location/Qualifiers
            source
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      738 ACAGAACAC 746
Db      1 ACAGAACTC 9

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RESULT 440
AR301543
LOCUS AR301543 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 124 from patent US 6538173.
ACCESSION AR301543
VERSION AR301543.1 GI:31689345
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz, E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 124 25-MAR-2003;
FEATURES
source
1. .11
/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 738 ACAGACAC 746
| | | | |
Db 3 ACCGACAC 11
RESULT 441
AR363438/c
LOCUS AR363438 11 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 10 from patent US 5214136.
ACCESSION AR363438
VERSION AR363438.1 GI:34425015
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Lin, K.-Y. and Matteucci, M.
TITLE Anthraquinone-derivatives oligonucleotides
JOURNAL Patent: US 5214136-A 10 25-MAY-1993;
FEATURES
source
1. .11
/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 732 CGAGAACAC 740
| | | | |
Db 9 GGAGAAAA 1
RESULT 442
AX098763
LOCUS AX098763 11 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 70 from Patent WO0120025.
ACCESSION AX098763
VERSION AX098763.1 GI:13538004
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Wojnowski, L. and Eiselt, R.
TITLE Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
JOURNAL diagnostic and therapeutic applications
Patent: WO 0120025-A 70 22-MAR-2001;
FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial"

Epidauros Biotechnologie AG (DE)
Location/Qualifiers
1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 735 GAAACAGAA 743
| | | | |
Db 2 GAAACAGTA 10
RESULT 443
AX098764/c
LOCUS AX098764 11 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 71 from Patent WO0120025.
ACCESSION AX098764
VERSION AX098764.1 GI:13538005
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Wojnowski, L. and Eiselt, R.
TITLE Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
JOURNAL diagnostic and therapeutic applications
Patent: WO 0120025-A 71 22-MAR-2001;
FEATURES
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/db_xref="taxon:32630"
/note="artificial"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 735 GAAACAGAA 743
| | | | |
Db 10 GAAACAGTA 2
RESULT 444
AX098769/c
LOCUS AX098769 11 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 76 from Patent WO0120025.
ACCESSION AX098769
VERSION AX098769.1 GI:13538010
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Wojnowski, L. and Eiselt, R.
TITLE Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
JOURNAL diagnostic and therapeutic applications
Patent: WO 0120025-A 76 22-MAR-2001;
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial"
Query Match 33.6%; Score 7.4; DB 1; Length 11;

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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 11 CAGAACCCC 3

RESULT 445
AX098770
LOCUS
DEFINITION Sequence 77 from Patent WO0120025.
ACCESSION AX098770
VERSION AX098770.1 GI:13538011
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Wojnowski, L. and Eiselt, R.
TITLE Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
JOURNAL diagnostic and therapeutic applications
Epidaurus Biotechnologie AG (DE)
FEATURES
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/organism="synthetic construct"
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/note="artificial"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 1 CAGAACCCC 9

RESULT 446
AX175318/c
LOCUS
DEFINITION Sequence 82 from Patent WO0144465.
ACCESSION AX175318
VERSION AX175318.1 GI:14598686
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Phillips, N.C. and Fillon, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 82 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
1..11
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAAC 744
Db 10 AAACAAAC 2

RESULT 447
AX393136/c
LOCUS
DEFINITION Sequence 66 from Patent WO0210217.
ACCESSION AX393136
VERSION AX393136.1 GI:19701186
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS St Croix, B., Kinzler, K.W. and Vogelstein, B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 66 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAACACAGA 742
Db 9 AGAACGACA 1

RESULT 448
AX470474/c
LOCUS
DEFINITION Sequence 51 from Patent WO02053773.
ACCESSION AX470474
VERSION AX470474.1 GI:22205599
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 51 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 11 CAGCACACC 3

RESULT 449
AX470533/c
LOCUS
DEFINITION Sequence 110 from Patent WO02053773.
ACCESSION AX470533
VERSION AX470533.1 GI:22205658
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro

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JOURNAL Patent: WO 02053773-A 110 11-JUL-2002;
FEATURES HENKEL KGAA (DE)
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1. .11
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/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 GGAGAACAA 740
Db 9 GGAGAACAA 1

RESULT 450
AX470707/c
LOCUS AX470707 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 284 from Patent WO02053773.
ACCESSION AX470707
VERSION AX470707.1 GI:22205832
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 284 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 738 ACAGAACAC 746
Db 9 ACAGAGCAC 1

RESULT 451
AX470708
LOCUS AX470708 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 285 from Patent WO02053773.
ACCESSION AX470708
VERSION AX470708.1 GI:22205833
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 285 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 737 AACAGAAC 745
Db 10 AAGAGAAC 2

RESULT 453
AX470961
LOCUS AX470961 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 538 from Patent WO02053773.
ACCESSION AX470961
VERSION AX470961.1 GI:22206086
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 538 11-JUL-2002;
HENKEL KGAA (DE)
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 737 AACAGAAC 745
Db 10 AAGAGAAC 2

RESULT 453
AX470961
LOCUS AX470961 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 538 from Patent WO02053773.
ACCESSION AX470961
VERSION AX470961.1 GI:22206086
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 538 11-JUL-2002;
HENKEL KGAA (DE)
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source
1. .11
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 735 GAACAGAA 743
Db 1 GAACAGAA 9

RESULT 454
AX471049
LOCUS AX471049 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 626 from Patent WO02053773.
ACCESSION AX471049
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VERSION AX471049.1 GI:22206174
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 626 11-JUL-2002;
HENKEL KGAA (DE)
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source Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAG 741
Db 1 GGGAAACAG 9
RESULT 455
AX471085/c
LOCUS AX471085 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 662 from Patent WO02053773.
ACCESSION AX471085
VERSION AX471085.1 GI:22206210
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 662 11-JUL-2002;
HENKEL KGAA (DE)
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 734 AGAAACAGA 742
Db 11 AGAAACAGA 3
RESULT 456
AX471104/c
LOCUS AX471104 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 681 from Patent WO02053773.
ACCESSION AX471104
VERSION AX471104.1 GI:22206229
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 681 11-JUL-2002;
HENKEL KGAA (DE)

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACAGAC 744
Db 9 AACACAGAC 1
RESULT 457
AX471541/c
LOCUS AX471541 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1118 from Patent WO02053773.
ACCESSION AX471541
VERSION AX471541.1 GI:22206666
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1118 11-JUL-2002;
HENKEL KGAA (DE)
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source Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGAACAC 746
Db 10 ACAGAACAC 2
RESULT 458
AX471703
LOCUS AX471703 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1280 from Patent WO02053773.
ACCESSION AX471703
VERSION AX471703.1 GI:22206828
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1280 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 739 CAGAACACC 747
Db 739 CAGAACACC 747

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Db      3  CAGGACACC 11
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RESULT 459
AX471709/c
LOCUS      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 1286 from Patent WO02053773.
ACCESSION  AX471709
VERSION     AX471709.1  GI:22206834
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL    Patent: WO 02053773-A 1286 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source
            1..11
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      735  GAAACAGAA 743
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Db      10  GAGACAGAA 2

RESULT 460
AX471743
LOCUS      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 1320 from Patent WO02053773.
ACCESSION  AX471743
VERSION     AX471743.1  GI:22206868
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL    Patent: WO 02053773-A 1320 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      735  GAAACAGAA 743
|||||
Db      10  GAGACAGAA 2

RESULT 460
AX471743
LOCUS      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 1320 from Patent WO02053773.
ACCESSION  AX471743
VERSION     AX471743.1  GI:22206868
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL    Patent: WO 02053773-A 1320 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      727  TGCCAGGAG 735
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Db      2  TGGCAGGAG 10

RESULT 461
AX472086
LOCUS      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 77 from Patent WO02053775.
ACCESSION  AX472086
VERSION     AX472086.1  GI:22207127
KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Huster,E., Haberl,M. and Wojnowski,L.
TITLE      Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
JOURNAL    Patent: WO 02053775-A 77 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      729  CCAGGAGAA 737
|||||
Db      2  CAAGGAGAA 10

RESULT 462
AX555201
LOCUS      11 bp      DNA      linear      PAT 27-NOV-2002
DEFINITION Sequence 37 from Patent WO02070720.
ACCESSION  AX555201
VERSION     AX555201.1  GI:25898729
KEYWORDS    synthetic construct
            synthetic construct
            artificial sequences.
SOURCE      Hayashizaki,Y. and Carninci,P.
ORGANISM    Hayashizaki,Y. and Carninci,P.
            Cloning vectors and method for molecular cloning
            Patent: WO 02070720-A 37 12-SEP-2002;
            Riken (JP)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="plasmid junction linker upper oligonucleotide"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      728  GCCAGGAGA 736
|||||
Db      2  GCCATGAGA 10

RESULT 463
AX623049/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 90 from Patent WO0203774.
ACCESSION  AX623049
VERSION     AX623049.1  GI:28450990
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 90 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers

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source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
10 CAGAAACACC 2

RESULT 464
AX623106/C
LOCUS
DEFINITION Sequence 147 from Patent WO02053774.
ACCESSION AX623106
VERSION AX623106.1 GI:28451047
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 147 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAC 739
10 AGGAGACAC 2

RESULT 465
AX623331
LOCUS
DEFINITION Sequence 372 from Patent WO02053774.
ACCESSION AX623331
VERSION AX623331.1 GI:28451272
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 372 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
10 GAAACAGAA 2

RESULT 466
AX623380/C
LOCUS
DEFINITION Sequence 421 from Patent WO02053774.
ACCESSION AX623380
VERSION AX623380.1 GI:28451321
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 421 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAAC 745
10 AACAGAAC 2

RESULT 467
AX623518/C
LOCUS
DEFINITION Sequence 559 from Patent WO02053774.
ACCESSION AX623518
VERSION AX623518.1 GI:28451459
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 559 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAG 742
9 AGAAACAG 1

RESULT 468
AX623551/C
LOCUS
DEFINITION Sequence 592 from Patent WO02053774.
ACCESSION AX623551
VERSION AX623551.1 GI:28451492
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 592 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/mole_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGCAACA 740
DB 9 GGAGCAACA 1

RESULT 469
AX623639/c
LOCUS AX623639 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 680 from Patent WO02053774.
ACCESSION AX623639
VERSION AX623639.1 GI:28451580
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 680 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/mole_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
DB 11 CAGAACACC 3

RESULT 470
AX623774/c
LOCUS AX623774 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 815 from Patent WO02053774.
ACCESSION AX623774
VERSION AX623774.1 GI:28451715
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 815 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/mole_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
DB 11 CAGAACACC 3

RESULT 471
AX623846
LOCUS AX623846 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 887 from Patent WO02053774.
ACCESSION AX623846
VERSION AX623846.1 GI:28451787
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 887 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/mole_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGATAAAC 739
DB 1 AGGATAAAC 9

RESULT 472
AX623862/c
LOCUS AX623862 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 903 from Patent WO02053774.
ACCESSION AX623862
VERSION AX623862.1 GI:28451803
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 903 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/mole_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAG 735
DB 9 TTCCAGGAG 1

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RESULT 473
AX624809
LOCUS
DEFINITION
Sequence 1850 from Patent WO02053774.
ACCESSION
AX624809
VERSION
AX624809.1 GI:28452750
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 1850 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACACAGAA 743
Db 2 GAACACAGAA 10

RESULT 474
AX624839
LOCUS
DEFINITION
Sequence 1880 from Patent WO02053774.
ACCESSION
AX624839
VERSION
AX624839.1 GI:28452780
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 1880 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 1 GGAACACAG 9

RESULT 475
AX625167
LOCUS
DEFINITION
Sequence 2208 from Patent WO02053774.
ACCESSION
AX625167
VERSION
AX625167.1 GI:28453108
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2208 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 AGAACACCG 748
Db 1 AGGACACCG 9

RESULT 477
AX625356/c
LOCUS
DEFINITION
Sequence 2397 from Patent WO02053774.
ACCESSION
AX625356
VERSION
AX625356.1 GI:28453297
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2397 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 AGAACACCG 748
Db 1 AGGACACCG 9

RESULT 477
AX625356/c
LOCUS
DEFINITION
Sequence 2397 from Patent WO02053774.
ACCESSION
AX625356
VERSION
AX625356.1 GI:28453297
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2397 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 AGAACACCG 748
Db 1 AGGACACCG 9

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REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2208 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACACAGAA 743
Db 2 GATACAGAA 10

RESULT 476
AX625224
LOCUS
DEFINITION
Sequence 2265 from Patent WO02053774.
ACCESSION
AX625224
VERSION
AX625224.1 GI:28453165
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2265 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 AGAACACCG 748
Db 1 AGGACACCG 9

RESULT 477
AX625356/c
LOCUS
DEFINITION
Sequence 2397 from Patent WO02053774.
ACCESSION
AX625356
VERSION
AX625356.1 GI:28453297
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2397 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 AGAACACCG 748
Db 1 AGGACACCG 9

RESULT 477
AX625356/c
LOCUS
DEFINITION
Sequence 2397 from Patent WO02053774.
ACCESSION
AX625356
VERSION
AX625356.1 GI:28453297
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2397 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 AGAACACCG 748
Db 1 AGGACACCG 9

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Query Match 33.6%; Score 7.4; DB 1; Length 11; PAT 21-FEB-2003
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGA 736
Db 10 GCAAGGAGA 2

RESULT 478
AX625496
LOCUS
DEFINITION Sequence 2537 from Patent WO02053774.
ACCESSION AX625496
VERSION AX625496.1 GI:28453437
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2537 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGA 736
Db 3 GTCAGGAGA 11

RESULT 479
AX625505
LOCUS
DEFINITION Sequence 2546 from Patent WO02053774.
ACCESSION AX625505
VERSION AX625505.1 GI:28453446
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2546 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAA 738
Db 1 CAGGAGGAA 9

RESULT 480

AX625671/c
LOCUS
DEFINITION Sequence 2712 from Patent WO02053774.
ACCESSION AX625671
VERSION AX625671.1 GI:28453612
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2712 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 GGAGAAACA 740
Db 9 GGAGAAAAA 1

RESULT 481
AX625851/c
LOCUS
DEFINITION Sequence 2892 from Patent WO02053774.
ACCESSION AX625851
VERSION AX625851.1 GI:28453889
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2892 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAA 738
Db 10 CAGGGGAAA 2

RESULT 482
AX625896/c
LOCUS
DEFINITION Sequence 2937 from Patent WO02053774.
ACCESSION AX625896
VERSION AX625896.1 GI:28453934
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1

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AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2937 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      728 GCCAGGACA 736
Db      9 GCCAGGATA 1

RESULT 483
AX625946
LOCUS      AX625946      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2987 from Patent WO02053774.
ACCESSION  AX625946
VERSION     AX625946.1 GI:28453984
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2987 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      735 GAAACAGAA 743
Db      1 GAAACAGAA 9

RESULT 484
AX626224/c
LOCUS      AX626224/c      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3265 from Patent WO02053774.
ACCESSION  AX626224
VERSION     AX626224.1 GI:28454262
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3265 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      736 AAACAGAC 744
Db      1 AAACAGAC 9

RESULT 486
AX626443/c
LOCUS      AX626443/c      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3484 from Patent WO02053774.
ACCESSION  AX626443
VERSION     AX626443.1 GI:28454481
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3484 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      739 CAGAACACC 747
Db      10 CAGAACACC 2

RESULT 487
AX626519/c
LOCUS      AX626519/c      11 bp      DNA      linear      PAT 21-FEB-2003

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[illegible]

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QY 729 CCAGGAGAA 737
Db 1 CCAGTAGAA 9

RESULT 492
AX626812/c
LOCUS AX626812 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3853 from Patent WO02053774.
ACCESSION AX626812
VERSION AX626812.1 GI:28454850
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3853 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACCA 745
Db 3 AACAGAACCA 11

RESULT 495
AX627101/c
LOCUS AX627101 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4142 from Patent WO02053774.
ACCESSION AX627101
VERSION AX627101.1 GI:28455139
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4142 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 9 CAGAACACC 1

RESULT 496
AX627201/c
LOCUS AX627201 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4242 from Patent WO02053774.
ACCESSION AX627201
VERSION AX627201.1 GI:28455239
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4242 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 734 AGAAGACAGA 742
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Db 9 AGACACAGA 1

RESULT 497
AX627513
LOCUS AX627513 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4554 from Patent WO02053774.
ACCESSION AX627513
VERSION AX627513.1 GI:28455551
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 4554 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGA 736
  ||| |||||
Db 3 GTCAGGAGA 11

RESULT 498
AX627584/c
LOCUS AX627584 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4625 from Patent WO02053774.
ACCESSION AX627584
VERSION AX627584.1 GI:28455622
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 4625 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    Location/Qualifiers
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        /mol_type="unassigned DNA"
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Query Match
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 737 AACAGACA 745
  ||| |||||
Db 9 AACAGACA 1
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FEATURES
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Query Match
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 738 ACAGAACAC 746
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Db 11 AAAGAACAC 3

RESULT 500
AX628002/c
LOCUS AX628002 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5043 from Patent WO02053774.
ACCESSION AX628002
VERSION AX628002.1 GI:28456040
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5043 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    Location/Qualifiers
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        /mol_type="unassigned DNA"
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Query Match
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 744
  ||| |||||
Db 9 AACAGAAC 1

RESULT 501
AX628045
LOCUS AX628045 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5086 from Patent WO02053774.
ACCESSION AX628045
VERSION AX628045.1 GI:28456083
KEYWORDS
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5086 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      729 CCAGGAGAA 737
Db      2 CCAGGAGCA 10

RESULT 502
AX628233/c
LOCUS      AX628233
DEFINITION Sequence 5274 from Patent WO02053774.
ACCESSION  AX628233
VERSION     AX628233.1 GI:28456271
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5274 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      738 ACAGAACAC 746
Db      10 ACAGAACAC 2

RESULT 503
AX628272
LOCUS      AX628272
DEFINITION Sequence 5313 from Patent WO02053774.
ACCESSION  AX628272
VERSION     AX628272.1 GI:28456310
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5313 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      735 GAAACAGAA 743
Db      2 GAAACGAA 10

RESULT 504
AX628283/c
LOCUS      AX628283
DEFINITION Sequence 5324 from Patent WO02053774.
ACCESSION  AX628283
VERSION     AX628283.1 GI:28456321
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5324 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      727 TGCCAGGAG 735
Db      11 TGACAGGAG 3

RESULT 505
AX628286
LOCUS      AX628286
DEFINITION Sequence 5327 from Patent WO02053774.
ACCESSION  AX628286
VERSION     AX628286.1 GI:28456324
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5327 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      739 CAGAACACC 747
Db      3 CAGGACACC 11

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RESULT 506
AX628357/c
LOCUS AX628357 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5398 from Patent WO02053774.
ACCESSION AX628357
VERSION AX628357.1 GI:28456395
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5398 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 739 CAGAACACC 747
Db 10 CAGAACAGC 2
|||||
|

RESULT 507
AX628361/c
LOCUS AX628361 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5402 from Patent WO02053774.
ACCESSION AX628361
VERSION AX628361.1 GI:28456399
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5402 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 739 CAGAACACC 747
Db 10 CAGAACAGC 2
|||||
|

RESULT 508
AX628382/c
LOCUS AX628382 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5423 from Patent WO02053774.
ACCESSION AX628382
VERSION AX628382.1 GI:28456420
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5423 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 729 CCAGCAGAA 737
Db 10 CCAGCAGAA 2
|||||
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RESULT 509
AX628396
LOCUS AX628396 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5437 from Patent WO02053774.
ACCESSION AX628396
VERSION AX628396.1 GI:28456434
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5437 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 732 GGAGAAACA 740
Db 10 GGAGGAACA 2
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RESULT 510
AX628417
LOCUS AX628417 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5458 from Patent WO02053774.
ACCESSION AX628417
VERSION AX628417.1 GI:28456455
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5458 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"			
Query Match	33.6%; Score 7.4; DB 1; Length 11;		
Best Local Similarity	88.9%; Pred. No. 2.7e-02;		
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	728 GCCAGGAGA 736		
Db	3 GCCAGGACA 11		
RESULT 511			
AX628539			
LOCUS	11 bp DNA	linear	PAT 21-FEB-2003
DEFINITION	Sequence 5580 from Patent WO02053774.		
ACCESSION	AX628539		
VERSION	AX628539.1 GI:28456577		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
1	Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5580 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)		
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source	1..11		
	Location/Qualifiers		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	33.6%; Score 7.4; DB 1; Length 11;		
Best Local Similarity	88.9%; Pred. No. 2.7e-02;		
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	732 GGAGAAACA 740		
Db	3 GGAGAAACA 11		
RESULT 512			
AX628543/c			
LOCUS	11 bp DNA	linear	PAT 21-FEB-2003
DEFINITION	Sequence 5584 from Patent WO02053774.		
ACCESSION	AX628543		
VERSION	AX628543.1 GI:28456581		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
1	Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5584 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)		
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source	1..11		
	Location/Qualifiers		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	33.6%; Score 7.4; DB 1; Length 11;		
Best Local Similarity	88.9%; Pred. No. 2.7e-02;		
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	735 GAAACAGAA 743		
Db	10 GAGACAGAA 2		
RESULT 515			
AX628860			
LOCUS	11 bp DNA	linear	PAT 21-FEB-2003
DEFINITION	Sequence 5901 from Patent WO02053774.		
ACCESSION	AX628860		
VERSION	AX628860.1 GI:28456898		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
1	Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5882 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)		
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source	1..11		
	Location/Qualifiers		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	33.6%; Score 7.4; DB 1; Length 11;		
Best Local Similarity	88.9%; Pred. No. 2.7e-02;		
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	728 GCCAGGAGA 736		
Db	3 GCCAGGACA 11		
RESULT 513			
AX628827/c			
LOCUS	11 bp DNA	linear	PAT 21-FEB-2003
DEFINITION	Sequence 5868 from Patent WO02053774.		
ACCESSION	AX628827		
VERSION	AX628827.1 GI:28456865		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
1	Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5868 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)		
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source	1..11		
	Location/Qualifiers		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	33.6%; Score 7.4; DB 1; Length 11;		
Best Local Similarity	88.9%; Pred. No. 2.7e-02;		
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	736 AAACAGAAC 744		
Db	9 AAATAGAAC 1		
RESULT 514			
AX628841			
LOCUS	11 bp DNA	linear	PAT 21-FEB-2003
DEFINITION	Sequence 5982 from Patent WO02053774.		
ACCESSION	AX628841		
VERSION	AX628841.1 GI:28456879		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
1	Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5882 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)		
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source	1..11		
	Location/Qualifiers		

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REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5901 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGAGAA 737
|||||
Db 1 CCAGTAGAA 9

RESULT 516
AX628903
LOCUS
AX628903
DEFINITION
Sequence 5944 from Patent WO02053774.
ACCESSION
AX628903
VERSION
AX628903.1 GI:28456941
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5944 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGACA 745
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Db 1 AACAGATA 9

RESULT 517
AX629070
LOCUS
AX629070
DEFINITION
Sequence 6111 from Patent WO02053774.
ACCESSION
AX629070
VERSION
AX629070.1 GI:28457108
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 6111 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
|||||
Db 1 GAGAAAGAG 9

RESULT 518
AX629180
LOCUS
AX629180
DEFINITION
Sequence 6221 from Patent WO02053774.
ACCESSION
AX629180
VERSION
AX629180.1 GI:28457218
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 6221 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGAG 735
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Db 3 TTCCAGGAG 11

RESULT 519
AX629375
LOCUS
AX629375
DEFINITION
Sequence 6416 from Patent WO02053774.
ACCESSION
AX629375
VERSION
AX629375.1 GI:28457413
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 6416 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAC 739
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Db 2 AGGGGAAC 10

RESULT 520
AX629412
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LOCUS       AX629412                      11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 6453 from Patent WO02053774.
ACCESSION    AX629412
VERSION      AX629412.1  GI:28457450
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1. Petersohn,D., Conradt,M. and Hofmann,K.
             Method for determining homeostasis of the skin
TITLE        Patent: WO 02053774-A 6453 11-JUL-2002;
JOURNAL      Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      733  GAGAAACAG 741
Db      3  GAGTAAACAG 11

RESULT 521
AX630196/c
LOCUS       AX630196                      11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 7237 from Patent WO02053774.
ACCESSION    AX630196
VERSION      AX630196.1  GI:28458234
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1. Petersohn,D., Conradt,M. and Hofmann,K.
             Method for determining homeostasis of the skin
TITLE        Patent: WO 02053774-A 7237 11-JUL-2002;
JOURNAL      Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
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             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      730  CAGGAGAAA 738
Db      11  CAGAAGAAA 3

RESULT 522
AX630470/c
LOCUS       AX630470                      11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 7511 from Patent WO02053774.
ACCESSION    AX630470
VERSION      AX630470.1  GI:28458508
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1. Petersohn,D., Conradt,M. and Hofmann,K.
             Method for determining homeostasis of the skin
TITLE        Patent: WO 02053774-A 7511 11-JUL-2002;
JOURNAL      Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731  AGGAGAAAC 739
Db      10  AGGAGACAC 2

RESULT 524
AX630752/c
LOCUS       AX630752                      11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 7793 from Patent WO02053774.
ACCESSION    AX630752
VERSION      AX630752.1  GI:28458790
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1. Petersohn,D., Conradt,M. and Hofmann,K.
             Method for determining homeostasis of the skin
TITLE        Patent: WO 02053774-A 7793 11-JUL-2002;
JOURNAL      Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731  AGGAGAAAC 739
Db      10  AGGAGACAC 2

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TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7511 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      739  CAGAACACC 747
Db      10  CAGAAAACC 2

RESULT 523
AX630527/c
LOCUS       AX630527                      11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 7568 from Patent WO02053774.
ACCESSION    AX630527
VERSION      AX630527.1  GI:28458565
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1. Petersohn,D., Conradt,M. and Hofmann,K.
             Method for determining homeostasis of the skin
TITLE        Patent: WO 02053774-A 7568 11-JUL-2002;
JOURNAL      Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
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             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731  AGGAGAAAC 739
Db      10  AGGAGACAC 2

RESULT 524
AX630752/c
LOCUS       AX630752                      11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 7793 from Patent WO02053774.
ACCESSION    AX630752
VERSION      AX630752.1  GI:28458790
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1. Petersohn,D., Conradt,M. and Hofmann,K.
             Method for determining homeostasis of the skin
TITLE        Patent: WO 02053774-A 7793 11-JUL-2002;
JOURNAL      Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731  AGGAGAAAC 739
Db      10  AGGAGACAC 2

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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
|||||
Db 3 GAAACAGGA 11

RESULT 525
AX630801/c
LOCUS AX630801 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7842 from Patent WO02053774.
ACCESSION AX630801
VERSION AX630801.1 GI:28458841
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7842 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACAA 745
|||||
Db 10 AACAGAACAA 2

RESULT 526
AX630939/c
LOCUS AX630939 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7980 from Patent WO02053774.
ACCESSION AX630939
VERSION AX630939.1 GI:28458981
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7980 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
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Db 9 AGAAACAGA 1

RESULT 527
AX630972/c
LOCUS AX630972 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8013 from Patent WO02053774.

ACCESSION AX630972
VERSION AX630972.1 GI:28459014
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8013 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAA 740
|||||
Db 9 GGAGAACAA 1

RESULT 528
AX631060/c
LOCUS AX631060 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8101 from Patent WO02053774.
ACCESSION AX631060
VERSION AX631060.1 GI:28459102
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8101 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
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Db 11 CAGAACACC 3

RESULT 529
AX631195/c
LOCUS AX631195 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8237 from Patent WO02053774.
ACCESSION AX631195
VERSION AX631195.1 GI:28459239
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8237 11-JUL-2002;

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FEATURES
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      /db_xref="taxon:9606"

Query Match
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  Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGACACACC 747
Db 11 CAGACACACC 3

RESULT 530
AX631267
LOCUS
  AX631267 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 8309 from Patent WO02053774.
ACCESSION
  AX631267
VERSION
  AX631267.1 GI:28459313
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE
    Method for determining homeostasis of the skin
  JOURNAL
    Patent: WO 02053774-A 8309 11-JUL-2002;
    Henkel Kommanditgesellschaft auf Aktien (DE)
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
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  Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAC 739
Db 1 AGGATTAAC 9

RESULT 531
AX631283/c
LOCUS
  AX631283 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 8325 from Patent WO02053774.
ACCESSION
  AX631283
VERSION
  AX631283.1 GI:28459329
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE
    Method for determining homeostasis of the skin
  JOURNAL
    Patent: WO 02053774-A 8325 11-JUL-2002;
    Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
  Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCACGAG 735
Db 9 TTCCAGGAG 1

RESULT 532
AX632230
LOCUS
  AX632230 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 9272 from Patent WO02053774.
ACCESSION
  AX632230
VERSION
  AX632230.1 GI:28467845
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE
    Method for determining homeostasis of the skin
  JOURNAL
    Patent: WO 02053774-A 9272 11-JUL-2002;
    Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
  Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 2 GAAGCAGAA 10

RESULT 533
AX632260
LOCUS
  AX632260 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 9302 from Patent WO02053774.
ACCESSION
  AX632260
VERSION
  AX632260.1 GI:28467875
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE
    Method for determining homeostasis of the skin
  JOURNAL
    Patent: WO 02053774-A 9302 11-JUL-2002;
    Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
  Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 1 GGGAAACAG 9

RESULT 534
AX632588
LOCUS
  AX632588 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 9630 from Patent WO02053774.
ACCESSION
  AX632588
VERSION
  AX632588.1 GI:28468203

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KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9630 11-JUL-2002; (DE)
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 735 GAAACAGAA 743
Db 2 GATACAGAA 10
RESULT 535
AX632645
LOCUS AX632645 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9687 from Patent WO02053774.
ACCESSION AX632645
VERSION AX632645.1 GI:28468260
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9687 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 740 AGAACACCG 748
Db 1 AGGACACCG 9
RESULT 536
AX632777/c
LOCUS AX632777 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9819 from Patent WO02053774.
ACCESSION AX632777
VERSION AX632777.1 GI:28468392
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9819 11-JUL-2002; (DE)
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers

source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCACGAGAA 736
Db 10 GCACGAGAA 2
RESULT 537
BD095115
LOCUS BD095115 11 bp DNA linear PAT 27-AUG-2002
DEFINITION A polynucleotide encoding mouse histidine decarboxylase.
ACCESSION BD095115
VERSION BD095115.1 GI:22640703
KEYWORDS WO 0132892-A/8.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE Otsu,H.
JOURNAL A polynucleotide encoding mouse histidine decarboxylase
COMMENT Patent: WO 0132892-A 8 10-MAY-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP,HIROSHI OTSU
OS Mus sp. (mouse)
PN WO 0132892-A/8
PD 10-MAY-2001
PF 01-NOV-2000 WO 2000JP007689
PR 02-NOV-1999 JP 99P 312559,23-MAR-2000 JP 00P 062953 PI
HIROSHI OTSU
PC C12N15/60,C12N9/88
CC A polynucleotide encoding mouse histidine decarboxylase FH
Key Location/Qualifiers
FT source
1. .11
/organism="Mus sp. (mouse)"
/Location/Qualifiers
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1. .11
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGACAC 746
Db 3 ACAGACAC 11
RESULT 538
BD124255
LOCUS BD124255 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124255
VERSION BD124255.1 GI:23219200
KEYWORDS JP 2002503460-A/86.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE Katz,E.H.
JOURNAL Compositions and method for healing wound
COMMENT Patent: JP 2002503460-A 86 05-FEB-2002;
THE WISTAR INSTITUTE
OS Mus musculus (mouse)

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PN JP 2002503460-A/86
PD 05-FEB-2002
PR 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1..11
FT Location/Qualifiers
1..11
/organism="Mus musculus (mouse)".
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source
1..11
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGAACAC 746
Db 1 ACAGAACTC 9
RESULT 539
BD124293
LOCUS BD124293 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124293
VERSION BD124293.1 GI:23219238
KEYWORDS JP 2002503460-A/124.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 11)
REFERENCE
AUTHORS Katz, E.H.
TITLE Compositions and method for healing wound
JOURNAL THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/124
PD 05-FEB-2002
PR 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1..11
FT Location/Qualifiers
1..11
/organism="Mus musculus (mouse)".
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source
1..11
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGAACAC 746
Db 3 ACCGAACAC 11
RESULT 540
AJ601274

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LOCUS AJ601274 11 bp DNA linear PLN 23-OCT-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
524A12
ACCESSION AJ601274
VERSION AJ601274.1 GI:37950902
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
REFERENCE
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446585
REFERENCE 2 (bases 1 to 11)
AUTHORS Balzerque, S.
JOURNAL Direct Submission
COMMENT Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (8) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplatane' (http://www.genoplatane.com and
http://genoplatane-info.infobiogen.fr).
FEATURES
Source
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassilewskija"
/db_xref="taxon:3702"
/clone="524A12"
/misc_feature 1..11
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/Note="T-DNA flanking sequence
left border"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 740 AGAACACCG 748
Db 2 AGAACACCG 10
RESULT 541
AX017048/c
LOCUS AX017048 8 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 11 from Patent WO9947706.
ACCESSION AX017048
VERSION AX017048.1 GI:10042014
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 8)
REFERENCE Schwarz, T. and Reeve, M.A.
AUTHORS Sequencing by hybridisation
TITLE Patent: WO 9947706-A 11 23-SEP-1999;
JOURNAL SCHWARZ TEREK (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN
(GB)

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FEATURES
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        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="Hba specific oligonucleotides"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 737
Db 7 AGGAGAA 1

RESULT 542
AX017049/c
LOCUS AX017049 8 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 12 from Patent WO9947706.
ACCESSION AX017049
VERSION AX017049.1 GI:10042015
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1 (bases 1 to 8)
    AUTHORS Schwarz,T. and Reeve,M.A.
    TITLE Sequencing by hybridisation
    JOURNAL Patent: WO 9947706-A 12 23-SEP-1999;
    SCHWARZ TEREK (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN
    (GB)
FEATURES
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        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="Hbs specific oligonucleotides"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 737
Db 8 AGGAGAA 2

RESULT 543
AX017086
LOCUS AX017086 8 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 49 from Patent WO9947706.
ACCESSION AX017086
VERSION AX017086.1 GI:10042052
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1 (bases 1 to 8)
    AUTHORS Schwarz,T. and Reeve,M.A.
    TITLE Sequencing by hybridisation
    JOURNAL Patent: WO 9947706-A 49 23-SEP-1999;
    SCHWARZ TEREK (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN
    (GB)
FEATURES
  source
    Location/Qualifiers
      1..8
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="Fluorescently labelled capture oligonucleotide"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 737
Db 8 AGGAGAA 2

RESULT 544
AX017087
LOCUS AX017087 8 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 50 from Patent WO9947706.
ACCESSION AX017087
VERSION AX017087.1 GI:10042053
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1 (bases 1 to 8)
    AUTHORS Schwarz,T. and Reeve,M.A.
    TITLE Sequencing by hybridisation
    JOURNAL Patent: WO 9947706-A 50 23-SEP-1999;
    SCHWARZ TEREK (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN
    (GB)
FEATURES
  source
    Location/Qualifiers
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        /db_xref="taxon:32630"
        /note="Fluorescently labelled capture oligonucleotide"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 737
Db 2 AGGAGAA 8

RESULT 545
AX573622/c
LOCUS AX573622 8 bp DNA linear PAT 07-JAN-2003
DEFINITION Sequence 32 from Patent WO02079467.
ACCESSION AX573622
VERSION AX573622.1 GI:27551292
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1
    AUTHORS Nielsen,P.E. and Good,L.
    TITLE Antibiotic-free bacterial strain selection with antisense molecules
    JOURNAL Patent: WO 02079467-A 32 10-OCT-2002;
    Koebenhavns Universitet (DK)
FEATURES
  source
    Location/Qualifiers
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        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="Peptide nucleic acid no. 1832"

misc_feature
  8
    /note="A lysine residue is linked to COOH-terminal of the
    PNA"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAG 741
Db 8 GAAACAG 2

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RESULT 546
BD217832/c
LOCUS      BD217832      8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence determination by hybridization.
ACCESSION  BD217832
VERSION    BD217832.1 GI:33027602
KEYWORDS   JP 2002509701-A/11.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS    Reeve,M.A. and Schwarz,T.
TITLE      Sequence determination by hybridization
JOURNAL    Patent: JP 2002509701-A 11 02-APR-2002;
COMMENT    NYCOMED AMERSHAM PLC
          PN JP 2002509701-A/11
          PD 02-APR-2002
          PF 19-MAR-1999 JP 2000536888
          PI MICHAEL ALAN REEVE,TEREK SCHWARZ
          PC C12Q1/69,C12N15/09,C12N15/00
          CC Description of Artificial Sequence:HBA SPECIFIC CC
          OLIGONUCLEOTIDE
          FH Key      Location/Qualifiers
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                      /organism='Artificial Sequence'.

FEATURES             source
LOCUS                 1..8
DEFINITION            /organism='synthetic construct'
ACCESSION              /mol_type='genomic DNA'
VERSION                /db_xref='taxon:32630'
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Query Match      31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      731 AGGAGAA 737
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Db      7 AGGAGAA 1

RESULT 547
BD217833/c
LOCUS      BD217833      8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence determination by hybridization.
ACCESSION  BD217833
VERSION    BD217833.1 GI:33027603
KEYWORDS   JP 2002509701-A/12.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS    Reeve,M.A. and Schwarz,T.
TITLE      Sequence determination by hybridization
JOURNAL    Patent: JP 2002509701-A 12 02-APR-2002;
COMMENT    NYCOMED AMERSHAM PLC
          PN JP 2002509701-A/12
          PD 02-APR-2002
          PF 19-MAR-1999 JP 2000536888
          PI MICHAEL ALAN REEVE,TEREK SCHWARZ
          PC C12Q1/69,C12N15/09,C12N15/00
          CC Description of Artificial Sequence:HBS SPECIFIC CC
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          FH Key      Location/Qualifiers
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FEATURES             source
LOCUS                 1..8
DEFINITION            /organism='synthetic construct'
ACCESSION              /mol_type='genomic DNA'
VERSION                /db_xref='taxon:32630'
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Query Match      31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      731 AGGAGAA 737
      |||||
Db      7 AGGAGAA 1

RESULT 548
BD217870
LOCUS      BD217870      8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence determination by hybridization.
ACCESSION  BD217870
VERSION    BD217870.1 GI:33027640
KEYWORDS   JP 2002509701-A/49.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS    Reeve,M.A. and Schwarz,T.
TITLE      Sequence determination by hybridization
JOURNAL    Patent: JP 2002509701-A 49 02-APR-2002;
COMMENT    NYCOMED AMERSHAM PLC
          OS Artificial Sequence
          PN JP 2002509701-A/49
          PD 02-APR-2002
          PF 19-MAR-1999 JP 2000536888
          PI MICHAEL ALAN REEVE,TEREK SCHWARZ
          PC C12Q1/69,C12N15/09,C12N15/00
          CC Description of Artificial Sequence:FLUORESCENTLY LABELLED CC
          CAPTURE
          CC OLIGONUCLEOTIDE
          FH Key      Location/Qualifiers
          FT source   1..8
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FEATURES             source
LOCUS                 1..8
DEFINITION            /organism='synthetic construct'
ACCESSION              /mol_type='genomic DNA'
VERSION                /db_xref='taxon:32630'
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Query Match      31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      731 AGGAGAA 737
      |||||
Db      2 AGGAGAA 8

RESULT 549
BD217871
LOCUS      BD217871      8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence determination by hybridization.
ACCESSION  BD217871
VERSION    BD217871.1 GI:33027641
KEYWORDS   JP 2002509701-A/50.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS    Reeve,M.A. and Schwarz,T.
TITLE      Sequence determination by hybridization
JOURNAL    Patent: JP 2002509701-A 50 02-APR-2002;
COMMENT    NYCOMED AMERSHAM PLC
          OS Artificial Sequence
          PN JP 2002509701-A/50
          PD 02-APR-2002
          PF 19-MAR-1999 JP 2000536888

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PR 19-MAR-1998 GB 9805918.1
PI MICHAEL ALAN REEVE, TEREK SCHWARZ
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: FLUORESCENTLY LABELLED CC
CAPTURE
CC OLIGONUCLEOTIDE Location/Qualifiers
FH Key 1..8
FT source /organism='Artificial Sequence'.
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            /organism='synthetic construct'
            /mol_type='genomic DNA'
            /db_xref='taxon:32630'

Query Match 31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 737
Db 1 AGGAGAA 7

RESULT 550
LOCUS AX350493/c 9 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 5 from Patent WO0179561.
ACCESSION AX350493
VERSION AX350493.1 GI:18616095
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 5 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
FEATURES
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            /mol_type='genomic DNA'
            /db_xref='taxon:9606'

Query Match 31.8%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 737
Db 8 AGGAGAA 2

RESULT 551
AX573621/c 9 bp DNA linear PAT 07-JAN-2003
LOCUS AX573621
DEFINITION Sequence 31 from Patent WO02079467.
ACCESSION AX573621
VERSION AX573621.1 GI:27551291
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Nielsen, P.E. and Good, L.
TITLE Antibiotic-free bacterial strain selection with antisense molecules
JOURNAL Patent: WO 02079467-A 31 10-OCT-2002;
Koebenhavns Universitet (DK)
FEATURES
    source
        Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
/note='Peptide nucleic acid no. 1876'
misc_feature 9
/note='A lysine residue is linked to COOH-terminal of the
ENA'

Query Match 31.8%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAAACAG 741
Db 9 GAAACAG 3

RESULT 552
LOCUS A06372 10 bp DNA linear PAT 26-AUG-1993
DEFINITION Nucleotide sequence 15 from patent number EP0139076.
ACCESSION A06372
VERSION A06372.1 GI:411246
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Mayer, H.
TITLE Human-Parathyroid hormone (human-PTH) producing hybrid vectors,
human-Parathyroid hormone gene, eucaryotic cells containing the
hybrid vector and their use
JOURNAL Patent: EP 0139076-A 15 02-MAY-1985;
Gesellschaft fuer Biotechnologische Forschung mbH (GBF)
FEATURES
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            /db_xref='taxon:32630'

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 737
Db 2 AGGAGAA 8

RESULT 553
AR018737 10 bp DNA linear PAT 05-DEC-1998
LOCUS AR018737
DEFINITION Sequence 19 from patent US 5783182.
ACCESSION AR018737
VERSION AR018737.1 GI:3973851
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Thompson, T.C.
TITLE Method for identifying metastatic sequences
JOURNAL Patent: US 5783182-A 19 21-JUL-1998;
FEATURES
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        Location/Qualifiers
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            /organism='unknown'
            /mol_type='unassigned DNA'

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 TGCCAGG 733
Db 727 TGCCAGG 733
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Db
4 TGCCAGG 10

RESULT 554
ARI07767/c
LOCUS ARI07767 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 13 from patent US 6110667.
ACCESSION ARI07767
VERSION ARI07767.1 GI:12823254
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 13 25-AUG-2000;
FEATURES
source
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Location/Qualifiers
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGA 734
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9 GCCAGGA 3

Db

RESULT 555
ARI076672
LOCUS ARI076672 10 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6312894.
ACCESSION ARI076672
VERSION ARI076672.1 GI:17919027
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hedgpeth,J., Afonina,I.A., Kutayavin,I.V., Lukhtanov,E.A.,
Belousov,E.S. and Meyer,R.B. Jr.
TITLE Hybridization and mismatch discrimination using oligonucleotides
conjugated to minor groove binders
JOURNAL Patent: US 6312894-A 3 06-NOV-2001;
FEATURES
source
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Location/Qualifiers
/mol_type="unassigned DNA"
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AACAGCA 742
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4 AACAGCA 10

Db

RESULT 556
BD238798/c
LOCUS BD238798 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238798
VERSION BD238798.1 GI:33048569
KEYWORDS JP 2002534056-A/216.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 341 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/341
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/090091 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
C12N1/15,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 CCAGGAG 735
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9 CCAGGAG 3

Db

RESULT 557
BD238923
LOCUS BD238923 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238923
VERSION BD238923.1 GI:33048693
KEYWORDS JP 2002534056-A/341.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 341 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/341
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 CCAGGAG 735
Db 4 CCAGGAG 10
RESULT 558
BD238950/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238950
VERSION BD238950.1 GI:33048720
KEYWORDS JP 2002534056-A/368.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
ROBERTS, B.L. and Shankara, S.
Preparation and use of superior vaccines
TITLE
JOURNAL Patent: JP 2002534056-A 368 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/368
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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Location/Qualifiers
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 CCAGGAG 735
Db 4 CCAGGAG 10
RESULT 558
BD238950/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238950
VERSION BD238950.1 GI:33048720
KEYWORDS JP 2002534056-A/368.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
ROBERTS, B.L. and Shankara, S.
Preparation and use of superior vaccines
TITLE
JOURNAL Patent: JP 2002534056-A 368 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/368
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
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/db_xref='taxon:9606'

C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 731 AGGAGAA 737
Db 10 AGGAGAA 4
RESULT 559
BD239270
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239270
VERSION BD239270.1 GI:33049040
KEYWORDS JP 2002534056-A/688.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
ROBERTS, B.L. and Shankara, S.
Preparation and use of superior vaccines
TITLE
JOURNAL Patent: JP 2002534056-A 688 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/688
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
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QY 737 AACAGAA 743
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 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD239336 10 bp DNA linear PAT 17-JUL-2003
 VERSION BD239336 GI:33049106
 KEYWORDS JP 2002534056-A/754.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Roberts, B.L. and Shankara, S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 754 15-OCT-2002;
 GENZYME CORP

COMMENT
 OS Homo sapiens (human)
 PN JP 2002534056-A/754
 PD 15-OCT-2002
 PF 18-JUN-1999 JP 2000554749
 PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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 08-DEC-1998 US 60/111715
 PI BRUCE L ROBERTS, SRINIVAS SHANKARA
 PC C12N1/19, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
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 Db 4 CCAGGAG 10

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 LOCUS
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD239499 10 bp DNA linear PAT 17-JUL-2003
 VERSION BD239499 GI:33049651
 KEYWORDS JP 2002534056-A/1299.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Roberts, B.L. and Shankara, S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 1299 15-OCT-2002;
 GENZYME CORP

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD239499
 VERSION BD239499.1 GI:33049269
 KEYWORDS JP 2002534056-A/917.
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens

REFERENCE 1 (bases 1 to 10)

AUTHORS Roberts, B.L. and Shankara, S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 917 15-OCT-2002;
 GENZYME CORP

COMMENT OS Homo sapiens (human)

PN JP 2002534056-A/917

PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

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19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR

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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR

08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS, SRINIVAS SHANKARA

PC C12N1/19, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC

G01N37/00,
 CC Preparation and use of superior vaccines

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BD239881

LOCUS

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD239881

VERSION BD239881.1 GI:33049651

KEYWORDS JP 2002534056-A/1299.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)

AUTHORS Roberts, B.L. and Shankara, S.

TITLE Preparation and use of superior vaccines

JOURNAL Patent: JP 2002534056-A 1299 15-OCT-2002;

GENZYME CORP

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PN JP 2002534056-A/1299
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08-DEC-1998 US 60/111715
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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DEFINITION
ACCESSION
VERSION
BD239958.1 GI:33049728
KEYWORDS
JP 2002534056-A/1376.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Roberts,B.L. and Shankara,S.
TITLE
Preparation and use of superior vaccines
JOURNAL
Patent: JP 2002534056-A 1376 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1376
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
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08-DEC-1998 US 60/111715
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PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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DEFINITION
ACCESSION
VERSION
BD240042.1 GI:33049812
KEYWORDS
JP 2002534056-A/1460.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Roberts,B.L. and Shankara,S.
TITLE
Preparation and use of superior vaccines
JOURNAL
Patent: JP 2002534056-A 1460 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1460
PD 15-OCT-2002
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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PC C12N15/00,C12N5/00,C12N15/00
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RESULT 565
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DEFINITION
ACCESSION
VERSION
BD240042.1 GI:33049812
KEYWORDS
JP 2002534056-A/1460.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Roberts,B.L. and Shankara,S.
TITLE
Preparation and use of superior vaccines
JOURNAL
Patent: JP 2002534056-A 1460 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1460
PD 15-OCT-2002
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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Qy 733 GAGAAAC 739
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Query Match 31.8%; Score 7; DB 1; Length 10;
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QY 727 TGCCAGG 733

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RESULT 565

BD240058/c

LOCUS BD240058 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD240058

VERSION BD240058.1 GI:33049828

KEYWORDS JP 2002534056-A/1476.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 10)

Robert, B.L. and Shankara, S.

Preparation and use of superior vaccines

TITLE Patent: JP 2002534056-A 1476 15-OCT-2002;

JOURNAL GENZYME CORP

OS Homo sapiens (human)

PN JP 2002534056-A/1476

PD 15-OCT-2002

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08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS, SRINIVAS SHANKARA

PC C12N15/09, C12N15/03, A61K39/00, A61P37/04, C12N1/15, PC

C12N1/19,

PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC

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CC Preparation and use of superior vaccines

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BD240326

LOCUS BD240326

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD240326

VERSION BD240326.1 GI:33050096

KEYWORDS JP 2002534056-A/1744.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 10)

Robert, B.L. and Shankara, S.

Preparation and use of superior vaccines

TITLE Patent: JP 2002534056-A 1744 15-OCT-2002;

JOURNAL GENZYME CORP

OS Homo sapiens (human)

PN JP 2002534056-A/1744

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08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS, SRINIVAS SHANKARA

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G01N37/00,

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CC Preparation and use of superior vaccines

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGG 734

Db 4 GCCAGG 10

RESULT 567

BD240451/c

LOCUS BD240451

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD240451

VERSION BD240451.1 GI:33050221

KEYWORDS JP 2002534056-A/1869.

SOURCE Homo sapiens (human)

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ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS      Roberts,B.L. and Shankara,S.
TITLE        Preparation and use of superior vaccines
JOURNAL      Patent: JP 2002534056-A 1869 15-OCT-2002;
GENZYME CORP
COMMENT      OS Homo sapiens (human)
PN JP 2002534056-A/1869
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 CCAGGAG 735
Db 10 CCAGGAG 4

RESULT 568
BD240471
LOCUS      BD240471 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD240471
VERSION     BD240471.1 GI:33050241
KEYWORDS   JP 2002534056-A/1869
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 1869 15-OCT-2002;
GENZYME CORP
COMMENT    OS Homo sapiens (human)
PN JP 2002534056-A/1869
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

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19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
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CC Preparation and use of superior vaccines
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACA 745
Db 2 CAGAACA 8

RESULT 569
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LOCUS      BD240713 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD240713
VERSION     BD240713.1 GI:33050483
KEYWORDS   JP 2002534056-A/2131
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 2131 15-OCT-2002;
GENZYME CORP
COMMENT    OS Homo sapiens (human)
PN JP 2002534056-A/2131
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
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19-JUN-1998 US 60/089992,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

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08-DEC-1998 US 60/111715
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PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
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CC Preparation and use of superior vaccines
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGCA 734
Db 10 GCCAGCA 4

RESULT 570
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LOCUS
DEFINITION
Hybridization and mismatch discrimination using oligonucleotides
conjugated to minor groove binders.
ACCESSION
BD260023
VERSION
BD260023.1 GI:33069793
KEYWORDS
JP 2002527040-A/3.
SOURCE
Escherichia coli
ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Hedgpeth, J., Afonina, I.A., Kutyavina, I.V., Lukhtanov, E.A.,
Belousov, E.S. and Jr, R.B.M.
TITLE
Hybridization and mismatch discrimination using oligonucleotides
conjugated to minor groove binders
JOURNAL
Patent: JP 2002527040-A 3 27-AUG-2002;
EPOCH BIOSCIENCES INC
COMMENT
OS Escherichia coli
PN JP 2002527040-A/3
PD 27-AUG-2002
PF 05-APR-1999 JP 2000542342
PR 03-APR-1998 US 09/054832
PI JOEL HEDGPETH, IRINA A AFONINA, IGOR V KUTYAVIN, EUGENY A PI
LUKHTANOV,
PC C12N15/09, C12N15/09, C07H21/02, C07H21/04, C12Q1/68, G01N21/78, PC
G01N33/483,
PC G01N33/53, G01N33/566, C12N15/00, C12N15/00
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oligonucleotides
CC conjugated to minor groove binders
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AACACGA 742

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Db 4 AACACGA 10

RESULT 571
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LOCUS
DEFINITION
Genes with human dendritic cell expression.
ACCESSION
E39508
VERSION
E39508.1 GI:18621599
KEYWORDS
JP 2000279181-A/41.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Hashimoto, S., Matsushima, K. and Suzuki, T.
TITLE
Genes with human dendritic cell expression
JOURNAL
Patent: JP 2000279181-A 41 10-OCT-2000;
SCIENCE & TECH AGENCY
COMMENT
OS Homo sapiens (human)
PN JP 2000279181-A/41
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
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PI SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGACAA 745
Db 2 CAGACAA 8

RESULT 572
E39646
LOCUS
DEFINITION
Genes with human dendritic cell expression.
ACCESSION
E39646
VERSION
E39646.1 GI:18621737
KEYWORDS
JP 2000279181-A/179.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Hashimoto, S., Matsushima, K. and Suzuki, T.
TITLE
Genes with human dendritic cell expression
JOURNAL
Patent: JP 2000279181-A 179 10-OCT-2000;
SCIENCE & TECH AGENCY
COMMENT
OS Homo sapiens (human)
PN JP 2000279181-A/179
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR
PI SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI
PC C12N15/09, C07K14/475, C07K16/18, C12N15/00
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 738 ACAGAAC 744
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Db 3 ACAGAAC 9

RESULT 573
E39648/c
LOCUS E39648 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39648
VERSION E39648.1 GI:18621739
KEYWORDS JP 2000279181-A/181.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Hashimoto,S., Matsushima,K. and Suzuki,T.
  Genes with human dendritic cell expression
  Patent: JP 2000279181-A 181 10-OCT-2000;
  JOURNAL SCIENCE & TECH AGENCY
COMMENT
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  PN JP 2000279181-A/181
  PD 10-OCT-2000
  PF 01-APR-1999 JP 1999095481
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 CCAGGAG 735
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Db 10 CCAGGAG 4

RESULT 574
E39691
LOCUS E39691 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39691
VERSION E39691.1 GI:18621782
KEYWORDS JP 2000279181-A/224.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Hashimoto,S., Matsushima,K. and Suzuki,T.
  Genes with human dendritic cell expression
  Patent: JP 2000279181-A 224 10-OCT-2000;
  JOURNAL SCIENCE & TECH AGENCY

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QY 727 TGCCAGG 733
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Db 9 TGCCAGG 3

RESULT 576
E54698/c
LOCUS E54698 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION E54698

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COMMENT
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  PN JP 2000279181-A/224
  PD 10-OCT-2000
  PF 01-APR-1999 JP 1999095481
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGA 734
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Db 2 GCCAGGA 8

RESULT 575
E39743/c
LOCUS E39743 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39743
VERSION E39743.1 GI:18621834
KEYWORDS JP 2000279181-A/276.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Hashimoto,S., Matsushima,K. and Suzuki,T.
  Genes with human dendritic cell expression
  Patent: JP 2000279181-A 276 10-OCT-2000;
  JOURNAL SCIENCE & TECH AGENCY
COMMENT
  OS Homo sapiens (human)
  PN JP 2000279181-A/276
  PD 10-OCT-2000
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Db 9 TGCCAGG 3

RESULT 576
E54698/c
LOCUS E54698 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION E54698

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VERSION E54698.1 GI:22556181
KEYWORDS JP 2001211883-A/50.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 50 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/50
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers.
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 740 AGAACAC 746
DB 10 AGAACAC 4

RESULT 577
E54746
LOCUS Human normal liver cell expression genes.
DEFINITION E54746
ACCESSION E54746
VERSION E54746.1 GI:22556229
KEYWORDS JP 2001211883-A/98.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 98 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/98
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
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QY 739 CAGAAC 745
DB 2 CAGAAC 8

RESULT 578
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LOCUS Human normal liver cell expression genes.
DEFINITION E54750
ACCESSION E54750
VERSION E54750.1 GI:22556233
KEYWORDS JP 2001211883-A/102.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 102 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/102
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
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FH Key Location/Qualifiers.
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Location/Qualifiers.
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 CCAGGAG 735
DB 10 CCAGGAG 4

RESULT 579
E58380/c
LOCUS Sequence 14 from patent US 5652106.
DEFINITION E58380
ACCESSION E58380
VERSION E58380.1 GI:2477618
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Plikaytis,B.B., Shinnick,T.M. and Crawford,J.T.
TITLE Rapid amplification-based subtyping of mycobacterium tuberculosis
JOURNAL Patent: US 5652106-A 14 29-JUL-1997;
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QY 742 AACACCG 748
DB 9 AACACCG 3

RESULT 580
AR282625
LOCUS

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DEFINITION Sequence 21 from patent US 6521747.
ACCESSION AR282625
VERSION AR282625.1 GI:29719223
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Anastasio,A.E., Finkel,K., Koshy,B. and Lee,H.
TITLE Haplotypes of the AGTR1 gene
JOURNAL Patent: US 6521747-A 21 18-FEB-2003;
FEATURES Location/Qualifiers
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAAACAG 741
Db 3 GAAACAG 9

RESULT 581
AR303410/c
LOCUS AR303410 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 135 from patent US 6544736.
ACCESSION AR303410
VERSION AR303410.1 GI:31692186
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 135 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 GGAGAAA 738
Db 9 GGAGAAA 3

RESULT 582
AR303594/c
LOCUS AR303594 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 319 from patent US 6544736.
ACCESSION AR303594
VERSION AR303594.1 GI:31692370
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 319 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAAACAG 741
Db 8 GAAACAG 2

RESULT 583
AR336847/c
LOCUS AR336847 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 22 from patent US 6566130.
ACCESSION AR336847
VERSION AR336847.1 GI:33722697
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 22 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 737
Db 9 AGGAGAA 3

RESULT 584
AR336854
LOCUS AR336854 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 29 from patent US 6566130.
ACCESSION AR336854
VERSION AR336854.1 GI:33722704
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 29 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 739 CAGAACAC 745
Db 2 CAGAACAC 8

RESULT 585
AR409234/c
LOCUS AR409234 10 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 52 from patent US 6632919.
ACCESSION AR409234
VERSION AR409234.1 GI:40159877
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Nielsen,P.E., Haaima,G. and Eldrup,A.B.
TITLE        Peptide nucleic acid monomers and oligomers
JOURNAL      Patent: US 6632919-A 52 14-OCT-2003;
FEATURES     Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      740 AGAACAC 746
Db      8 AGAACAC 2

RESULT 586
LOCUS      AR409238
DEFINITION Sequence 56 from patent US 6632919.
ACCESSION  AR409238
VERSION     AR409238.1 GI:40159881
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Nielsen,P.E., Haaima,G. and Eldrup,A.B.
TITLE        Peptide nucleic acid monomers and oligomers
JOURNAL      Patent: US 6632919-A 56 14-OCT-2003;
FEATURES     Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      740 AGAACAC 746
Db      8 AGAACAC 2

RESULT 587
LOCUS      AX112968
DEFINITION Sequence 15 from Patent WO0127267.
ACCESSION  AX112968
VERSION     AX112968.1 GI:13939403
KEYWORDS
SOURCE      Mus sp.
ORGANISM     Mus sp.
REFERENCE    1
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL      Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
            Genes differentially expressed in tri cells and their use in the
            manufacture of immunoregulatory compositions
            Patent: WO 0127267-A 15 19-APR-2001;
FEATURES     Location/Qualifiers
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            /organism="Mus sp."
            /mol_type="unassigned DNA"
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Query Match      31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      740 AGAACAC 746
Db      8 AGAACAC 2

RESULT 588
LOCUS      AX113021/c
DEFINITION Sequence 68 from Patent WO0127267.
ACCESSION  AX113021
VERSION     AX113021.1 GI:13939456
KEYWORDS
SOURCE      Mus sp.
ORGANISM     Mus sp.
REFERENCE    1
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL      Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
            Genes differentially expressed in tri cells and their use in the
            manufacture of immunoregulatory compositions
            Patent: WO 0127267-A 68 19-APR-2001;
FEATURES     Location/Qualifiers
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            /organism="Mus sp."
            /mol_type="unassigned DNA"
            /db_xref="taxon:10095"

Query Match      31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      742 AACACCG 748
Db      4 AACACCG 10

RESULT 589
LOCUS      AX152386
DEFINITION Sequence 301 from Patent WO0138577.
ACCESSION  AX152386
VERSION     AX152386.1 GI:14534037
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 301 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES     Location/Qualifiers
            1..10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      727 TGCCAGG 733
Db      7 TGCCAGG 1

RESULT 589
LOCUS      AX152386
DEFINITION Sequence 301 from Patent WO0138577.
ACCESSION  AX152386
VERSION     AX152386.1 GI:14534037
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 301 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES     Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      727 TGCCAGG 733
Db      7 TGCCAGG 1

RESULT 590
LOCUS      AX152442/c
DEFINITION Sequence 728 from Patent WO0127267.
ACCESSION  AX152442
VERSION     AX152442.1 GI:13939403
KEYWORDS
SOURCE      Mus sp.
ORGANISM     Mus sp.
REFERENCE    1
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL      Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
            Genes differentially expressed in tri cells and their use in the
            manufacture of immunoregulatory compositions
            Patent: WO 0127267-A 728 19-APR-2001;
FEATURES     Location/Qualifiers
            1..10
            /organism="Mus sp."
            /mol_type="unassigned DNA"
            /db_xref="taxon:10095"

Query Match      31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGA 734
Db      3 GCCAGGA 9

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LOCUS AX152442 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 357 from Patent WO0138577.
ACCESSION AX152442
VERSION AX152442.1 GI:14534093
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 357 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 727 TGCCAGG 733
Db 9 TGCCAGG 3
RESULT 591
AX152463
LOCUS AX152463 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 378 from Patent WO0138577.
ACCESSION AX152463
VERSION AX152463.1 GI:14534114
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 378 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 739 CAGAACA 745
Db 2 CAGAACA 8
RESULT 592
AX152464
LOCUS AX152464 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 379 from Patent WO0138577.
ACCESSION AX152464
VERSION AX152464.1 GI:14534115
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.

TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 379 31-MAY-2001;
The Johns Hopkins University (US)
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source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 739 CAGAACA 745
Db 2 CAGAACA 8
RESULT 593
AX152485/c
LOCUS AX152485 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 400 from Patent WO0138577.
ACCESSION AX152485
VERSION AX152485.1 GI:14534136
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 400 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 727 TGCCAGG 733
Db 8 TGCCAGG 2
RESULT 594
AX152786/c
LOCUS AX152786 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 701 from Patent WO0138577.
ACCESSION AX152786
VERSION AX152786.1 GI:14534437
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 701 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
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source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 727 TGCCAGG 733
Db 8 TGCCAGG 2

FEATURES		The Johns Hopkins University (US)			
source		Location/Qualifiers			
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		/mol_type="unassigned DNA"			
		/db_xref="taxon:9606"			
Query Match		31.8%; Score 7; DB 1; Length 10;			
Best Local Similarity		100.0%; Pred. No. 2.9e+02;			
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy		733 GAGAAAC 739			
Db		1 GAGAAAC 7			
RESULT 600					
AX153258					
LOCUS		AX153258		10 bp DNA	
DEFINITION		Sequence 1173 from Patent WO0138577.		linear	
ACCESSION		AX153258		PAT 22-JUN-2001	
VERSION		AX153258.1			
KEYWORDS		GI:14534909			
SOURCE		Homo sapiens (human)			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS		Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.			
TITLE		Human transcriptomes			
JOURNAL		Patent: WO 0138577-A 1173 31-MAY-2001;			
FEATURES		The Johns Hopkins University (US)			
source		Location/Qualifiers			
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		/organism="Homo sapiens"			
		/mol_type="unassigned DNA"			
		/db_xref="taxon:9606"			
Query Match		31.8%; Score 7; DB 1; Length 10;			
Best Local Similarity		100.0%; Pred. No. 2.9e+02;			
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy		729 CCAGGAG 735			
Db		4 CCAGGAG 10			
RESULT 601					
AX153267					
LOCUS		AX153267		10 bp DNA	
DEFINITION		Sequence 1182 from Patent WO0138577.		linear	
ACCESSION		AX153267		PAT 22-JUN-2001	
VERSION		AX153267.1			
KEYWORDS		GI:14534918			
SOURCE		Homo sapiens (human)			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS		Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.			
TITLE		Human transcriptomes			
JOURNAL		Patent: WO 0138577-A 1182 31-MAY-2001;			
FEATURES		The Johns Hopkins University (US)			
source		Location/Qualifiers			
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		/organism="Homo sapiens"			
		/mol_type="unassigned DNA"			
		/db_xref="taxon:9606"			
Query Match		31.8%; Score 7; DB 1; Length 10;			
Best Local Similarity		100.0%; Pred. No. 2.9e+02;			
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy		728 GCCAGGA 734			
Db		4 GCCAGGA 10			
RESULT 604					
AX153505					
LOCUS		AX153505		10 bp DNA	
DEFINITION		Sequence 1420 from Patent WO0138577.		linear	
ACCESSION		AX153505		PAT 22-JUN-2001	
VERSION		AX153505.1			
KEYWORDS		GI:14535156			
SOURCE		Homo sapiens (human)			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS		Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.			
TITLE		Human transcriptomes			
JOURNAL		Patent: WO 0138577-A 1418 31-MAY-2001;			
FEATURES		The Johns Hopkins University (US)			
source		Location/Qualifiers			
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		/organism="Homo sapiens"			
		/mol_type="unassigned DNA"			
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Query Match		31.8%; Score 7; DB 1; Length 10;			
Best Local Similarity		100.0%; Pred. No. 2.9e+02;			
Matches		7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 1420 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES     Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match   31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGA 734
Db 4 GCCAGGA 10
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RESULT 605
LOCUS      AX153594
DEFINITION Sequence 1509 from Patent WO0138577.
ACCESSION AX153594
VERSION    AX153594.1 GI:14535245
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE       Human transcriptomes
JOURNAL     Patent: WO 0138577-A 1509 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES    Location/Qualifiers
              source
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                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match   31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACCA 745
Db 2 CAGAACCA 8
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RESULT 606
LOCUS      AX301719
DEFINITION Sequence 433 from Patent WO0185941.
ACCESSION AX301719
VERSION    AX301719.1 GI:17382802
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Versteeg,R. and Caron,H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 433 15-NOV-2001;
              Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES    Location/Qualifiers

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source
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  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match   31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACCA 745
Db 2 CAGAACCA 8
|||||

RESULT 607
LOCUS      AX391458
DEFINITION Sequence 21 from Patent EP1184456.
ACCESSION AX391458
VERSION    AX391458.1 GI:19700068
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS     Anastasio,A.E., Koshy,B., Finkel,K. and Lee,H.H.
TITLE       Haplotypes of the agtr1 gene
JOURNAL     Patent: EP 1184456-A 21 06-MAR-2002;
              Genaisance Pharmaceuticals, Inc. (US)
FEATURES    Location/Qualifiers
              source
                1..10
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match   31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAG 741
Db 3 GAAACAG 9
|||||

RESULT 608
LOCUS      AX573620/c
DEFINITION Sequence 30 from Patent WO02079467.
ACCESSION AX573620
VERSION    AX573620.1 GI:27551290
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE   1
AUTHORS     Nielsen,P.B. and Good,L.
TITLE       Antibiotic-free bacterial strain selection with antisense molecules
JOURNAL     Patent: WO 02079467-A 30 10-OCT-2002;
              Koebenhavns Univesitet (DK)
FEATURES    Location/Qualifiers
              source
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Peptide nucleic acid no. 1833"
              misc_feature
                10
                /note="A lysine residue is linked to COOH-terminal of the PNA"

Query Match   31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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Qy 735 GAAACAG 741
Db 10 GAAACAG 4
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RESULT 609
AX753457/c
LOCUS AX753457 10 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 2 from Patent EPI310556.
ACCESSION AX753457
VERSION AX753457.1 GI:32166217
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
AUTHORS Composition and methods for the identification of lung tumor cells
TITLE Patent: EP 1310556-A 2 14-MAY-2003;
JOURNAL GENZYME CORPORATION (US)
JOURNAL
FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 729 CCAGGAG 735
Db 7 CCAGGAG 1
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RESULT 610
BD007771
LOCUS BD007771 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007771
VERSION BD007771.1 GI:18636144
KEYWORDS JP 2001069993-A/47.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 47 21-MAR-2001;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2001069993-A/47
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/53//A61K45/00, PC
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PC A61P31/00,C12P21/08,C12N15/00
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 CAGGAGA 736
Db 7 CAGGAGA 1
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RESULT 612
BD007949
LOCUS BD007949 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007949
VERSION BD007949.1 GI:18636322
KEYWORDS JP 2001069993-A/225.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 225 21-MAR-2001;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2001069993-A/225
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 739 CAGGACA 745
Db 2 CAGGACA 8
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RESULT 611
BD007849/c
LOCUS BD007849 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007849
VERSION BD007849.1 GI:18636222
KEYWORDS JP 2001069993-A/125.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 125 21-MAR-2001;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2001069993-A/125
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/53//A61K45/00, PC
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FT source
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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A61P29/00,
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGA 734
DB 2 GCCAGGA 8

RESULT 613
LOCUS BD007979/c 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007979
VERSION BD007979.1 GI:18636352
KEYWORDS JP 2001069993-A/255.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
TITLE Patent: JP 2001069993-A 255 21-MAR-2001,
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/255
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
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FT source 1..10
/organism='Homo sapiens (human)'
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FEATURES
source
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 TGCCAGG 733
DB 9 TGCCAGG 3

RESULT 614
LOCUS BD008032 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD008032
VERSION BD008032.1 GI:18636405
KEYWORDS JP 2001069993-A/308.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 308 21-MAR-2001,
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/308
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
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FEATURES
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGACAA 745
DB 2 CAGACAA 8

RESULT 615
LOCUS BD065275/c 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065275
VERSION BD065275.1 GI:23610878
KEYWORDS JP 2001509017-A/211.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 10)
Velculescu,V.B., Vogelstein,B. and Kinzler,K.W.
Characterization of the yeast transcriptome
TITLE Patent: JP 2001509017-A 211 10-JUL-2001,
JOURNAL THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/211
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
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/organism='Saccharomyces cerevisiae (yeast)'
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source
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 729 CCAGGAG 735
Db 10 CCAGGAG 4

RESULT 616
BD083173 10 bp DNA linear PAT 27-AUG-2002
LOCUS Human matured/activated dendritic cell expression genes.
DEFINITION
ACCESSION BD083173
VERSION BD083173.1 GI:22628783
KEYWORDS JP 2001327293-A/94.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
COMMENT Human matured/activated dendritic cell expression genes
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/94
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 739 CAGAACA 745
Db 2 CAGAACA 8

RESULT 617
BD083179/c 10 bp DNA linear PAT 27-AUG-2002
LOCUS Human matured/activated dendritic cell expression genes.
DEFINITION
ACCESSION BD083179
VERSION BD083179.1 GI:22628789
KEYWORDS JP 2001327293-A/100.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
COMMENT Human matured/activated dendritic cell expression genes
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/100
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
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PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC

FEATURES
source
1..10
Location/Qualifiers.

Qy 727 TGCCAGG 733
Db 8 TGCCAGG 2

RESULT 618
BD083230/c 10 bp DNA linear PAT 27-AUG-2002
LOCUS Human matured/activated dendritic cell expression genes.
DEFINITION
ACCESSION BD083230
VERSION BD083230.1 GI:22628840
KEYWORDS JP 2001327293-A/151.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
COMMENT Human matured/activated dendritic cell expression genes
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/151
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
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FEATURES
source
1..10
Location/Qualifiers.

Qy 727 TGCCAGG 733
Db 8 TGCCAGG 2

RESULT 619
BD083361 10 bp DNA linear PAT 27-AUG-2002
LOCUS Human matured/activated dendritic cell expression genes.
DEFINITION
ACCESSION BD083361
VERSION BD083361.1 GI:22628971
KEYWORDS JP 2001327293-A/282.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
COMMENT Human matured/activated dendritic cell expression genes
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/282
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562

FEATURES
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Location/Qualifiers.

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PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
NAGAI
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        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 738 CAGAAGC 744
DB 3 CAGAAGC 9

RESULT 620
BD161207
LOCUS
    10 bp DNA linear PAT 17-JAN-2003
DEFINITION
    Human activated Th1 and Th2 cell expression genes.
ACCESSION
    BD161207
VERSION
    BD161207.1 GI:278666965
KEYWORDS
    JP 2002186482-A/29.
SOURCE
    Homo sapiens (human)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 10)
AUTHORS
    Nagai, S., Matsushima, K. and Hashimoto, S.
TITLE
    Human activated Th1 and Th2 cell expression genes
JOURNAL
    Patent: JP 2002186482-A 29 02-JUL-2002;
    JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT
    OS Homo sapiens (human)
    PN JP 2002186482-A/29
    PD 02-JUL-2002
    PF 19-DEC-2000 JP 2000385816
    PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
    C12N15/09, C07K14/47, C07K16/18, C12P21/08, C12N15/00 CC Human
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    Best Local Similarity
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    Matches
        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACA 745
DB 2 CAGAACA 8

RESULT 621
BD161244
LOCUS
    10 bp DNA linear PAT 17-JAN-2003
DEFINITION
    Human activated Th1 and Th2 cell expression genes.
ACCESSION
    BD161244
VERSION
    BD161244.1 GI:27867002
KEYWORDS
    JP 2002186482-A/66.
SOURCE
    Homo sapiens (human)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 10)

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AUTHORS
    Nagai, S., Matsushima, K. and Hashimoto, S.
TITLE
    Human activated Th1 and Th2 cell expression genes
JOURNAL
    Patent: JP 2002186482-A 66 02-JUL-2002;
    JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT
    OS Homo sapiens (human)
    PN JP 2002186482-A/66
    PD 02-JUL-2002
    PF 19-DEC-2000 JP 2000385816
    PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
    C12N15/09, C07K14/47, C07K16/18, C12P21/08, C12N15/00 CC Human
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QY 739 CAGAACA 745
DB 2 CAGAACA 8

RESULT 622
BD161338/c
LOCUS
    10 bp DNA linear PAT 17-JAN-2003
DEFINITION
    Human activated Th1 and Th2 cell expression genes.
ACCESSION
    BD161338
VERSION
    BD161338.1 GI:27867096
KEYWORDS
    JP 2002186482-A/160.
SOURCE
    Homo sapiens (human)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 10)
AUTHORS
    Nagai, S., Matsushima, K. and Hashimoto, S.
TITLE
    Human activated Th1 and Th2 cell expression genes
JOURNAL
    Patent: JP 2002186482-A 160 02-JUL-2002;
    JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT
    OS Homo sapiens (human)
    PN JP 2002186482-A/160
    PD 02-JUL-2002
    PF 19-DEC-2000 JP 2000385816
    PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
    C12N15/09, C07K14/47, C07K16/18, C12P21/08, C12N15/00 CC Human
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    Best Local Similarity
        100.0%; Pred. No. 2.9e+02;
    Matches
        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGA 734
DB 7 GCCAGGA 1

RESULT 623
BD161404/c
LOCUS
    10 bp DNA linear PAT 17-JAN-2003

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DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161404
VERSION BD161404.1 GI:27867162
KEYWORDS JP 2002186482-A/226
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 226 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/226
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
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/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGA 734
DB 9 GCCAGGA 3
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RESULT 624
BD161472
LOCUS Human activated Th1 and Th2 cell expression genes.
DEFINITION Human activated Th1 and Th2 cell expression genes
ACCESSION BD161472
VERSION BD161472.1 GI:27867230
KEYWORDS JP 2002186482-A/294
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 294 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/294
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
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DEFINITION Human liver disease-expressing genes
ACCESSION BD166678
VERSION BD166678.1 GI:27872490
KEYWORDS JP 2002209591-A/223
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 223 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/223
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
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QY 733 GAGAAAC 739
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RESULT 625
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LOCUS Human liver disease-expressing genes.
DEFINITION Human liver disease-expressing genes
ACCESSION BD166539
VERSION BD166539.1 GI:27872351
KEYWORDS JP 2002209591-A/84
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 84 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/84
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
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DB 9 CCAGGAG 3
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RESULT 626
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LOCUS Human liver disease-expressing genes.
DEFINITION Human liver disease-expressing genes
ACCESSION BD166678
VERSION BD166678.1 GI:27872490
KEYWORDS JP 2002209591-A/223
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 223 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/223
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
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DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167093.1 GI:27872905
VERSION     JP 2002209591-A/638.
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE     Human liver disease-expressing genes
JOURNAL   Patent: JP 2002209591-A 638 30-JUL-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002209591-A/638
          PD 30-JUL-2002
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          PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
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DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167149.1 GI:27872961
VERSION     JP 2002209591-A/694.
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE     Human liver disease-expressing genes
JOURNAL   Patent: JP 2002209591-A 694 30-JUL-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002209591-A/694
          PD 30-JUL-2002
          PF 19-JAN-2001 JP 2001012328
          PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
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Query Match 31.8%; Score 7; DB 1; Length 10;
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Db 10 AGAACAC 4
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RESULT 632
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DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167220.1 GI:27873032
VERSION     JP 2002209591-A/765.
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE     Human liver disease-expressing genes
JOURNAL   Patent: JP 2002209591-A 765 30-JUL-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002209591-A/765
          PD 30-JUL-2002
          PF 19-JAN-2001 JP 2001012328
          PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
          YAMASHITA
          PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
          PC C12P21/08,
          PC C12N15/00,
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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Qy 740 AGAACAC 746
Db 10 AGAACAC 4
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RESULT 633
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LOCUS      BD225309              10 bp    DNA        linear    PAT 17-JUL-2003
DEFINITION Methods for the diagnosis and treatment of lung cancer.
ACCESSION  BD225309.1 GI:33035079
VERSION     JP 2002509706-A/8.
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Jen,J., Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE     Methods for the diagnosis and treatment of lung cancer
JOURNAL   Patent: JP 2002509706-A 8 02-APR-2002;
          GENZYME CORP,JOHN HOPKINS UNIVERSITY

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COMMENT      OS      Artificial Sequence
PN          JP 2002509706-A/8
PD          02-APR-2002
PF          30-MAR-1999 JP 2000540746
PR          31-MAR-1998 US 60/080044
PI          JIN JEN GARY A BEAUDRY,STEPHEN L MADDEN,ARTHUR H BERTELSEN PC
C12N15/09,A61K45/00,A61K48/00,A61P35/00,C12Q1/68,G01N33/50, PC
G01N33/574,
PC          C12N15/00
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DB      7 CCAGGAG 1

RESULT 634
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DEFINITION      BD225320.1 GI:33035090
ACCESSION      BD225320
VERSION      BD225320.1 GI:33035090
KEYWORDS      JP 2002509707-A/2.
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE      Compositions and methods for the identification of lung tumor cells
JOURNAL      Patent: JP 2002509707-A 2 02-APR-2002;
            GENZYME CORP

COMMENT      OS      Artificial Sequence
PN          JP 2002509707-A/2
PD          02-APR-2002
PF          30-MAR-1999 JP 2000541180
PR          31-MAR-1998 US 60/080037
PI          GARY A BEAUDRY,STEPHEN L MADDEN,ARTHUR H BERTELSEN PC
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PC          C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
G01N33/566//
PC          A61K45/00,A61P35/00,C12N15/00,C12N5/00 CC
C12N15/09,A61K45/00,A61P35/00,C12N15/00,C12N5/00 CC
Compositions and methods for the identification of lung tumor
cells
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QY      729 CCAGGAG 735
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Job time : 3 secs

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C 259	9.4	42.7	13	1	ABC30258	Oligonucleotide SE
C 260	9.4	42.7	13	1	ABF96837	Oligonucleotide SE
261	9.4	42.7	13	1	ABC83625	Oligonucleotide SE
C 262	9.4	42.7	13	1	ABC37749	Oligonucleotide SE
C 263	9.4	42.7	13	1	ABF75624	Oligonucleotide SE
C 264	9.4	42.7	13	1	ABC82727	Oligonucleotide SE
C 265	9.4	42.7	13	1	ABC58200	Oligonucleotide SE
C 266	9.4	42.7	13	1	ABC37748	Oligonucleotide SE
C 267	9.4	42.7	13	1	ABF24394	Oligonucleotide SE
C 268	9.4	42.7	13	1	ABF30260	Oligonucleotide SE
C 269	9.4	42.7	13	1	ABC72270	Oligonucleotide SE
C 270	9.4	42.7	13	1	ABC51768	Oligonucleotide SE
C 271	9.4	42.7	13	1	ABC57782	Oligonucleotide SE
C 272	9.4	42.7	13	1	ABC58201	Oligonucleotide SE
273	9.4	42.7	13	1	ABC11964	Oligonucleotide SE
274	9.4	42.7	13	1	ABF24377	Oligonucleotide SE
275	9.4	42.7	13	1	ABF74449	Oligonucleotide SE
C 276	9.4	42.7	13	1	ABF75625	Oligonucleotide SE
C 277	9.4	42.7	13	1	ABF56387	Oligonucleotide SE
C 278	9.4	42.7	13	1	ABH15112	Oligonucleotide SE
C 279	9.4	42.7	13	1	ABF66157	Oligonucleotide SE
280	9.4	42.7	13	1	ABF66269	Oligonucleotide SE
C 281	9.4	42.7	13	1	ABC67296	Oligonucleotide SE
C 282	9.4	42.7	13	1	ABC50423	Oligonucleotide SE
C 283	9.4	42.7	13	1	ABC77826	Oligonucleotide SE
C 284	9.4	42.7	13	1	ABF24376	Oligonucleotide SE
C 285	9.4	42.7	13	1	ABF24395	Oligonucleotide SE
C 286	9.4	42.7	13	1	ABF80900	Oligonucleotide SE
C 287	9.4	42.7	13	1	ABC51769	Oligonucleotide SE
C 288	9.4	42.7	13	1	ABC57783	Oligonucleotide SE
C 289	9.4	42.7	13	1	ABC10581	Oligonucleotide SE
C 290	9.4	42.7	13	1	ABF96836	Oligonucleotide SE
C 291	9.4	42.7	13	1	ABH23091	Oligonucleotide SE
C 292	9.4	42.7	13	1	ABF75626	Oligonucleotide SE
C 293	9.4	42.7	13	1	ABC71282	Oligonucleotide SE
294	9.4	42.7	13	1	ABC51769	Oligonucleotide SE
C 295	9.4	42.7	13	1	ABC83627	Oligonucleotide SE
C 296	9.4	42.7	13	1	ABC66042	Oligonucleotide SE
C 297	9.4	42.7	13	1	ABF25407	Oligonucleotide SE
C 298	9.4	42.7	13	1	ABF74292	Oligonucleotide SE
C 299	9.4	42.7	13	1	ABF74448	Oligonucleotide SE
C 300	9.4	42.7	13	1	ABF66159	Oligonucleotide SE
C 301	9.4	42.7	13	1	ABF66268	Oligonucleotide SE
C 302	9.4	42.7	13	1	ABH50906	Oligonucleotide SE
C 303	9.4	42.7	13	1	ABC57781	Oligonucleotide SE
C 304	9.4	42.7	13	1	ABF66156	Oligonucleotide SE
C 305	9.4	42.7	13	1	ABC73158	Oligonucleotide SE
C 306	9.4	42.7	13	1	ABC66043	Oligonucleotide SE
C 307	9.4	42.7	13	1	ABF30261	Oligonucleotide SE
C 308	9.4	42.7	13	1	ABF80901	Oligonucleotide SE
C 309	9.4	42.7	13	1	ABF66158	Oligonucleotide SE
C 310	9.4	42.7	13	1	ABC67297	Oligonucleotide SE
C 311	9.4	42.7	13	1	ABC56821	Oligonucleotide SE
C 312	9.4	42.7	13	1	ABH19618	Oligonucleotide SE
C 313	9.4	42.7	13	1	ABF87397	Oligonucleotide SE
C 314	9.4	42.7	13	1	ABH54888	Oligonucleotide SE
C 315	9.4	42.7	13	1	ABC27521	Oligonucleotide SE
C 316	9.4	42.7	13	1	ABC11965	Oligonucleotide SE
C 317	9.4	42.7	13	1	ABH14817	Oligonucleotide SE
C 318	9.4	42.7	13	1	ABH14817	Oligonucleotide SE
C 319	9.4	42.7	13	1	ABC72271	Oligonucleotide SE
C 320	9.4	42.7	13	1	ABC72902	Oligonucleotide SE
C 321	9.4	42.7	13	1	ABC83626	Oligonucleotide SE
C 322	9.4	42.7	13	1	ABF56386	Oligonucleotide SE
C 323	9.4	42.7	13	1	ABF87396	Oligonucleotide SE
C 324	9.4	42.7	13	1	ABH50907	Oligonucleotide SE
325	9.4	42.7	13	1	ABC71283	Oligonucleotide SE

1	ABC72903	Oligonucleotide SE
1	ABC50422	Oligonucleotide SE
1	ABC6820	Oligonucleotide SE
1	ABC82728	Oligonucleotide SE
1	ABF30259	Oligonucleotide SE
1	ABH19619	Oligonucleotide SE
1	ABF50801	Oligonucleotide SE
1	ABH48837	Oligonucleotide SE
1	ABF75627	Oligonucleotide SE
1	ABF56510	Oligonucleotide SE
1	ABF72819	Oligonucleotide SE
1	AAT76263	Rod opsin hammerhe
1	AAT76249	Human IL6 receptor
1	AAX54053	Human IL-6 recepto
1	AAX54039	Human IL-6 recepto
1	AAX54623	Endothelial moocy
1	AAA33483	Low adenosine anti
1	AAA34070	Human adenosine re
1	AAA33497	Low adenosine anti
1	AAF20192	Human endothelial
1	AAF19619	Human IL6 receptor
1	AAF19605	Human IL6 receptor
1	AA655226	Modified end-block
1	AA57799	Anisense oligonuc
1	AAAL37793	RNA region of modi
1	ABQ75477	Influenza C virus
1	ABK15512	Influenza C, 3, co
1	ABZ95399	Human IL-6 recepto
1	ABZ95886	Human monocyte act
1	ABZ95313	Human IL-6 recepto
1	ACF63279	Human phosphodiect
1	AQ78386	Anisense oligonuc
1	AAA19155	Human TIE-2 target
1	AA55188	Multiple antisense
1	AA34635	Human adenosine re
1	AAZ20757	Human multiple tar
1	AAZ21460	Human multiple tar
1	ABZ97154	Human MTA oligonuc
1	AAZ96451	Human nucleic acid
1	AAZ79493	Human dendritic ce
1	AAZ79359	Human dendritic ce
1	AA286656	Metastatic breast
1	AAH20544	Human MTR1 intron9
1	AAF70411	Human DRD2 polymor
1	AAF42486	Yeast NCRF Gene SA
1	AA519577	Primer-extension o
1	AA598810	Colony stimulating
1	ABL99040	Mouse neuronal reg
1	ABK96032	Human LIPE gene po
1	ABK81376	Human FOS gene all
1	ABV78423	Human Th1 cell pre
1	AB199152	Human PCDH2 ASO PC
1	AAAL39543	CCBP2 detecting AS
1	AA54592	Prostaglandin D sy
1	AAA34039	Human adenosine re
1	AAF20161	Human prostaglandi
1	AB086412	Human skin stress/
1	ABV71807	Human skin EST 959
1	ABV62393	Human skin EST 179
1	ABV69814	Human skin EST 760
1	ABV65662	Human skin EST 344
1	ABV64386	Human skin EST 217
1	ABV64098	Human skin EST 188
1	ABV71519	Human skin EST 930
1	ABV67302	Human skin EST 508
1	ABA89897	ESR-alpha gene Liv
1	ABA89949	ESR-alpha gene Cor
1	ABZ95855	Human prostaglandi
1	AAA93388	DNA encoding proca
1	AA93381	DNA encoding proca
1	AA27581	DNA encoding proca
1	AAA27588	DNA encoding proca
1	ABS71506	DNA encoding prote

399	9	40.9	12	1	ABS71499	DNA encoding prote	C 472	8.8	40.0	12	1	ABI233606	Oligonucleotide pr
C 400	9	40.9	12	1	PAL46301	Human M33 protein	C 473	8.8	40.0	12	1	ABI30553	Oligonucleotide pr
C 401	9	40.9	12	1	ADC19373	Protease recogniti	474	8.8	40.0	12	1	ABI46968	Oligonucleotide pr
C 402	9	40.9	12	1	ADC18387	Protease recogniti	475	8.8	40.0	12	1	ABI67539	Oligonucleotide pr
C 403	9	40.9	13	1	ABF34134	Oligonucleotide SE	476	8.8	40.0	12	1	ABI65215	Oligonucleotide pr
C 404	9	40.9	13	1	ABF34135	Oligonucleotide SE	477	8.8	40.0	12	1	ABI23702	Oligonucleotide pr
C 405	9	40.9	13	1	ABF24040	Oligonucleotide SE	C 478	8.8	40.0	12	1	ABI47510	Oligonucleotide pr
C 406	9	40.9	13	1	ABC80017	Oligonucleotide SE	C 479	8.8	40.0	12	1	ABI26708	Oligonucleotide pr
C 407	9	40.9	13	1	ABF24041	Oligonucleotide SE	C 480	8.8	40.0	12	1	ABH1408	Oligonucleotide pr
C 408	9	40.9	13	1	ABC80016	Oligonucleotide SE	C 481	8.8	40.0	12	1	ABH1826	Oligonucleotide pr
C 409	9	40.9	13	1	ABF81152	Oligonucleotide SE	482	8.8	40.0	12	1	ABI08687	Oligonucleotide pr
C 410	9	40.9	13	1	ABF81154	Oligonucleotide SE	483	8.8	40.0	12	1	ABI15833	Oligonucleotide pr
C 411	9	40.9	13	1	ABF81155	Oligonucleotide SE	C 484	8.8	40.0	12	1	AA520481	Oligonucleotide us
C 412	9	40.9	13	1	ABH65494	Oligonucleotide SE	C 485	8.8	40.0	12	1	ADD71434	Stimulus-responsiv
C 413	9	40.9	13	1	ABC62666	Oligonucleotide SE	486	8.8	40.0	12	1	ABE14282	Optineurin promote
C 414	9	40.9	13	1	ABF34137	Oligonucleotide SE	487	8.8	40.0	13	1	AA79398	HLA-DR typing prob
C 415	9	40.9	13	1	ABF81153	Oligonucleotide SE	488	8.8	40.0	13	1	AAV06763	Target oligonucleo
C 416	9	40.9	13	1	ABC62667	Oligonucleotide SE	C 489	8.8	40.0	13	1	AAV42361	Transition point o
C 417	9	40.9	13	1	ABH65495	Oligonucleotide SE	490	8.8	40.0	13	1	AAV16594	Probe H30 used to
C 418	9	40.9	13	1	ABF34136	Oligonucleotide SE	C 491	8.8	40.0	13	1	AAV81348	Mouse agouti wild
C 419	8.8	40.0	12	1	AAA05941	Human XIAP IRES po	C 492	8.8	40.0	13	1	AA556464	Locked nucleoside
C 420	8.8	40.0	12	1	AAA05942	Human XIAP IRES w	C 493	8.8	40.0	13	1	AA556496	Locked nucleoside
C 421	8.8	40.0	12	1	AA05946	Human XIAP IRES w	C 494	8.8	40.0	13	1	AAA62335	Mouse wild-type ag
C 422	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 495	8.8	40.0	13	1	ABC76054	Oligonucleotide SE
C 423	8.8	40.0	12	1	ABH75799	Oligonucleotide pr	C 496	8.8	40.0	13	1	ABC09298	Oligonucleotide SE
C 424	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 497	8.8	40.0	13	1	ABC09299	Oligonucleotide SE
C 425	8.8	40.0	12	1	ABH75799	Oligonucleotide pr	C 498	8.8	40.0	13	1	ABC64866	Oligonucleotide SE
C 426	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 499	8.8	40.0	13	1	ABF24769	Oligonucleotide SE
C 427	8.8	40.0	12	1	ABH75799	Oligonucleotide pr	500	8.8	40.0	13	1	ABF43128	Oligonucleotide SE
C 428	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	501	8.8	40.0	13	1	ABF43129	Oligonucleotide SE
C 429	8.8	40.0	12	1	ABH75799	Oligonucleotide pr	502	8.8	40.0	13	1	ABH02517	Oligonucleotide SE
C 430	8.8	40.0	12	1	ABH68614	Oligonucleotide pr	C 503	8.8	40.0	13	1	ABC48561	Oligonucleotide SE
C 431	8.8	40.0	12	1	ABH89478	Oligonucleotide pr	C 504	8.8	40.0	13	1	ABC24672	Oligonucleotide SE
C 432	8.8	40.0	12	1	ABH66990	Oligonucleotide pr	C 505	8.8	40.0	13	1	ABC76052	Oligonucleotide SE
C 433	8.8	40.0	12	1	ABH67357	Oligonucleotide pr	C 506	8.8	40.0	13	1	ABF07388	Oligonucleotide SE
C 434	8.8	40.0	12	1	ABH74521	Oligonucleotide pr	507	8.8	40.0	13	1	ABF07389	Oligonucleotide SE
C 435	8.8	40.0	12	1	ABH75098	Oligonucleotide pr	508	8.8	40.0	13	1	ABC82381	Oligonucleotide SE
C 436	8.8	40.0	12	1	ABH88943	Oligonucleotide pr	C 509	8.8	40.0	13	1	ABC37925	Oligonucleotide SE
C 437	8.8	40.0	12	1	ABH67468	Oligonucleotide pr	510	8.8	40.0	13	1	ABC64865	Oligonucleotide SE
C 438	8.8	40.0	12	1	ABH75557	Oligonucleotide pr	511	8.8	40.0	13	1	ABF23389	Oligonucleotide SE
C 439	8.8	40.0	12	1	ABH80821	Oligonucleotide pr	C 512	8.8	40.0	13	1	ABH19990	Oligonucleotide SE
C 440	8.8	40.0	12	1	ABH22903	Oligonucleotide pr	C 513	8.8	40.0	13	1	ABF48664	Oligonucleotide SE
C 441	8.8	40.0	12	1	ABH76378	Oligonucleotide pr	514	8.8	40.0	13	1	ABF73772	Oligonucleotide SE
C 442	8.8	40.0	12	1	ABH70170	Oligonucleotide pr	515	8.8	40.0	13	1	ABF82673	Oligonucleotide SE
C 443	8.8	40.0	12	1	ABH73681	Oligonucleotide pr	516	8.8	40.0	13	1	ABH40261	Oligonucleotide SE
C 444	8.8	40.0	12	1	ABH04383	Oligonucleotide pr	517	8.8	40.0	13	1	ABH41118	Oligonucleotide SE
C 445	8.8	40.0	12	1	ABH79549	Oligonucleotide pr	518	8.8	40.0	13	1	ABC24673	Oligonucleotide SE
C 446	8.8	40.0	12	1	ABH07767	Oligonucleotide pr	C 519	8.8	40.0	13	1	ABC29854	Oligonucleotide SE
C 447	8.8	40.0	12	1	ABH33484	Oligonucleotide pr	C 520	8.8	40.0	13	1	ABF23388	Oligonucleotide SE
C 448	8.8	40.0	12	1	ABH53341	Oligonucleotide pr	C 521	8.8	40.0	13	1	ABH29482	Oligonucleotide SE
C 449	8.8	40.0	12	1	ABH17388	Oligonucleotide pr	522	8.8	40.0	13	1	ABH29485	Oligonucleotide SE
C 450	8.8	40.0	12	1	ABH05666	Oligonucleotide pr	C 523	8.8	40.0	13	1	ABF59006	Oligonucleotide SE
C 451	8.8	40.0	12	1	ABH84329	Oligonucleotide pr	C 524	8.8	40.0	13	1	ABH40262	Oligonucleotide SE
C 452	8.8	40.0	12	1	ABH16214	Oligonucleotide pr	525	8.8	40.0	13	1	ABC48960	Oligonucleotide SE
C 453	8.8	40.0	12	1	ABH17624	Oligonucleotide pr	526	8.8	40.0	13	1	ABC32957	Oligonucleotide SE
C 454	8.8	40.0	12	1	ABH70326	Oligonucleotide pr	527	8.8	40.0	13	1	ABC79524	Oligonucleotide SE
C 455	8.8	40.0	12	1	ABH11213	Oligonucleotide pr	528	8.8	40.0	13	1	ABF27769	Oligonucleotide SE
C 456	8.8	40.0	12	1	ABH12547	Oligonucleotide pr	529	8.8	40.0	13	1	ABF39592	Oligonucleotide SE
C 457	8.8	40.0	12	1	ABH25965	Oligonucleotide pr	C 530	8.8	40.0	13	1	ABH25372	Oligonucleotide SE
C 458	8.8	40.0	12	1	ABH48399	Oligonucleotide pr	531	8.8	40.0	13	1	ABH02516	Oligonucleotide SE
C 459	8.8	40.0	12	1	ABH30861	Oligonucleotide pr	C 532	8.8	40.0	13	1	ABF82574	Oligonucleotide SE
C 460	8.8	40.0	12	1	ABH86305	Oligonucleotide pr	533	8.8	40.0	13	1	ABH34757	Oligonucleotide SE
C 461	8.8	40.0	12	1	ABH72010	Oligonucleotide pr	C 534	8.8	40.0	13	1	ABH42798	Oligonucleotide SE
C 462	8.8	40.0	12	1	ABH65974	Oligonucleotide pr	C 535	8.8	40.0	13	1	ABH43252	Oligonucleotide SE
C 463	8.8	40.0	12	1	ABH97184	Oligonucleotide pr	536	8.8	40.0	13	1	ABH53941	Oligonucleotide SE
C 464	8.8	40.0	12	1	ABH98666	Oligonucleotide pr	537	8.8	40.0	13	1	ABH54081	Oligonucleotide SE
C 465	8.8	40.0	12	1	ABH08983	Oligonucleotide pr	538	8.8	40.0	13	1	ABC94297	Oligonucleotide SE
C 466	8.8	40.0	12	1	ABH47139	Oligonucleotide pr	539	8.8	40.0	13	1	ABC23145	Oligonucleotide SE
C 467	8.8	40.0	12	1	ABH58619	Oligonucleotide pr	C 540	8.8	40.0	13	1	ABC61654	Oligonucleotide SE
C 468	8.8	40.0	12	1	ABH70467	Oligonucleotide pr	541	8.8	40.0	13	1	ABC82380	Oligonucleotide SE
C 469	8.8	40.0	12	1	ABH71132	Oligonucleotide pr	C 542	8.8	40.0	13	1	ABF30658	Oligonucleotide SE
C 470	8.8	40.0	12	1	ABH44609	Oligonucleotide pr	543	8.8	40.0	13	1	ABH19407	Oligonucleotide SE
C 471	8.8	40.0	12	1	ABH77488	Oligonucleotide pr	544	8.8	40.0	13	1	ABH02515	Oligonucleotide SE

545	8.8	40.0	13	1	ABH42937	Oligonucleotide SE
546	8.8	40.0	13	1	ABH42938	Oligonucleotide SE
547	8.8	40.0	13	1	ABH48474	Oligonucleotide SE
548	8.8	40.0	13	1	ABC32956	Oligonucleotide SE
549	8.8	40.0	13	1	ABC87410	Oligonucleotide SE
550	8.8	40.0	13	1	ABH42939	Oligonucleotide SE
551	8.8	40.0	13	1	ABH48475	Oligonucleotide SE
552	8.8	40.0	13	1	ABH54080	Oligonucleotide SE
553	8.8	40.0	13	1	ABC01518	Oligonucleotide SE
554	8.8	40.0	13	1	ABC01519	Oligonucleotide SE
555	8.8	40.0	13	1	ABC29855	Oligonucleotide SE
556	8.8	40.0	13	1	ABC07303	Oligonucleotide SE
557	8.8	40.0	13	1	ABC09300	Oligonucleotide SE
558	8.8	40.0	13	1	ABC87411	Oligonucleotide SE
559	8.8	40.0	13	1	ABH24319	Oligonucleotide SE
560	8.8	40.0	13	1	ABF49924	Oligonucleotide SE
561	8.8	40.0	13	1	ABF56045	Oligonucleotide SE
562	8.8	40.0	13	1	ABH33790	Oligonucleotide SE
563	8.8	40.0	13	1	ABH34756	Oligonucleotide SE
564	8.8	40.0	13	1	ABC94294	Oligonucleotide SE
565	8.8	40.0	13	1	ABC06155	Oligonucleotide SE
566	8.8	40.0	13	1	ABC37605	Oligonucleotide SE
567	8.8	40.0	13	1	ABF24592	Oligonucleotide SE
568	8.8	40.0	13	1	ABF41880	Oligonucleotide SE
569	8.8	40.0	13	1	ABF41881	Oligonucleotide SE
570	8.8	40.0	13	1	ABC27868	Oligonucleotide SE
571	8.8	40.0	13	1	ABC32873	Oligonucleotide SE
572	8.8	40.0	13	1	ABC09301	Oligonucleotide SE
573	8.8	40.0	13	1	ABC59860	Oligonucleotide SE
574	8.8	40.0	13	1	ABF27768	Oligonucleotide SE
575	8.8	40.0	13	1	ABF48665	Oligonucleotide SE
576	8.8	40.0	13	1	ABH40263	Oligonucleotide SE
577	8.8	40.0	13	1	ABH41119	Oligonucleotide SE
578	8.8	40.0	13	1	ABC67855	Oligonucleotide SE
579	8.8	40.0	13	1	ABC94296	Oligonucleotide SE
580	8.8	40.0	13	1	ABC69697	Oligonucleotide SE
581	8.8	40.0	13	1	ABC76055	Oligonucleotide SE
582	8.8	40.0	13	1	ABC55567	Oligonucleotide SE
583	8.8	40.0	13	1	ABC07302	Oligonucleotide SE
584	8.8	40.0	13	1	ABC88808	Oligonucleotide SE
585	8.8	40.0	13	1	ABF24593	Oligonucleotide SE
586	8.8	40.0	13	1	ABF73773	Oligonucleotide SE
587	8.8	40.0	13	1	ABH25373	Oligonucleotide SE
588	8.8	40.0	13	1	ABF56044	Oligonucleotide SE
589	8.8	40.0	13	1	ABH10380	Oligonucleotide SE
590	8.8	40.0	13	1	ABH36000	Oligonucleotide SE
591	8.8	40.0	13	1	ABH40318	Oligonucleotide SE
592	8.8	40.0	13	1	ABH40319	Oligonucleotide SE
593	8.8	40.0	13	1	ABH42948	Oligonucleotide SE
594	8.8	40.0	13	1	ABC39716	Oligonucleotide SE
595	8.8	40.0	13	1	ABC64867	Oligonucleotide SE
596	8.8	40.0	13	1	ABH29484	Oligonucleotide SE
597	8.8	40.0	13	1	ABH82672	Oligonucleotide SE
598	8.8	40.0	13	1	ABH40318	Oligonucleotide SE
599	8.8	40.0	13	1	ABH40319	Oligonucleotide SE
600	8.8	40.0	13	1	ABH45233	Oligonucleotide SE
601	8.8	40.0	13	1	ABH53840	Oligonucleotide SE
602	8.8	40.0	13	1	ABC67854	Oligonucleotide SE
603	8.8	40.0	13	1	ABH19405	Oligonucleotide SE
604	8.8	40.0	13	1	ABH42979	Oligonucleotide SE
605	8.8	40.0	13	1	ABH42949	Oligonucleotide SE
606	8.8	40.0	13	1	ABC76053	Oligonucleotide SE
607	8.8	40.0	13	1	ABC59861	Oligonucleotide SE
608	8.8	40.0	13	1	ABC39717	Oligonucleotide SE
609	8.8	40.0	13	1	ABF24768	Oligonucleotide SE
610	8.8	40.0	13	1	ABH19991	Oligonucleotide SE
611	8.8	40.0	13	1	ABF49925	Oligonucleotide SE
612	8.8	40.0	13	1	ABH29483	Oligonucleotide SE
613	8.8	40.0	13	1	ABF59007	Oligonucleotide SE
614	8.8	40.0	13	1	ABH36001	Oligonucleotide SE
615	8.8	40.0	13	1	ABC69696	Oligonucleotide SE
616	8.8	40.0	13	1	ABC55566	Oligonucleotide SE
617	8.8	40.0	13	1	ABC31753	Oligonucleotide SE
1	ABH02514	13	1	ABH02514	Oligonucleotide SE	
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837	8	36.4	10	1	AAO96884	HIV-1 NL4-3 nef ge	C 910	8	36.4	11	1	ABV71634	Human skin EST 942
838	8	36.4	10	1	AAO96883	HIV-1 NL4-3 nef ge	C 911	8	36.4	11	1	ABV64213	Human skin EST 199
839	8	36.4	10	1	AAZ78109	Human dendritic ce	C 912	8	36.4	11	1	ABV64254	Human skin EST 204
840	8	36.4	10	1	AAZ80857	Metastatic breast	C 913	8	36.4	11	1	ABV65655	Human skin EST 344
841	8	36.4	10	1	AAZ82836	Metastatic breast	C 914	8	36.4	11	1	ABL91967	Human Pan-Endothel
842	8	36.4	10	1	AAZ83679	Metastatic breast	C 915	8	36.4	11	1	ABQ81877	Kaposi's Sarcoma s
843	8	36.4	10	1	AAZ81170	Metastatic breast	C 916	8	36.4	11	1	ABQ71892	DNA tag used to id
844	8	36.4	10	1	AAZ86201	Metastatic breast	C 917	8	36.4	12	1	AAZ34991	Antisense oligonuc
845	8	36.4	10	1	AAZ81797	Metastatic breast	C 918	8	36.4	12	1	AAZ34986	Antisense oligonuc
846	8	36.4	10	1	AAZ83594	Metastatic breast	C 919	8	36.4	12	1	AAZ14823	Triple helix third
847	8	36.4	10	1	AAZ82358	Metastatic breast	C 920	8	36.4	12	1	ABH74751	Oligonucleotide pr
848	8	36.4	10	1	AAZ83845	Metastatic breast	C 921	8	36.4	12	1	ABH73910	Oligonucleotide pr
849	8	36.4	10	1	AAZ81230	Metastatic breast	C 922	8	36.4	12	1	ABH45370	Oligonucleotide pr
850	8	36.4	10	1	AAZ85663	Metastatic breast	C 923	8	36.4	12	1	ABH68872	Oligonucleotide pr
851	8	36.4	10	1	AAH63186	Human colon epithe	C 924	8	36.4	12	1	ABH55796	Oligonucleotide pr
852	8	36.4	10	1	AAH63245	Human colon epithe	C 925	8	36.4	12	1	ABH73752	Oligonucleotide pr
853	8	36.4	10	1	AAH63239	Human colon epithe	C 926	8	36.4	12	1	ABH79664	Oligonucleotide pr
854	8	36.4	10	1	AAH64481	Human colon epithe	C 927	8	36.4	12	1	ABH05358	Oligonucleotide pr
855	8	36.4	10	1	AAH63237	Human colon epithe	C 928	8	36.4	12	1	ABH85801	Oligonucleotide pr
856	8	36.4	10	1	AAF37890	Yeast NORF gene SA	C 929	8	36.4	12	1	ABH85921	Oligonucleotide pr
857	8	36.4	10	1	AAF35950	Yeast NORF gene SA	C 930	8	36.4	12	1	ABH19120	Oligonucleotide pr
858	8	36.4	10	1	AAF41069	Yeast NORF gene SA	C 931	8	36.4	12	1	ABH19497	Oligonucleotide pr
859	8	36.4	10	1	AAF38498	Yeast NORF gene SA	C 932	8	36.4	12	1	ABH76928	Oligonucleotide pr
860	8	36.4	10	1	AAF38885	Yeast NORF gene SA	C 933	8	36.4	12	1	ABH64170	Oligonucleotide pr
861	8	36.4	10	1	AAF33978	Yeast NORF gene SA	C 934	8	36.4	12	1	ABH00251	Oligonucleotide pr
862	8	36.4	10	1	AAF35089	Yeast NORF gene SA	C 935	8	36.4	12	1	ABH81115	Oligonucleotide pr
863	8	36.4	10	1	ABK24254	Retinaldehyde-bind	C 936	8	36.4	12	1	ABH38150	Oligonucleotide pr
864	8	36.4	10	1	ABK69700	Human SCV2A gene a	C 937	8	36.4	12	1	ABH56943	Oligonucleotide pr
865	8	36.4	10	1	ABL42788	Human maturation/a	C 938	8	36.4	12	1	ABH05035	Oligonucleotide pr
866	8	36.4	10	1	ABL48074	Human CSF3 gene al	C 939	8	36.4	12	1	ABH93562	Oligonucleotide pr
867	8	36.4	10	1	ABV93817	Human PRKFB2 PCR P	C 940	8	36.4	12	1	ABH80366	Oligonucleotide pr
868	8	36.4	10	1	ABV78493	Human COP9 SAGE ta	C 941	8	36.4	12	1	ABH34495	Oligonucleotide pr
869	8	36.4	10	1	ABK23469	Transcript tag DNA	C 942	8	36.4	12	1	ABH05034	Oligonucleotide pr
870	8	36.4	10	1	ABK96609	Human interleukin	C 943	8	36.4	12	1	ABH71127	Oligonucleotide pr
871	8	36.4	10	1	ABK96611	Human interleukin	C 944	8	36.4	12	1	ABH95691	Oligonucleotide pr
872	8	36.4	10	1	AAH19962	Primer-extension o	C 945	8	36.4	12	1	ABH63697	Oligonucleotide pr
873	8	36.4	10	1	AAH43004	Human cerberus 1 (C 946	8	36.4	12	1	ABH04086	Oligonucleotide pr
874	8	36.4	10	1	ABL45804	Human MMP13 gene a	C 947	8	36.4	12	1	ABH76407	Oligonucleotide pr
875	8	36.4	10	1	ABN81268	Oligonucleotide pr	C 948	8	36.4	12	1	ABH49832	Oligonucleotide pr
876	8	36.4	10	1	ACC78771	Normal estrogen re	C 949	8	36.4	12	1	ABH96106	Oligonucleotide pr
877	8	36.4	10	1	AAD58112	Leader DNA #2 used	C 950	8	36.4	12	1	ABH01362	Oligonucleotide pr
878	8	36.4	10	1	ADD71433	Stimulus-responsiv	C 951	8	36.4	12	1	ABH80835	Oligonucleotide pr
879	8	36.4	11	1	AAF82244	DNA sequence that	C 952	8	36.4	12	1	ADH52664	Human ALT2 gene in
880	8	36.4	11	1	ABA01034	Mutational DNA exo	C 953	8	36.4	12	1	ADH52660	Human ALT2 gene in
881	8	36.4	11	1	AAO57524	Polypyrimidine-ric	C 954	8	36.4	12	1	ACD40404	Human APL1 CDNA f
882	8	36.4	11	1	AAO57526	Polypyrimidine-ric	C 955	7.8	35.5	11	1	AAZ18763	Murine C57BL/6 SAG
883	8	36.4	11	1	AAI64929	Human Cream1 prote	C 956	7.8	35.5	11	1	AAZ54601	Eosinophil derived
884	8	36.4	11	1	ABQ87632	Human skin stress/	C 957	7.8	35.5	11	1	AAZ14702	Triple helix formi
885	8	36.4	11	1	ABQ86959	Human skin stress/	C 958	7.8	35.5	11	1	AAA34048	Human adenosine re
886	8	36.4	11	1	ABQ86697	Human skin stress/	C 959	7.8	35.5	11	1	AAZ20170	Human eosinophil d
887	8	36.4	11	1	ABV68978	Human skin EST 476	C 960	7.8	35.5	11	1	AAZ70541	Rice alpha-amylase
888	8	36.4	11	1	ABV70231	Human skin EST 801	C 961	7.8	35.5	11	1	ABQ87289	Human skin stress/
889	8	36.4	11	1	ABV71675	Human skin EST 946	C 962	7.8	35.5	11	1	ABQ86542	Human skin stress/
890	8	36.4	11	1	ABV67502	Human skin EST 528	C 963	7.8	35.5	11	1	ABV63070	Human skin EST 856
891	8	36.4	11	1	ABV67881	Human skin EST 566	C 964	7.8	35.5	11	1	ABV64588	Human skin EST 237
892	8	36.4	11	1	ABV71609	Human skin EST 939	C 965	7.8	35.5	11	1	ABV67546	Human skin EST 533
893	8	36.4	11	1	ABV64703	Human skin EST 248	C 966	7.8	35.5	11	1	ABV67900	Human skin EST 568
894	8	36.4	11	1	ABV65140	Human skin EST 292	C 967	7.8	35.5	11	1	ABV70317	Human skin EST 870
895	8	36.4	11	1	ABV62451	Human skin EST 237	C 968	7.8	35.5	11	1	ABV65569	Human skin EST 335
896	8	36.4	11	1	ABV64507	Human skin EST 229	C 969	7.8	35.5	11	1	ABV68950	Human skin EST 673
897	8	36.4	11	1	ABV62810	Human skin EST 596	C 970	7.8	35.5	11	1	ABV65783	Human skin EST 356
898	8	36.4	11	1	ABV65528	Human skin EST 331	C 971	7.8	35.5	11	1	ABV69415	Human skin EST 720
899	8	36.4	11	1	ABV68871	Human skin EST 665	C 972	7.8	35.5	11	1	ABV63496	Human skin EST 128
900	8	36.4	11	1	ABV69872	Human skin EST 765	C 973	7.8	35.5	11	1	ABV69104	Human skin EST 699
901	8	36.4	11	1	ABV66245	Human skin EST 403	C 974	7.8	35.5	11	1	ABV63121	Human skin EST 907
902	8	36.4	11	1	ABV64188	Human skin EST 197	C 975	7.8	35.5	11	1	ABV64498	Human skin EST 228
903	8	36.4	11	1	ABV69727	Human skin EST 751	C 976	7.8	35.5	11	1	ABV70542	Human skin EST 832
904	8	36.4	11	1	ABV66934	Human skin EST 472	C 977	7.8	35.5	11	1	ABV63621	Human skin EST 140
905	8	36.4	11	1	ABV71928	Human skin EST 971	C 978	7.8	35.5	11	1	ABV67609	Human skin EST 639
906	8	36.4	11	1	ABV62306	Human skin EST 92	C 979	7.8	35.5	11	1	ABV68198	Human skin EST 598
907	8	36.4	11	1	ABV67368	Human skin EST 515	C 980	7.8	35.5	11	1	ABV72009	Human skin EST 979
908	8	36.4	11	1	ABV68010	Human skin EST 579	C 981	7.8	35.5	11	1	ABV66736	Human skin EST 452
909	8	36.4	11	1	ABV68605	Human skin EST 639	C 982	7.8	35.5	11	1	ABV69413	Human skin EST 719

983	7.8	35.5	11	1	ABV70065	Human skin EST 785	1056	7.8	35.5	12	1	AB112030	Oligonucleotide pr
984	7.8	35.5	11	1	ABV71919	Human skin EST 970	c1057	7.8	35.5	12	1	AB145744	Oligonucleotide pr
985	7.8	35.5	11	1	ABV62644	Human skin EST 430	1058	7.8	35.5	12	1	AB156179	Oligonucleotide pr
c 986	7.8	35.5	11	1	ABV61108	Human skin EST 389	c1059	7.8	35.5	12	1	AB171623	Oligonucleotide pr
987	7.8	35.5	11	1	ABV65524	Human skin EST 431	1060	7.8	35.5	12	1	AB160839	Oligonucleotide pr
c 988	7.8	35.5	11	1	ABV69076	Human skin EST 686	c1061	7.8	35.5	12	1	AB118875	Oligonucleotide pr
989	7.8	35.5	11	1	ABV68102	Human skin EST 686	1062	7.8	35.5	12	1	ABH69811	Oligonucleotide pr
990	7.8	35.5	11	1	ABV68680	Human skin EST 646	c1063	7.8	35.5	12	1	ABH69375	Oligonucleotide pr
991	7.8	35.5	11	1	ABV69886	Human skin EST 767	1064	7.8	35.5	12	1	ABH71578	Oligonucleotide pr
992	7.8	35.5	11	1	ABV62465	Human skin EST 251	c1065	7.8	35.5	12	1	ABH98926	Oligonucleotide pr
c 993	7.8	35.5	11	1	ABV65390	Human skin EST 317	c1066	7.8	35.5	12	1	ABH75639	Oligonucleotide pr
994	7.8	35.5	11	1	ABV70491	Human skin EST 827	1067	7.8	35.5	12	1	ABH75709	Oligonucleotide pr
995	7.8	35.5	11	1	ABV71042	Human skin EST 882	c1068	7.8	35.5	12	1	ABH77101	Oligonucleotide pr
996	7.8	35.5	11	1	AB191951	Human Pan-Endothel	1069	7.8	35.5	12	1	ABH77342	Oligonucleotide pr
c 997	7.8	35.5	11	1	AB295864	Human eosinophil d	1070	7.8	35.5	12	1	ABH78437	Oligonucleotide pr
998	7.8	35.5	11	1	ABX71876	DNA tag used to id	c1071	7.8	35.5	12	1	AB129767	Oligonucleotide pr
999	7.8	35.5	11	1	ACA61506	Modified promoter	1072	7.8	35.5	12	1	AB131517	Oligonucleotide pr
1000	7.8	35.5	11	1	ACA61501	Modified promoter	c1073	7.8	35.5	12	1	ABH81430	Oligonucleotide pr
1001	7.8	35.5	12	1	AAQ30191	Sequence of probe/	c1074	7.8	35.5	12	1	ABH84641	Oligonucleotide pr
c1002	7.8	35.5	12	1	AAQ88668	Human mitochondria	c1075	7.8	35.5	12	1	AB110189	Oligonucleotide pr
1003	7.8	35.5	12	1	AAT11908	Antisense DNA to i	1076	7.8	35.5	12	1	AB111030	Oligonucleotide pr
1004	7.8	35.5	12	1	AAV05933	Translation rate c	c1077	7.8	35.5	12	1	ABH86856	Oligonucleotide pr
c1005	7.8	35.5	12	1	AAT63016	TNF-alpha mRNA ser	c1078	7.8	35.5	12	1	ABH86857	Oligonucleotide pr
1006	7.8	35.5	12	1	AAV53018	CCR-5 gene targeti	c1079	7.8	35.5	12	1	AB139657	Oligonucleotide pr
1007	7.8	35.5	12	1	AAV16650	Probe H30 used to	1080	7.8	35.5	12	1	ABH91152	Oligonucleotide pr
1008	7.8	35.5	12	1	AAQ08771	Antioxidant respon	c1081	7.8	35.5	12	1	AB141426	Oligonucleotide pr
1009	7.8	35.5	12	1	AAQ14842	Triple helix formi	c1082	7.8	35.5	12	1	AB116969	Oligonucleotide pr
1010	7.8	35.5	12	1	AAQ14964	Triple helix formi	c1083	7.8	35.5	12	1	ABH67263	Oligonucleotide pr
1011	7.8	35.5	12	1	AAQ14828	Triple helix formi	1084	7.8	35.5	12	1	AB142846	Oligonucleotide pr
1012	7.8	35.5	12	1	AAQ22069	Probe analyte #1.	c1085	7.8	35.5	12	1	AB167458	Oligonucleotide pr
1013	7.8	35.5	12	1	AAQ93383	DNA encoding caspa	c1086	7.8	35.5	12	1	AB168462	Oligonucleotide pr
1014	7.8	35.5	12	1	AAQ0712	VSGF derived short	c1087	7.8	35.5	12	1	AB168928	Oligonucleotide pr
1015	7.8	35.5	12	1	AAQ27583	DNA encoding caspa	1088	7.8	35.5	12	1	AB157057	Oligonucleotide pr
c1016	7.8	35.5	12	1	AAQ88229	pp32 upstream cons	c1089	7.8	35.5	12	1	AB172322	Oligonucleotide pr
1017	7.8	35.5	12	1	AAH20822	Complex PCR amplif	c1090	7.8	35.5	12	1	AB162385	Oligonucleotide pr
c1018	7.8	35.5	12	1	AAQ61471	Wildtype influenza	c1091	7.8	35.5	12	1	AB163323	Oligonucleotide pr
c1019	7.8	35.5	12	1	AB117626	Oligonucleotide pr	1092	7.8	35.5	12	1	AB177334	Oligonucleotide pr
c1020	7.8	35.5	12	1	ABH94714	Oligonucleotide pr	c1093	7.8	35.5	12	1	AB117457	Oligonucleotide pr
c1021	7.8	35.5	12	1	ABH69699	Oligonucleotide pr	c1094	7.8	35.5	12	1	ABH94174	Oligonucleotide pr
1022	7.8	35.5	12	1	ABH95393	Oligonucleotide pr	1095	7.8	35.5	12	1	ABH96946	Oligonucleotide pr
1023	7.8	35.5	12	1	AB122321	Oligonucleotide pr	c1096	7.8	35.5	12	1	ABH99367	Oligonucleotide pr
c1024	7.8	35.5	12	1	ABH97378	Oligonucleotide pr	c1097	7.8	35.5	12	1	AB125367	Oligonucleotide pr
c1025	7.8	35.5	12	1	ABH98878	Oligonucleotide pr	c1098	7.8	35.5	12	1	AB126855	Oligonucleotide pr
1026	7.8	35.5	12	1	AB100237	Oligonucleotide pr	c1099	7.8	35.5	12	1	AB101762	Oligonucleotide pr
1027	7.8	35.5	12	1	ABH75522	Oligonucleotide pr	1100	7.8	35.5	12	1	AB103834	Oligonucleotide pr
1028	7.8	35.5	12	1	AB103349	Oligonucleotide pr	c1101	7.8	35.5	12	1	AB105890	Oligonucleotide pr
c1029	7.8	35.5	12	1	ABH79106	Oligonucleotide pr	c1102	7.8	35.5	12	1	AB105981	Oligonucleotide pr
c1030	7.8	35.5	12	1	AB129614	Oligonucleotide pr	c1103	7.8	35.5	12	1	ABH81103	Oligonucleotide pr
c1031	7.8	35.5	12	1	AB130078	Oligonucleotide pr	c1104	7.8	35.5	12	1	ABH81845	Oligonucleotide pr
1032	7.8	35.5	12	1	AB107757	Oligonucleotide pr	1105	7.8	35.5	12	1	AB132585	Oligonucleotide pr
c1033	7.8	35.5	12	1	ABH84262	Oligonucleotide pr	1106	7.8	35.5	12	1	ABH83841	Oligonucleotide pr
c1034	7.8	35.5	12	1	ABH84262	Oligonucleotide pr	c1107	7.8	35.5	12	1	ABH83992	Oligonucleotide pr
c1035	7.8	35.5	12	1	ABH92118	Oligonucleotide pr	1108	7.8	35.5	12	1	AB109859	Oligonucleotide pr
c1036	7.8	35.5	12	1	AB146539	Oligonucleotide pr	c1109	7.8	35.5	12	1	ABH85351	Oligonucleotide pr
c1037	7.8	35.5	12	1	AB168995	Oligonucleotide pr	c1110	7.8	35.5	12	1	AB135476	Oligonucleotide pr
1038	7.8	35.5	12	1	AB169973	Oligonucleotide pr	c1111	7.8	35.5	12	1	ABH89723	Oligonucleotide pr
c1039	7.8	35.5	12	1	AB156400	Oligonucleotide pr	1112	7.8	35.5	12	1	AB141302	Oligonucleotide pr
1040	7.8	35.5	12	1	AB157976	Oligonucleotide pr	c1113	7.8	35.5	12	1	AB146706	Oligonucleotide pr
c1041	7.8	35.5	12	1	AB161268	Oligonucleotide pr	c1114	7.8	35.5	12	1	AB149128	Oligonucleotide pr
1042	7.8	35.5	12	1	AB176796	Oligonucleotide pr	c1115	7.8	35.5	12	1	AB149581	Oligonucleotide pr
1043	7.8	35.5	12	1	AB166989	Oligonucleotide pr	c1116	7.8	35.5	12	1	AB152144	Oligonucleotide pr
c1044	7.8	35.5	12	1	AB117663	Oligonucleotide pr	1117	7.8	35.5	12	1	AB167896	Oligonucleotide pr
c1045	7.8	35.5	12	1	ABH93682	Oligonucleotide pr	1118	7.8	35.5	12	1	AB155064	Oligonucleotide pr
c1046	7.8	35.5	12	1	ABH94122	Oligonucleotide pr	c1119	7.8	35.5	12	1	AB160846	Oligonucleotide pr
1047	7.8	35.5	12	1	ABH70233	Oligonucleotide pr	1120	7.8	35.5	12	1	ABH67704	Oligonucleotide pr
1048	7.8	35.5	12	1	ABH70846	Oligonucleotide pr	1121	7.8	35.5	12	1	AB117899	Oligonucleotide pr
1049	7.8	35.5	12	1	ABH71165	Oligonucleotide pr	1122	7.8	35.5	12	1	ABH68620	Oligonucleotide pr
c1050	7.8	35.5	12	1	ABH96584	Oligonucleotide pr	c1123	7.8	35.5	12	1	ABH68620	Oligonucleotide pr
c1051	7.8	35.5	12	1	AB123586	Oligonucleotide pr	1124	7.8	35.5	12	1	AB119218	Oligonucleotide pr
c1052	7.8	35.5	12	1	AB124526	Oligonucleotide pr	1125	7.8	35.5	12	1	ABH95505	Oligonucleotide pr
c1053	7.8	35.5	12	1	AB102156	Oligonucleotide pr	1126	7.8	35.5	12	1	ABH73050	Oligonucleotide pr
c1054	7.8	35.5	12	1	AB102367	Oligonucleotide pr	1127	7.8	35.5	12	1	ABH98296	Oligonucleotide pr
1055	7.8	35.5	12	1	AB135801	Oligonucleotide pr	c1128	7.8	35.5	12	1	ABH98427	Oligonucleotide pr

1129	7.8	35.5	12	1	ABH98584	Oligonucleotide pr	c1202	7.8	35.5	12	1	ABH98694	Oligonucleotide pr
1130	7.8	35.5	12	1	ABH76538	Oligonucleotide pr	c1203	7.8	35.5	12	1	ABH75214	Oligonucleotide pr
1131	7.8	35.5	12	1	ABH77615	Oligonucleotide pr	1204	7.8	35.5	12	1	ABH81321	Oligonucleotide pr
c1132	7.8	35.5	12	1	ABH03493	Oligonucleotide pr	1205	7.8	35.5	12	1	ABH06387	Oligonucleotide pr
1133	7.8	35.5	12	1	ABH04382	Oligonucleotide pr	1206	7.8	35.5	12	1	ABH06563	Oligonucleotide pr
c1134	7.8	35.5	12	1	ABH79505	Oligonucleotide pr	c1207	7.8	35.5	12	1	ABH08091	Oligonucleotide pr
1135	7.8	35.5	12	1	ABH05140	Oligonucleotide pr	1208	7.8	35.5	12	1	ABH35927	Oligonucleotide pr
c1136	7.8	35.5	12	1	ABH81597	Oligonucleotide pr	c1209	7.8	35.5	12	1	ABH37823	Oligonucleotide pr
1137	7.8	35.5	12	1	ABH31926	Oligonucleotide pr	c1210	7.8	35.5	12	1	ABH37865	Oligonucleotide pr
c1138	7.8	35.5	12	1	ABH82802	Oligonucleotide pr	c1211	7.8	35.5	12	1	ABH37856	Oligonucleotide pr
1139	7.8	35.5	12	1	ABH33250	Oligonucleotide pr	1212	7.8	35.5	12	1	ABH40033	Oligonucleotide pr
c1140	7.8	35.5	12	1	ABH09315	Oligonucleotide pr	1213	7.8	35.5	12	1	ABH41019	Oligonucleotide pr
c1141	7.8	35.5	12	1	ABH84745	Oligonucleotide pr	c1214	7.8	35.5	12	1	ABH42044	Oligonucleotide pr
1142	7.8	35.5	12	1	ABH13398	Oligonucleotide pr	1215	7.8	35.5	12	1	ABH43358	Oligonucleotide pr
c1143	7.8	35.5	12	1	ABH88743	Oligonucleotide pr	1216	7.8	35.5	12	1	ABH48485	Oligonucleotide pr
1144	7.8	35.5	12	1	ABH89349	Oligonucleotide pr	1217	7.8	35.5	12	1	ABH48743	Oligonucleotide pr
c1145	7.8	35.5	12	1	ABH15497	Oligonucleotide pr	1218	7.8	35.5	12	1	ABH56761	Oligonucleotide pr
1146	7.8	35.5	12	1	ABH48367	Oligonucleotide pr	c1219	7.8	35.5	12	1	ABH71030	Oligonucleotide pr
c1147	7.8	35.5	12	1	ABH50627	Oligonucleotide pr	1220	7.8	35.5	12	1	ABH59260	Oligonucleotide pr
1148	7.8	35.5	12	1	ABH68739	Oligonucleotide pr	c1221	7.8	35.5	12	1	ABH52103	Oligonucleotide pr
c1149	7.8	35.5	12	1	ABH58123	Oligonucleotide pr	c1222	7.8	35.5	12	1	ABH52770	Oligonucleotide pr
1150	7.8	35.5	12	1	ABH72256	Oligonucleotide pr	c1223	7.8	35.5	12	1	ABH17816	Oligonucleotide pr
c1151	7.8	35.5	12	1	ABH74036	Oligonucleotide pr	1224	7.8	35.5	12	1	ABH19044	Oligonucleotide pr
1152	7.8	35.5	12	1	ABH68860	Oligonucleotide pr	1225	7.8	35.5	12	1	ABH72846	Oligonucleotide pr
c1153	7.8	35.5	12	1	ABH94151	Oligonucleotide pr	c1226	7.8	35.5	12	1	ABH72970	Oligonucleotide pr
1154	7.8	35.5	12	1	ABH94621	Oligonucleotide pr	1227	7.8	35.5	12	1	ABH73930	Oligonucleotide pr
c1155	7.8	35.5	12	1	ABH94759	Oligonucleotide pr	c1228	7.8	35.5	12	1	ABH73392	Oligonucleotide pr
1156	7.8	35.5	12	1	ABH21173	Oligonucleotide pr	c1229	7.8	35.5	12	1	ABH75112	Oligonucleotide pr
c1157	7.8	35.5	12	1	ABH96687	Oligonucleotide pr	c1230	7.8	35.5	12	1	ABH26439	Oligonucleotide pr
1158	7.8	35.5	12	1	ABH22082	Oligonucleotide pr	c1231	7.8	35.5	12	1	ABH76862	Oligonucleotide pr
c1159	7.8	35.5	12	1	ABH77376	Oligonucleotide pr	1232	7.8	35.5	12	1	ABH128082	Oligonucleotide pr
1160	7.8	35.5	12	1	ABH73248	Oligonucleotide pr	1233	7.8	35.5	12	1	ABH83179	Oligonucleotide pr
c1161	7.8	35.5	12	1	ABH73280	Oligonucleotide pr	1234	7.8	35.5	12	1	ABH33614	Oligonucleotide pr
1162	7.8	35.5	12	1	ABH72336	Oligonucleotide pr	c1235	7.8	35.5	12	1	ABH84624	Oligonucleotide pr
c1163	7.8	35.5	12	1	ABH73413	Oligonucleotide pr	c1236	7.8	35.5	12	1	ABH35866	Oligonucleotide pr
1164	7.8	35.5	12	1	ABH98987	Oligonucleotide pr	c1237	7.8	35.5	12	1	ABH97594	Oligonucleotide pr
c1165	7.8	35.5	12	1	ABH74242	Oligonucleotide pr	1238	7.8	35.5	12	1	ABH38254	Oligonucleotide pr
1166	7.8	35.5	12	1	ABH74441	Oligonucleotide pr	c1239	7.8	35.5	12	1	ABH89924	Oligonucleotide pr
c1167	7.8	35.5	12	1	ABH25571	Oligonucleotide pr	1240	7.8	35.5	12	1	ABH15677	Oligonucleotide pr
1168	7.8	35.5	12	1	ABH75743	Oligonucleotide pr	c1241	7.8	35.5	12	1	ABH16497	Oligonucleotide pr
c1169	7.8	35.5	12	1	ABH01324	Oligonucleotide pr	1242	7.8	35.5	12	1	ABH48091	Oligonucleotide pr
1170	7.8	35.5	12	1	ABH02443	Oligonucleotide pr	1243	7.8	35.5	12	1	ABH50311	Oligonucleotide pr
c1171	7.8	35.5	12	1	ABH03120	Oligonucleotide pr	1244	7.8	35.5	12	1	ABH51092	Oligonucleotide pr
1172	7.8	35.5	12	1	ABH29661	Oligonucleotide pr	1245	7.8	35.5	12	1	ABH53202	Oligonucleotide pr
c1173	7.8	35.5	12	1	ABH06318	Oligonucleotide pr	c1246	7.8	35.5	12	1	ABH57058	Oligonucleotide pr
1174	7.8	35.5	12	1	ABH07219	Oligonucleotide pr	c1247	7.8	35.5	12	1	ABH72935	Oligonucleotide pr
c1175	7.8	35.5	12	1	ABH82668	Oligonucleotide pr	c1248	7.8	35.5	12	1	ABH92402	Oligonucleotide pr
1176	7.8	35.5	12	1	ABH09948	Oligonucleotide pr	c1249	7.8	35.5	12	1	ABH17866	Oligonucleotide pr
c1177	7.8	35.5	12	1	ABH86977	Oligonucleotide pr	c1250	7.8	35.5	12	1	ABH68546	Oligonucleotide pr
1178	7.8	35.5	12	1	ABH73777	Oligonucleotide pr	1251	7.8	35.5	12	1	ABH70569	Oligonucleotide pr
c1179	7.8	35.5	12	1	ABH13567	Oligonucleotide pr	1252	7.8	35.5	12	1	ABH71401	Oligonucleotide pr
1180	7.8	35.5	12	1	ABH39120	Oligonucleotide pr	1253	7.8	35.5	12	1	ABH97515	Oligonucleotide pr
c1181	7.8	35.5	12	1	ABH14455	Oligonucleotide pr	c1254	7.8	35.5	12	1	ABH72725	Oligonucleotide pr
1182	7.8	35.5	12	1	ABH15116	Oligonucleotide pr	c1255	7.8	35.5	12	1	ABH97698	Oligonucleotide pr
c1183	7.8	35.5	12	1	ABH48138	Oligonucleotide pr	1256	7.8	35.5	12	1	ABH722807	Oligonucleotide pr
1184	7.8	35.5	12	1	ABH50150	Oligonucleotide pr	c1257	7.8	35.5	12	1	ABH74520	Oligonucleotide pr
c1185	7.8	35.5	12	1	ABH51368	Oligonucleotide pr	1258	7.8	35.5	12	1	ABH75109	Oligonucleotide pr
1186	7.8	35.5	12	1	ABH54086	Oligonucleotide pr	1259	7.8	35.5	12	1	ABH101097	Oligonucleotide pr
c1187	7.8	35.5	12	1	ABH68359	Oligonucleotide pr	1260	7.8	35.5	12	1	ABH101648	Oligonucleotide pr
1188	7.8	35.5	12	1	ABH158539	Oligonucleotide pr	c1261	7.8	35.5	12	1	ABH102112	Oligonucleotide pr
c1189	7.8	35.5	12	1	ABH72502	Oligonucleotide pr	c1262	7.8	35.5	12	1	ABH128665	Oligonucleotide pr
1190	7.8	35.5	12	1	ABH58927	Oligonucleotide pr	1263	7.8	35.5	12	1	ABH30226	Oligonucleotide pr
c1191	7.8	35.5	12	1	ABH15454	Oligonucleotide pr	1264	7.8	35.5	12	1	ABH06388	Oligonucleotide pr
1192	7.8	35.5	12	1	ABH75528	Oligonucleotide pr	c1265	7.8	35.5	12	1	ABH107748	Oligonucleotide pr
c1193	7.8	35.5	12	1	ABH62507	Oligonucleotide pr	1266	7.8	35.5	12	1	ABH108342	Oligonucleotide pr
1194	7.8	35.5	12	1	ABH177328	Oligonucleotide pr	c1267	7.8	35.5	12	1	ABH109340	Oligonucleotide pr
c1195	7.8	35.5	12	1	ABH65867	Oligonucleotide pr	1268	7.8	35.5	12	1	ABH35703	Oligonucleotide pr
1196	7.8	35.5	12	1	ABH166074	Oligonucleotide pr	1269	7.8	35.5	12	1	ABH86393	Oligonucleotide pr
c1197	7.8	35.5	12	1	ABH93366	Oligonucleotide pr	1270	7.8	35.5	12	1	ABH111951	Oligonucleotide pr
1198	7.8	35.5	12	1	ABH86864	Oligonucleotide pr	c1271	7.8	35.5	12	1	ABH14631	Oligonucleotide pr
c1199	7.8	35.5	12	1	ABH21464	Oligonucleotide pr	1272	7.8	35.5	12	1	ABH49237	Oligonucleotide pr
1200	7.8	35.5	12	1	ABH221306	Oligonucleotide pr	c1273	7.8	35.5	12	1	ABH50288	Oligonucleotide pr
c1201	7.8	35.5	12	1	ABH23106	Oligonucleotide pr	1274	7.8	35.5	12	1	ABH52148	Oligonucleotide pr

1275	7.8	35.5	12	1	ABH73267	Oligonucleotide pr	c1348	7.8	35.5	12	1	ABH97185	Oligonucleotide pr
c1276	7.8	35.5	12	1	ABH73949	Oligonucleotide pr	c1349	7.8	35.5	12	1	ABH97831	Oligonucleotide pr
1277	7.8	35.5	12	1	ABH77744	Oligonucleotide pr	1350	7.8	35.5	12	1	ABH72992	Oligonucleotide pr
1278	7.8	35.5	12	1	ABH77997	Oligonucleotide pr	c1351	7.8	35.5	12	1	ABH73017	Oligonucleotide pr
c1279	7.8	35.5	12	1	ABH95109	Oligonucleotide pr	c1352	7.8	35.5	12	1	ABH98307	Oligonucleotide pr
c1280	7.8	35.5	12	1	ABH121172	Oligonucleotide pr	1353	7.8	35.5	12	1	ABH73368	Oligonucleotide pr
c1281	7.8	35.5	12	1	ABH121190	Oligonucleotide pr	1354	7.8	35.5	12	1	ABH73404	Oligonucleotide pr
c1282	7.8	35.5	12	1	ABH96220	Oligonucleotide pr	c1355	7.8	35.5	12	1	ABH74633	Oligonucleotide pr
c1283	7.8	35.5	12	1	ABH72581	Oligonucleotide pr	c1356	7.8	35.5	12	1	ABH74718	Oligonucleotide pr
1284	7.8	35.5	12	1	ABH72752	Oligonucleotide pr	c1357	7.8	35.5	12	1	ABH74718	Oligonucleotide pr
c1285	7.8	35.5	12	1	ABH97940	Oligonucleotide pr	c1358	7.8	35.5	12	1	ABH74718	Oligonucleotide pr
1286	7.8	35.5	12	1	ABH98624	Oligonucleotide pr	c1359	7.8	35.5	12	1	ABH78687	Oligonucleotide pr
1287	7.8	35.5	12	1	ABH124220	Oligonucleotide pr	c1360	7.8	35.5	12	1	ABH79704	Oligonucleotide pr
c1288	7.8	35.5	12	1	ABH124220	Oligonucleotide pr	1361	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1289	7.8	35.5	12	1	ABH125115	Oligonucleotide pr	c1362	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1290	7.8	35.5	12	1	ABH101758	Oligonucleotide pr	1363	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1291	7.8	35.5	12	1	ABH77031	Oligonucleotide pr	c1364	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1292	7.8	35.5	12	1	ABH77113	Oligonucleotide pr	1365	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1293	7.8	35.5	12	1	ABH77616	Oligonucleotide pr	1366	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1294	7.8	35.5	12	1	ABH78361	Oligonucleotide pr	c1367	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1295	7.8	35.5	12	1	ABH103124	Oligonucleotide pr	c1368	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1296	7.8	35.5	12	1	ABH131761	Oligonucleotide pr	c1369	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1297	7.8	35.5	12	1	ABH109326	Oligonucleotide pr	c1370	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1298	7.8	35.5	12	1	ABH134513	Oligonucleotide pr	c1371	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1299	7.8	35.5	12	1	ABH84458	Oligonucleotide pr	c1372	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1300	7.8	35.5	12	1	ABH137162	Oligonucleotide pr	c1373	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1301	7.8	35.5	12	1	ABH86327	Oligonucleotide pr	1374	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1302	7.8	35.5	12	1	ABH14362	Oligonucleotide pr	c1375	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1303	7.8	35.5	12	1	ABH14363	Oligonucleotide pr	c1376	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1304	7.8	35.5	12	1	ABH90392	Oligonucleotide pr	1377	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1305	7.8	35.5	12	1	ABH116970	Oligonucleotide pr	1378	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1306	7.8	35.5	12	1	ABH144222	Oligonucleotide pr	c1379	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1307	7.8	35.5	12	1	ABH147512	Oligonucleotide pr	1380	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1308	7.8	35.5	12	1	ABH148414	Oligonucleotide pr	c1381	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1309	7.8	35.5	12	1	ABH150966	Oligonucleotide pr	c1382	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1310	7.8	35.5	12	1	ABH154291	Oligonucleotide pr	1383	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1311	7.8	35.5	12	1	ABH155063	Oligonucleotide pr	1384	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1312	7.8	35.5	12	1	ABH171186	Oligonucleotide pr	c1385	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1313	7.8	35.5	12	1	ABH171208	Oligonucleotide pr	c1386	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1314	7.8	35.5	12	1	ABH158196	Oligonucleotide pr	c1387	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1315	7.8	35.5	12	1	ABH158935	Oligonucleotide pr	c1388	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1316	7.8	35.5	12	1	ABH179820	Oligonucleotide pr	c1389	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1317	7.8	35.5	12	1	ABH69142	Oligonucleotide pr	c1390	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1318	7.8	35.5	12	1	ABH94123	Oligonucleotide pr	c1391	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1319	7.8	35.5	12	1	ABH120151	Oligonucleotide pr	c1392	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1320	7.8	35.5	12	1	ABH71164	Oligonucleotide pr	1393	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1321	7.8	35.5	12	1	ABH98267	Oligonucleotide pr	1394	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1322	7.8	35.5	12	1	ABH75051	Oligonucleotide pr	1395	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1323	7.8	35.5	12	1	ABH125979	Oligonucleotide pr	1396	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1324	7.8	35.5	12	1	ABH101553	Oligonucleotide pr	1397	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1325	7.8	35.5	12	1	ABH76553	Oligonucleotide pr	1398	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1326	7.8	35.5	12	1	ABH76703	Oligonucleotide pr	c1399	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1327	7.8	35.5	12	1	ABH107551	Oligonucleotide pr	1400	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1328	7.8	35.5	12	1	ABH84047	Oligonucleotide pr	c1401	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1329	7.8	35.5	12	1	ABH109185	Oligonucleotide pr	c1402	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1330	7.8	35.5	12	1	ABH109325	Oligonucleotide pr	c1403	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1331	7.8	35.5	12	1	ABH135772	Oligonucleotide pr	1404	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1332	7.8	35.5	12	1	ABH111212	Oligonucleotide pr	1405	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1333	7.8	35.5	12	1	ABH111567	Oligonucleotide pr	c1406	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1334	7.8	35.5	12	1	ABH113745	Oligonucleotide pr	c1407	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1335	7.8	35.5	12	1	ABH88930	Oligonucleotide pr	c1408	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1336	7.8	35.5	12	1	ABH114657	Oligonucleotide pr	1409	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1337	7.8	35.5	12	1	ABH116501	Oligonucleotide pr	c1411	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1338	7.8	35.5	12	1	ABH147270	Oligonucleotide pr	1412	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1340	7.8	35.5	12	1	ABH147997	Oligonucleotide pr	1413	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1341	7.8	35.5	12	1	ABH172376	Oligonucleotide pr	1414	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1342	7.8	35.5	12	1	ABH174526	Oligonucleotide pr	1415	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1343	7.8	35.5	12	1	ABH68976	Oligonucleotide pr	1416	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1344	7.8	35.5	12	1	ABH94359	Oligonucleotide pr	c1417	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1345	7.8	35.5	12	1	ABH69746	Oligonucleotide pr	c1418	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
c1346	7.8	35.5	12	1	ABH70048	Oligonucleotide pr	1419	7.8	35.5	12	1	ABH81788	Oligonucleotide pr
1347	7.8	35.5	12	1	ABH95193	Oligonucleotide pr	1420	7.8	35.5	12	1	ABH81788	Oligonucleotide pr

ALIGNMENTS

1421	7.8	35.5	12	1	ABI65216	Oligonucleotide pr
1422	7.8	35.5	12	1	ABI80460	Oligonucleotide pr
1423	7.8	35.5	12	1	ABI67260	Oligonucleotide pr
1424	7.8	35.5	12	1	ASH68427	Oligonucleotide pr
1425	7.8	35.5	12	1	ABI20393	Oligonucleotide pr
1426	7.8	35.5	12	1	ASH73762	Oligonucleotide pr
1427	7.8	35.5	12	1	ASH75483	Oligonucleotide pr
1428	7.8	35.5	12	1	ABI28569	Oligonucleotide pr
1429	7.8	35.5	12	1	ASH79548	Oligonucleotide pr
1430	7.8	35.5	12	1	ASH80335	Oligonucleotide pr
1431	7.8	35.5	12	1	ASH80462	Oligonucleotide pr
1432	7.8	35.5	12	1	ABI05650	Oligonucleotide pr
1433	7.8	35.5	12	1	ABI06182	Oligonucleotide pr
1434	7.8	35.5	12	1	ABI32093	Oligonucleotide pr
1435	7.8	35.5	12	1	ASH84551	Oligonucleotide pr
1436	7.8	35.5	12	1	ABI13475	Oligonucleotide pr
1437	7.8	35.5	12	1	ASH90450	Oligonucleotide pr
1438	7.8	35.5	12	1	ABI15662	Oligonucleotide pr
1439	7.8	35.5	12	1	ABI49818	Oligonucleotide pr
1440	7.8	35.5	12	1	ABI52057	Oligonucleotide pr
1441	7.8	35.5	12	1	ABI52706	Oligonucleotide pr
1442	7.8	35.5	12	1	ABI53175	Oligonucleotide pr
1443	7.8	35.5	12	1	ABI76815	Oligonucleotide pr
1444	7.8	35.5	12	1	ABI78370	Oligonucleotide pr
1445	7.8	35.5	12	1	ABI78401	Oligonucleotide pr
1446	7.8	35.5	12	1	ABI66145	Oligonucleotide pr
1447	7.8	35.5	12	1	ABI82035	Oligonucleotide pr
1448	7.8	35.5	12	1	ABI17694	Oligonucleotide pr
1449	7.8	35.5	12	1	ASH92991	Oligonucleotide pr
1450	7.8	35.5	12	1	ASH94505	Oligonucleotide pr
1451	7.8	35.5	12	1	ASH95694	Oligonucleotide pr
1452	7.8	35.5	12	1	ASH71751	Oligonucleotide pr
1453	7.8	35.5	12	1	ASH72328	Oligonucleotide pr
1454	7.8	35.5	12	1	ABI23966	Oligonucleotide pr
1455	7.8	35.5	12	1	ASH74796	Oligonucleotide pr
1456	7.8	35.5	12	1	ASH76081	Oligonucleotide pr
1457	7.8	35.5	12	1	ABI26715	Oligonucleotide pr
1458	7.8	35.5	12	1	ABI02659	Oligonucleotide pr
1459	7.8	35.5	12	1	ABI03308	Oligonucleotide pr
1460	7.8	35.5	12	1	ABI28965	Oligonucleotide pr
1461	7.8	35.5	12	1	ASH79806	Oligonucleotide pr
1462	7.8	35.5	12	1	ASH80068	Oligonucleotide pr
1463	7.8	35.5	12	1	ABI05818	Oligonucleotide pr
1464	7.8	35.5	12	1	ABI06252	Oligonucleotide pr
1465	7.8	35.5	12	1	ABI09548	Oligonucleotide pr
1466	7.8	35.5	12	1	ASH88308	Oligonucleotide pr
1467	7.8	35.5	12	1	ASH89677	Oligonucleotide pr
1468	7.8	35.5	12	1	ABI41860	Oligonucleotide pr
1469	7.8	35.5	12	1	ABI43273	Oligonucleotide pr
1470	7.8	35.5	12	1	ABI46462	Oligonucleotide pr
1471	7.8	35.5	12	1	ABI47815	Oligonucleotide pr
1472	7.8	35.5	12	1	ABI49456	Oligonucleotide pr
1473	7.8	35.5	12	1	ABI54085	Oligonucleotide pr
1474	7.8	35.5	12	1	ABI68631	Oligonucleotide pr
1475	7.8	35.5	12	1	ABI57978	Oligonucleotide pr
1476	7.8	35.5	12	1	APF2714	Multiple allele de
1477	7.8	35.5	12	1	AAI37779	3' conserved RNA r
1478	7.8	35.5	12	1	AAI37802	Modified 3' RNA re
1479	7.8	35.5	12	1	ABS71501	DNA encoding prote
1480	7.8	35.5	12	1	ABQ75462	Modified influenza
1481	7.8	35.5	12	1	ABQ75461	Influenza virus C
1482	7.8	35.5	12	1	AKS9290	Hepatitis C virus
1483	7.8	35.5	12	1	AKS15139	Wild type Influenz
1484	7.8	35.5	12	1	ASH39657	Luc (luciferase)-1</

RESULT 1
AAL49614/c
ID AAL49614 standard; DNA; 21 BP

XX
AC AAL49614;

27-NOV-2002 (first entry)

XX Tumour differentiation effecting protein TL4 related PCR primer #18

XX Mouse; tumour differentiation; rhabdosarcoma; leiomyosarcoma; rat; ss;
KW muscular dystrophy; uterine myoma; cytostatic; plasmic change; TL4;
KW human; PCR; primer.

OS Unidentified.

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PN
W0200266049-A1XX
30-3110-3003
PP

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XX Plasmic change agents and antibodies to them for diagnosis, and treatment
PT of tumours of muscle tissue and of muscular dystrophy,
PT

Example 1: Page 127: 136pp; Japanese.

XX The present invention relates to plasmic change agents with cell
CC differentiation activity containing protein TL4. These can be used in the
CC treatment, prevention and diagnosis of rhabdosarcoma, leiomyosarcoma,
CC muscular dystrophy and uterine myeloma. The present sequence is a PCR
CC primer used in the exemplification of the invention

Sequence 21 BP: 1 A; 5 C; 6 G; 9 T; 0 U; 0 Other; 0 X

Query Match 95.5%: Score 21: DB 1: Length 21:

Best Local Similarity 100.0%; Pred. No. 8.5;

Matches	21;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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OV 727 TGCCAGGAGAAACAGAACACC 747

db 21 TGGCAGGAGAAACAGAACACC 1

RESULT 2

РЕЗУЛТАТ
АВТ05081/С

ID ABT05081 standard; DNA; 18 BP.

AC ABT05081:

11-OCT-2002 (first entry)

XX
DE TNFR1 expression modulation related antisense oligo SEQ ID No 111

XX Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW human; ds.
KW

Homosapiens.

XX
PN
W0200248168-21

XX XX

PD 20-JUN-2002.
XX
PF 22-OCT-2001; 2001WO-US051224.
XX
PR 24-OCT-2000; 2000US-00695451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowser LM, Zhang H, Dean NM;
PI WPI; 2002-583481/62.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding tumor
PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
XX Example 18; Page 56; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human oligonucleotide relating
CC to the TNFR1 of the invention
XX
SQ Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 81.8%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAACAGAAC 744
DB 18 TGCCAGGAGAAACAGAAC 1
RESULT 3
ID ABT05082/c
XX ABT05082 standard; DNA; 18 BP.
XX
AC ABT05082;
XX
XX 11-OCT-2002 (first entry)
XX
DE TNFR1 expression modulation related antisense oligo SEQ ID No 112.
XX
KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW human; ds.
XX
OS Homo sapiens.
XX
XX WO200248168-A1.
XX
XX 20-JUN-2002.
XX
XX 22-OCT-2001; 2001WO-US051224.
XX
XX 24-OCT-2000; 2000US-00695451.
XX
XX (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowser LM, Zhang H, Dean NM;
PI WPI; 2002-583481/62.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding tumor

PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
XX Example 18; Page 56; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human oligonucleotide relating
CC to the TNFR1 of the invention
XX
SQ Sequence 18 BP; 0 A; 4 C; 5 G; 9 T; 0 U; 0 Other;
Query Match 81.8%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 CCAGGAGAAACAGAAC 746
DB 18 CCAGGAGAAACAGAAC 1
RESULT 4
ID ABT05083/c
XX ABT05083 standard; DNA; 18 BP.
XX
AC ABT05083;
XX
XX 11-OCT-2002 (first entry)
XX
DE TNFR1 expression modulation related antisense oligo SEQ ID No 113.
XX
KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW human; ds.
XX
OS Homo sapiens.
XX
XX WO200248168-A1.
XX
XX 20-JUN-2002.
XX
XX 22-OCT-2001; 2001WO-US051224.
XX
XX 24-OCT-2000; 2000US-00695451.
XX
XX (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowser LM, Zhang H, Dean NM;
PI WPI; 2002-583481/62.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding tumor
PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
XX Example 18; Page 56; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting

CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human oligonucleotide relating
CC to the TNFR1 of the invention
XX
SQ Sequence 18 BP; 0 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 81.8%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGAACACCG 748
|||||
Db 18 AGGAGAAACAGAACACCG 1

RESULT 5
AAZ48521/c
ID AAZ48521 standard; DNA; 18 BP.
XX
AC AAZ48521;
XX
DT 31-MAR-2000 (first entry)
XX
DE Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18914.
XX
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
XX inflammation; tumour formation; TNFR1; anticancer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US6007995-A.
XX
PD 28-DEC-1999.
XX
PF 26-JUN-1998; 98US-00106038.
XX
PR 26-JUN-1998; 98US-00106038.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowser LM;
XX
PT WPI; 2000-105333/09.
XX
PT Antisense inhibition of tumor necrosis factor type 1 expression for
PT diagnosis, treatment and prevention of disease, particularly tumors.
XX
PS Claim 1; Col 25; 34pp; English.
XX
CC The invention provides antisense compounds targeted to human tumour
CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC can be used in a method of inhibiting the expression of TNFR1 human cells
CC or tissues. The antisense compounds specifically hybridize with one or
CC more nucleic acids encoding TNFR1 modulating the function of nucleic acid
CC molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC produced. The antisense compounds and method are useful as research
CC reagents and diagnostics, and in the treatment and prophylaxis of
CC infection, inflammation or tumour formation. Sequences AAZ48482-565
CC represent antisense oligos used for inhibition of the human TNFR1 mRNA
XX
SQ Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

RESULT 6
ABT05017/c
ID ABT05017 standard; DNA; 18 BP.
XX
AC ABT05017;
XX
DT 11-OCT-2002 (first entry)
XX
DE TNFR1 expression modulation related antisense oligo SEQ ID No 47.
XX
KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW human; ds.
XX
OS Homo sapiens.
XX
PN WO200248168-A1.
XX
PD 20-JUN-2002.
XX
PF 22-OCT-2001; 2001WO-US051224.
XX
PR 24-OCT-2000; 2000US-00695451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowser LM, Zhang H, Dean NW;
XX
PT WPI; 2002-583481/62.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding tumor
PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
PS Example 10; Page 45; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human oligonucleotide relating
CC to the TNFR1 of the invention
XX
SQ Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 77.3%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 GGAGAAACAGAACACCG 748
|||||
Db 18 GGAGAAACAGAACACCG 2

RESULT 7
AAT16398/c
ID AAT16398 standard; DNA; 18 BP.
XX
AC AAT16398;
XX
DT 13-SEP-1996 (first entry)
XX
DE Primer #1 for SWS32359 human obesity gene.
XX
KW Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
KW food intake; energy expenditure; high blood pressure; cholesterol; human;
KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay; PCR;


```

XX WPI; 2000-302788/26.
DR
XX Modifying body weight of an animal comprises administering mammalian
PT obesity polypeptide obtained from humans and murine.
XX
XX Example 10; Col 133-134; 153pp; English.
XX
XX This invention describes a novel method for modifying body weight of an
CC animal which comprises administering mammalian obesity (OB) polypeptide.
CC The products of the invention have anorectic activity. The OB polypeptide
CC at a dose of 5 mg/g/day in 300 micro litres of PBS was injected
CC intraperitoneally into mice. Control mice were injected with PBS
CC dialysate of the recombinant protein. The body weight of the mice was
CC noted. The results shows that recombinant the OB polypeptide is capable
CC of reducing a body weight and is found to be effective when it is
CC administered daily. The OB polypeptide acts as a part of the signalling
CC pathway by which adipose tissue communicates with the brain and other
CC organs. (i) is useful for modulating body weight of an animal especially
CC humans. This sequence represents a PCR primer used in the amplification
CC of a human OB protein described in the method of the invention
XX
XX Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
SQ
Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 730 CAGGAGAAACACACAC 746
DB 18 CAGGAGAAACACACAC 2
|||||
RESULT 10
AAC62673/c
ID AAC62673 standard; DNA; 18 BP.
XX
XX AAC62673;
XX
XX 01-FEB-2001 (first entry)
XX
XX Human OB gene sequence tagged-site-specific PCR primer #7.
XX
XX Human; mouse; anabolic; cytostatic; immunostimulant;
KW OB polypeptide inhibitor; body weight; obesity; OB gene; cancer; AIDS;
KW anorexia nervosa; hypertension; heart disease; Type II diabetes;
KW PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6124439-A.
XX
XX 26-SEP-2000.
XX
XX 07-JUN-1995; 95US-00488214.
XX
XX 17-AUG-1994; 94US-00292345.
XX
XX 30-NOV-1994; 94US-00347563.
XX
XX 10-MAY-1995; 95US-00438431.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Proenca R, Zhang Y, Friedman JM;
XX
XX WPI; 2000-611018/58.
XX
XX Novel antibody to mammalian obesity polypeptide useful for diagnosis and
PT treatment of weight loss associated with disorders such as cancer, AIDS.
XX and anorexia nervosa.
XX
XX Example 10; Col 80; 150pp; English.
XX
XX The present sequence is a PCR primer which was used in an invention
CC

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CC relating to the control of body weight of animals including humans.
CC Antibodies against the mammalian obesity (OB) polypeptide have been
CC identified. The antibodies are useful for modulating the activity of OB
CC to control body weight and fat content and/or to treat certain
CC pathological conditions in which there is abnormal depression or
CC elevation of body weight. The antibodies are used to treat weight loss
CC associated with cancer, AIDS and anorexia nervosa. They are useful for
CC the diagnosis of nutritional disorders such as obesity and diseases
CC associated with obesity, such as hypertension, heart disease and Type II
CC diabetes. The kits are used to determine the presence or amount of OB in
XX the blood or plasma of an individual
XX
XX Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
SQ
Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 730 CAGGAGAAACACACAC 746
DB 18 CAGGAGAAACACACAC 2
|||||
RESULT 11
ABX89547/c
ID ABX89547 standard; DNA; 18 BP.
XX
XX ABX89547;
XX
XX 08-MAY-2003 (first entry)
XX
XX Human sequence tagged specific PCR primer sWss2359 #1.
XX
XX ss; human; obese polypeptide; body weight; PCR; ob polypeptide; leptin;
KW adipocyte; appetite reduction; cosmetic; primer; fat deposit reduction;
KW improved body appearance; heart disease; obesity; agriculture;
KW nutritional disorder; cancer associated weight loss; type II diabetes;
KW obesity associated disease; AIDS associated weight loss; hypertension;
KW gene therapy.
XX
XX Homo sapiens.
XX
XX US2002107211-A1.
XX
XX 08-AUG-2002.
XX
XX 13-DEC-2000; 2000US-00736084.
XX
XX 07-JUN-1995; 95US-00485943.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Friedman JM, Halaas JL, Gajiwala K, Burley SK, Zhang Y;
XX Proenca R, Maffei M;
XX
XX WPI; 2002-722695/78.
XX
XX New obese polypeptide useful for inducing reduction of body weight in an
PT animal, for preparing a composition for treating obesity, disease
PT associated with obesity such as hypertension, heart disease or type II
PT diabetes.
XX
XX Example 10; Page 44; 144pp; English.
XX
XX The invention relates to an obese (ob) polypeptide, also known as leptin,
CC expressed predominantly by adipocytes and capable of inducing reduction
CC of body weight in an animal. The polypeptide is useful for monitoring
CC therapeutic treatment of a disease associated with elevated or decreased
CC levels of ob polypeptide in a mammalian subject; for use in
CC radioimmunoassays for measuring fat and/or plasma levels of ob protein or
CC for detecting the presence and level of receptor for ob on tissues, such
CC as hypothalamus; for screening expression libraries to isolate active
CC receptors; for use in cosmetics by improving body appearance by reducing
CC

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CC fat deposits or appetite or both and is used independently or in
 CC conjugation with other cosmetic strategies e.g. surgery for its cosmetic
 CC effect; for identifying agonists or antagonists that affect its activity
 CC and has potential agricultural uses e.g. increasing the body weight of
 CC animals. Nucleic acid encoding the polypeptide is useful for identifying
 CC mutation in ob nucleotide, in gene therapy for obesity and in the
 CC measurement of its encoded RNA and protein in nutritional disorders. A
 CC host cell transfected with a vector expressing the polypeptide is useful
 CC in the preparation of modulators of the polypeptide and its nucleic acid.
 CC An immunogenic fragment of the polypeptide is useful for preparing an
 CC antibody. The antibody is useful for measuring the presence of the
 CC polypeptide in a sample; for evaluating the level of ob polypeptide in a
 CC biological sample to detect or diagnose the presence of a disease
 CC associated with elevated or decreased levels of ob polypeptide in a
 CC mammalian subject; for imaging ob polypeptide in situ. A composition
 CC comprising the polypeptide is useful for reducing body weight of an
 CC animal, in particular humans. A composition comprising an antagonist of
 CC the polypeptide is useful for increasing body weight of an animal.
 CC Compositions containing the polypeptide and the antagonist are useful for
 CC treating obesity, weight loss associated with cancer or AIDS, disease
 CC associated with obesity such as hypertension, heart disease or type II
 CC diabetes. The present sequence represents a human sequence tagged
 CC specific PCR primer
 XX
 SQ Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 59;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 730 CAGGAGAAACAGACAC 746
 |||||
 DB 18 CAGGAGAAACAGACAC 2

RESULT 12
 ABL61421/c
 ID ABL61421 standard; DNA; 18 BP.
 XX
 AC ABL61421;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE Human Ob gene STS sN5S2359 AFVa0652g9 PCR primer #1.
 XX
 KW Ob; human; obese; adiposity; body weight; anorectic; anabolic; PCR;
 KW primer; chromosome 7; STS; sequence tagged site; 7q31.3;
 KW microsatellite marker; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6350730-B1.
 XX
 PD 26-FEB-2002.
 XX
 PF 07-JUN-1995; 95US-00488223.
 XX
 PR 17-AUG-1994; 94US-00292345.
 PR 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 XX
 PA (UVRQ) UNIV ROCKEFELLER.
 XX
 PI Friedman JM, Zhang Y, Proenca R;
 XX
 DR WPI; 2002-412914/44.
 XX
 PT Modifying the body weight of an animal comprises administering an obese
 PT gene (OB) polypeptide analog.
 XX
 PS Example 10; Col 79-80; 152pp; English.
 XX
 CC This invention describes a novel method of modifying the body weight of

CC an animal comprising administering an obese gene (OB) polypeptide
 CC analogue, capable of modulating body weight and adiposity. The invention
 CC has anorectic and anabolic activity. ABL61415-ABL61468 represent PCR
 CC primers used in the detection of sequence tagged sites (STS's) and
 CC microsatellite markers used in the mapping of the human Ob gene onto
 CC chromosome 7. These genetic markers represent an important tool for
 CC studying the possible role of the Ob gene in inherited forms of human
 CC obesity
 XX
 SQ Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 59;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 730 CAGGAGAAACAGACAC 746
 |||||
 DB 18 CAGGAGAAACAGACAC 2

RESULT 13
 ABX96407/c
 ID ABX96407 standard; DNA; 18 BP.
 XX
 AC ABX96407;
 XX
 DT 13-MAY-2003 (first entry)
 XX
 DE Human obese (ob) gene associated PCR primer #7.
 XX
 KW OB polypeptide; obese polypeptide; leptin; body weight; obesity;
 KW weight gain; protein therapy; weight loss; cancer; AIDS; human;
 KW acquired immunodeficiency syndrome; anorexia nervosa; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6471956-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 07-JUN-1995; 95US-00488225.
 XX
 PR 17-AUG-1994; 94US-00292345.
 PR 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 XX
 PA (UVRQ) UNIV ROCKEFELLER.
 XX
 PI Friedman JM, Zhang Y, Proenca R;
 XX
 DR WPI; 2003-298093/29.
 XX
 PT New human or mouse OB polypeptide, also referred to as leptin
 PT polypeptide, which is capable of modulating body weight, useful for
 PT treating obesity.
 XX
 PS Example 10; Col 79-80; 153pp; English.
 XX
 CC The invention describes an OB (obese) polypeptide (also referred as
 CC leptin) (I), capable of modulating body weight, comprising amino acids 22
 CC - 167 of a human or mouse OB polypeptide sequence of 167 amino acids
 CC (S1), given in the specification, or amino acids 22 - 166 a human or
 CC mouse OB polypeptide sequence of 166 amino acids (S2), given in the
 CC specification. The OB polypeptide is useful for reducing body weight in
 CC conditions of obesity, and as a target for neutralising antibodies which
 CC results in weight gain (protein therapy), for treating weight loss
 CC associated with cancer, acquired immunodeficiency syndrome (AIDS) or
 CC anorexia nervosa. This sequence represents a primer associated with the
 CC isolation of the human obese (ob) or leptin gene
 XX
 SQ Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGAACAC 746
|||||
Db 18 CAGGAGAAACAGAACAC 2

RESULT 14
AAH85678/c
ID AAH85678 standard; DNA; 19 BP.

XX AAH85678;

XX 04-DEC-2000 (first entry)

DT Cyclin B1 ribozyme binding site #7.

DE Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

XX Mammalia.

XX WO200032765-A2.

XX 08-JUN-2000.

XX 06-DEC-1999; 99WO-US028772.

XX 04-DEC-1998; 98US-0110954P.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JW;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.

XX Disclosure; Page 96; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAH82415 to AAH86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment

XX Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 CGAGAAACAGAACACCG 748
|||||
Db 19 CGAGAAACAGAACACCG 3

RESULT 15
AAH60840/c
ID AAH60840 standard; DNA; 19 BP.

XX AAH60840;

XX 10-SEP-2001 (first entry)

DT Cyclin B1 ribozyme binding site SEQ ID NO:3264.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;

recognition site; target; ribozyme binding site; eye disease; vulnary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200130362-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US029500.

XX 26-OCT-1999; 99US-0161532P.

XX (IMMU-) IMMUSOL INC.

XX Robbins JM, Tritz R;

XX WPI; 2001-300427/31.

XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.

XX Example 1; Page 309; 408pp; English.

XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiproliferative,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention

XX Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 CGAGAAACAGAACACCG 748
|||||
Db 19 CGAGAAACAGAACACCG 3

RESULT 16
AAV14108/c
ID AAV14108 standard; DNA; 18 BP.

XX AAV14108;

XX 27-AUG-2003 (revised)

DT 19-MAY-1998 (first entry)

XX

DE Probe HBP-274 for RT pol region of HBV.
 XX Probe; hepatitis B virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.
 XX Synthetic.
 OS Hepatitis B virus.
 XX WO9740193-A2.
 PN 30-OCT-1997.
 PD 21-APR-1997; 97WO-EP002002.
 XX 19-APR-1996; 96EP-00870053.
 XX (INNO-) INNOGENETICS NV.
 XX Stuyver L, Rossau R, Maertens G;
 PI WPI; 1997-535867/49.
 DR Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.
 XX Claim 5; Fig 1; 80pp; English.
 XX This sequence represents a probe for the RT pol region of hepatitis B
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (i) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (i) with a combination of at least
 CC 2 nucleotide probes, which are applied to known locations on a solid
 CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 18 BP; 1 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 SQ Query Match 68.2%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAACACAGA 742
 DB 18 GCCAGGAGAACACAGA 4
 RESULT 17
 AAD22805/c
 ID AAD22805 standard; DNA; 22 BP.
 XX AAD22805;
 AC AAD22805;
 XX 26-FEB-2002 (first entry)
 DT Human EMR2 specific nested PCR primer, 3'-1.
 DE Human; EGF-like molecule containing mucin-like hormone receptor-2; EMR2;
 KW epidermal growth factor; therapy; acute inflammation; injury; infection;
 KW meningitis; pneumonia; chronic inflammation; chronic tissue damage;
 KW rheumatoid arthritis; septic shock; atherosclerosis; autoimmune disease;
 KW diabetes; Alzheimer's disease; autoimmunity; intravascular coagulation;
 KW clotting; fibrinolysis; thrombosis; embolism; wound repair; angiogenesis;
 KW haematopoiesis; blood disorder; anaemia; agranulocytosis; migration;
 KW myeloid leukaemia; anastomosis; vascular malformation; congenital disease;
 KW wound healing; Marfan syndrome; hereditary haemorrhagic telangiectasia;
 KW HHT; tumour; infection; cancer; asthma; anorexia; Parkinson's disease;
 KW bulimia; hypotension; acute heart failure; hypertension; osteoporosis;
 KW urinary retention; angina pectoris; myocardial infarction; allergy;
 KW ulcer; benign prostatic hypertrophy; neurological disorder; anxiety;
 KW schizophrenia; manic depression; delirium; dementia; mental retardation;
 KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS WO200179296-A1.
 PN 25-OCT-2001.
 PD 17-APR-2001; 2001WO-GB001729.
 XX 13-APR-2000; 2000GB-00009181.
 XX (ISIS-) ISIS INNOVATION LTD.
 XX Lin H, Gordon D, McKnight AJ, Stacey M;
 PI WPI; 2002-026015/03.
 DR Novel human epidermal growth factor-like molecule containing mucin-like
 PT hormone receptor-2 polypeptide, useful for treating acute and chronic
 PT inflammation, chronic tissue damages and for wound healing.
 XX Example; Page 49; 118pp; English.
 XX The patent discloses human epidermal growth factor (EGF)-like molecule
 CC containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic
 CC acids encoding them. EMR2 sequences are useful for treating acute
 CC inflammation caused by injury or infection (e.g. meningitis and
 CC pneumonia), chronic inflammation (e.g. rheumatoid arthritis), chronic
 CC tissue damages, septic shock, atherosclerosis, repair and autoimmune
 CC disease processes, diabetes, Alzheimer's disease, processes such as
 CC killing of targets by degranulation, chemotaxis and leukocyte
 CC recruitment, induction and effector mechanism of innate and acquired
 CC autoimmunity. They are also useful for treating conditions involving
 CC clotting, fibrinolysis, intravascular coagulation, thrombosis and
 CC embolism, wound repair and angiogenesis, haematopoiesis and blood
 CC disorders such as anaemia, agranulocytosis, migration, retention and
 CC activation or deactivation of phagocytes, myeloid leukaemia, anaemia,
 CC general disorders of connective tissue (e.g. vascular malfunction, wound
 CC healing) and congenital diseases such as hereditary haemorrhagic
 CC telangiectasia (HHT) and Marfan syndrome. They are also useful for
 CC controlling tumour formation and metastasis, for treating macrophage
 CC giant cells in bacterially-induced granuloma. Sequences of the invention
 CC are useful in the preparation of a medicament for use in a method of
 CC therapy of a condition or disease associated with EMR2 polypeptide and in
 CC the preparation of a diagnostic agent for use in the method of diagnosis
 CC of a condition or disease associated with EMR2 polypeptide. Antibodies
 CC against EMR2 are useful for treating infections such as bacterial,
 CC fungal, protozoan and viral infections, particularly infections caused by
 CC HIV-1 or HIV-2, pain, cancers, anorexia, Parkinson's disease,
 CC bulimia, hypotension, acute heart failure, hypertension, osteoporosis,
 CC urinary retention, angina pectoris, myocardial infarction, ulcers,
 CC allergies, benign prostatic hypertrophy, psychotic and neurological
 CC disorders including anxiety, schizophrenia, manic depression, delirium,
 CC dementia, severe mental retardation, dyskinesias such as Huntington's
 CC disease or Gilles de la Tourette's syndrome. The present DNA sequence is
 CC nested PCR primer, 3'-1 which is specific for human EMR2 cDNAs
 XX Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other;
 SQ Query Match 66.4%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 85;

		Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	727 TCCGAGGAGAACAGACACC 747	
Db	22 TCCGAGGAGAACAGACACC 2	
RESULT 18		
AD	AAD22809/c	
ID	AAD22809 standard; DNA; 22 BP.	
XX	AAD22809;	
AC	AAD22809;	
XX		
DT	26-FEB-2002 (first entry)	
XX		
DE	Human EMR2 specific RT-PCR primer #1.	
XX		
KW	Human; EGF-like molecule containing mucin-like hormone receptor-2; EMR2;	
KW	epidermal growth factor; therapy; acute inflammation; injury; infection;	
KW	meningitis; pneumonia; chronic inflammation; chronic tissue damage;	
KW	rheumatoid arthritis; septic shock; atherosclerosis; autoimmune disease;	
KW	diabetes; Alzheimer's disease; autoimmunity; intravascular coagulation;	
KW	clotting; fibrinolysis; thrombosis; embolism; wound repair; angiogenesis;	
KW	haematopoiesis; blood disorder; anaetropenia; agranulocytosis; migration;	
KW	myeloid leukaemia; anaemia; vascular malfunction; congenital disease;	
KW	wound healing; Marfan syndrome; hereditary haemorrhagic telangiectasia;	
KW	HHT; tumour; infection; cancer; asthma; anorexia; Parkinson's disease;	
KW	bulimia; hypotension; acute heart failure; hypertension; osteoporosis;	
KW	urinary retention; angina pectoris; myocardial infarction; allergy;	
KW	ulcer; benign prostatic hypertrophy; neurological disorder; anxiety;	
KW	schizophrenia; manic depression; delirium; dementia; mental retardation;	
KW	dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;	
KW	reverse transcription; RT-PCR primer; ss.	
OS	Homo sapiens.	
XX		
PN	WO200179296-A1.	
PD	25-OCT-2001.	
XX		
PF	17-APR-2001; 2001WO-GB001729.	
XX		
PR	13-APR-2000; 2000GB-00009181.	
XX	(ISIS-) ISIS INNOVATION LTD.	
PI	Lin H, Gordon D, Mcknight AJ, Stacey M;	
XX		
DR	WPI; 2002-026015/03.	
XX		
PT	Novel human epidermal growth factor-like molecule containing mucin-like	
XX	hormone receptor-2 polypeptide, useful for treating acute and chronic	
XX	inflammation, chronic tissue damages and for wound healing.	
XX		
PS	Example; Page 50; 118pp; English.	
XX		
CC	The patent discloses human epidermal growth factor (EGF)-like molecule	
CC	containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic	
CC	acids encoding them. EMR2 sequences are useful for treating acute	
CC	inflammation caused by injury or infection (e.g. meningitis and	
CC	pneumonia), chronic inflammation (e.g. rheumatoid arthritis), chronic	
CC	tissue damages, septic shock, atherosclerosis, repair and autoimmune	
CC	disease processes, diabetes, Alzheimer's disease, processes such as	
CC	killing of targets by degradation, chemotaxis and leukocyte	
CC	recruitment, induction and effector mechanism of innate and acquired	
CC	autoimmunity. They are also useful for treating conditions involving	
CC	clotting, fibrinolysis, intravascular coagulation, thrombosis and	
CC	embolism, wound repair and angiogenesis, haematopoiesis and blood	
CC	disorders such as anaetropenia, agranulocytosis, migration, retention and	
CC	activation or deactivation of phagocytes, myeloid leukaemia, anaemia,	
CC	general disorders of connective tissue (e.g. vascular malfunction, wound	
CC	healing) and congenital diseases such as hereditary haemorrhagic	
CC	telangiectasia (HHT) and Marfan syndrome. They are also useful for	

CC	controlling tumour formation and metastasis, for treating macrophage	
CC	giant cells in bacterially-induced granuloma. Sequences of the invention	
CC	are useful in the preparation of a medicament for use in a method of	
CC	therapy of a condition or disease associated with EMR2 polypeptide and in	
CC	the preparation of a diagnostic agent for use in the method of diagnosis	
CC	of a condition or disease associated with EMR2 polypeptide. Antibodies	
CC	against EMR2 are useful for treating infections such as bacterial,	
CC	fungal, protozoan and viral infections, particularly infections caused by	
CC	HIV-1 or HIV-2, pain, cancers, asthma, anorexia, Parkinson's disease,	
CC	bulimia, hypotension, acute heart failure, hypertension, osteoporosis,	
CC	urinary retention, angina pectoris, myocardial infarction, ulcers,	
CC	allergies, benign prostatic hypertrophy, psychotic and neurological	
CC	disorders including anxiety, schizophrenia, manic depression, delirium,	
CC	dementia, severe mental retardation, dyskinesias such as Huntington's	
CC	disease or Gilles de la Tourette's syndrome. The present DNA sequence is a	
CC	reverse transcription (RT)-PCR primer which is specific for human EMR2	
CC	cDNA sequences	
XX		
SQ	Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other;	
Query Match 66.4%; Score 14.6; DB 1; Length 22;		
Best Local Similarity 81.0%; Pred. No. 85;		
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
QY	727 TCCGAGGAGAACAGACACC 747	
Db	22 TCCGAGGAGAACAGACACC 2	
RESULT 19		
AD	AAD22815/c	
ID	AAD22815 standard; DNA; 22 BP.	
XX		
AC	AAD22815;	
XX		
DT	26-FEB-2002 (first entry)	
XX		
DE	Human EMR2 7 transmembrane domain identifying primer #1.	
XX		
KW	Human; EGF-like molecule containing mucin-like hormone receptor-2; EMR2;	
KW	epidermal growth factor; therapy; acute inflammation; injury; infection;	
KW	meningitis; pneumonia; chronic inflammation; chronic tissue damage;	
KW	rheumatoid arthritis; septic shock; atherosclerosis; autoimmune disease;	
KW	diabetes; Alzheimer's disease; autoimmunity; intravascular coagulation;	
KW	clotting; fibrinolysis; thrombosis; embolism; wound repair; angiogenesis;	
KW	haematopoiesis; blood disorder; anaetropenia; agranulocytosis; migration;	
KW	myeloid leukaemia; anaemia; vascular malfunction; congenital disease;	
KW	wound healing; Marfan syndrome; hereditary haemorrhagic telangiectasia;	
KW	HHT; tumour; infection; cancer; asthma; anorexia; Parkinson's disease;	
KW	bulimia; hypotension; acute heart failure; hypertension; osteoporosis;	
KW	urinary retention; angina pectoris; myocardial infarction; allergy;	
KW	ulcer; benign prostatic hypertrophy; neurological disorder; anxiety;	
KW	schizophrenia; manic depression; delirium; dementia; mental retardation;	
KW	dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;	
KW	reverse transcription; RT-PCR primer; ss.	
OS	Homo sapiens.	
XX		
PN	WO200179296-A1.	
PD	25-OCT-2001.	
XX		
PF	17-APR-2001; 2001WO-GB001729.	
XX		
PR	13-APR-2000; 2000GB-00009181.	
XX	(ISIS-) ISIS INNOVATION LTD.	
PI	Lin H, Gordon D, Mcknight AJ, Stacey M;	
XX		
DR	WPI; 2002-026015/03.	
XX		
PT	Novel human epidermal growth factor-like molecule containing mucin-like	
XX	hormone receptor-2 polypeptide, useful for treating acute and chronic	
XX	inflammation, chronic tissue damages and for wound healing.	
XX		
PS	Example; Page 50; 118pp; English.	
XX		
CC	The patent discloses human epidermal growth factor (EGF)-like molecule	
CC	containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic	
CC	acids encoding them. EMR2 sequences are useful for treating acute	
CC	inflammation caused by injury or infection (e.g. meningitis and	
CC	pneumonia), chronic inflammation (e.g. rheumatoid arthritis), chronic	
CC	tissue damages, septic shock, atherosclerosis, repair and autoimmune	
CC	disease processes, diabetes, Alzheimer's disease, processes such as	
CC	killing of targets by degradation, chemotaxis and leukocyte	
CC	recruitment, induction and effector mechanism of innate and acquired	
CC	autoimmunity. They are also useful for treating conditions involving	
CC	clotting, fibrinolysis, intravascular coagulation, thrombosis and	
CC	embolism, wound repair and angiogenesis, haematopoiesis and blood	
CC	disorders such as anaetropenia, agranulocytosis, migration, retention and	
CC	activation or deactivation of phagocytes, myeloid leukaemia, anaemia,	
CC	general disorders of connective tissue (e.g. vascular malfunction, wound	
CC	healing) and congenital diseases such as hereditary haemorrhagic	
CC	telangiectasia (HHT) and Marfan syndrome. They are also useful for	

Novel human epidermal growth factor-like molecule containing mucin-like

PT hormone receptor-2 polypeptide, useful for treating acute and chronic
 XX inflammation, chronic tissue damages and for wound healing.
 PS Example; Page 51; 118pp; English.
 XX

The patent discloses human epidermal growth factor (EGF)-like molecule
 CC containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic
 CC acids encoding them. EMR2 sequences are useful for treating acute
 CC inflammation caused by injury or infection (e.g. meningitis and
 CC pneumonia), chronic inflammation (e.g. rheumatoid arthritis), chronic
 CC tissue damages, septic shock, atherosclerosis, repair and autoimmune
 CC disease processes, diabetes, Alzheimer's disease, processes such as
 CC killing of targets by degranulation, chemotaxis and leukocyte
 CC recruitment, induction and effector mechanism of innate and acquired
 CC autoimmunity. They are also useful for treating conditions involving
 CC clotting, fibrinolysis, intravascular coagulation, thrombosis and
 CC embolism, wound repair and angiogenesis, haematopoiesis and blood
 CC disorders such as anaeropenia, granulocytosis, migration, retention and
 CC activation or deactivation of phagocytes, myeloid leukaemia, anaemia,
 CC general disorders of connective tissue (e.g. vascular malfunction, wound
 CC healing) and congenital diseases such as hereditary haemorrhagic
 CC telangiectasia (HHT) and Marfan syndrome. They are also useful for
 CC controlling tumour formation and metastasis, for treating macrophage
 CC giant cells in bacterially-induced granuloma. Sequences of the invention
 CC are useful in the preparation of a medicament for use in a method of
 CC therapy of a condition or disease associated with EMR2 polypeptide and in
 CC the preparation of a diagnostic agent for use in the method of diagnosis
 CC of a condition or disease associated with EMR2 polypeptide. Antibodies
 CC against EMR2 are useful for treating infections such as bacterial,
 CC fungal, protozoan and viral infections, particularly infections caused by
 CC HIV-1 or HIV-2, pain, cancers, asthma, anorexia, Parkinson's disease,
 CC bulimia, hypotension, acute heart failure, hypertension, osteoporosis,
 CC urinary retention, angina pectoris, myocardial infarction, ulcers,
 CC allergies, benign prostatic hypertrophy, psychotic and neurological
 CC disorders including anxiety, schizophrenia, manic depression, delirium,
 CC dementia, severe mental retardation, dyskinesias such as Huntington's
 CC disease or Gilles de la Tourette's syndrome. The present DNA sequence is a
 CC PCR primer which is used for identifying the 7 transmembrane domain (7TM)
 CC of EMR2 transcript
 XX

SQ Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other;
 Query Match 66.4%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 85;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 727 TCCGAGGAGAACAGACACC 747
 Db 22 TCCGAGGAGAACAGACACC 2

RESULT 20
 AAA85677/c
 ID AAA85677 standard; DNA; 19 BP.
 XX
 AC AAA85677;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Cyclin B1 ribozyme binding site #6.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX Mammalia.
 XX WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US028772.
 XX
 PR 04-DEC-1998; 98US-0110954P.
 XX

PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 DR WPI; 2000-412314/35.
 XX

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 XX
 PS Disclosure; Page 96; 109pp; English.
 XX

XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX

SQ Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 65.5%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 86;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAACACCG 748
 Db 19 GAGAAACAGAACACCG 4

RESULT 21
 AAH60839/c
 ID AAH60839 standard; DNA; 19 BP.
 XX
 AC AAH60839;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Cyclin B1 ribozyme binding site SEQ ID NO:3263.
 XX

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX

XX Homo sapiens.
 OS Synthetic.
 XX
 XX WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US029500.
 XX
 PR 26-OCT-1999; 99US-0161532P.
 XX
 XX (IMMU-) IMMUSOL INC.
 XX
 XX Robbins JM, Tritz R;
 XX
 XX WPI; 2001-300427/31.
 XX

XX Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 PT

XX Example 1; Page 309; 408pp; English.

PS The present invention describes a method for treating a proliferative

XX skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in

CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a

CC nucleic acid molecule (II) comprising a promoter operably linked to a

CC nucleic acid segment encoding (I). (I) can have antipsoriatic,

CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulnary, keratolytic and virucide activities, and

CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin

CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of

CC prematurity and retinal detachment, and for treating and preventing

CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn

CC scar. AAH57577 to AAH62099 represent sequences used in the

CC exemplification of the present invention

XX

XX Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 65.5%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 86;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAACAGACACCG 748

||||| |||||

Db 19 GAGAGCAGACACCG 4

RESULT 22

AAH5941/C

ID AAH5941 standard; DNA; 19 BP.

XX

AC AAH5941;

XX

XX 04-DEC-2000 (first entry)

XX

DE Cdc 25 hs ribozyme binding site #49.

XX

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

XX

XX Mammalia.

OS

XX WO200032765-A2.

XX

PD 08-JUN-2000.

XX

XX 06-DEC-1999; 99WO-US028772.

XX

XX 04-DEC-1998; 98US-0110954P.

XX

XX (IMMU-) IMMUSOL INC.

PA

XX

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

PI

XX

XX WPI; 2000-412314/35.

DR

XX

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves

PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,

PT PCNA and Cyclin B1.

PT

XX

XX Disclosure; Page 100; 109pp; English.

PS

XX

XX The present invention relates to a hairpin or hammerhead ribozyme,

XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase

CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.

CC

CC Representative examples of ribozyme recognition sites are given in

CC AAA82415 to AAA86787. The ribozyme of the invention is useful for

CC inhibiting restenosis by introduction of the ribozyme into cells. The

CC ribozyme is resistant to endonuclease activity and hence is efficient in

XX restenosis treatment

XX Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;

Query Match 64.5%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 92;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAGACACC 747

||||| |||||

Db 19 CCAGGAGAAACAGACACC 1

RESULT 23

AAH61103/C

ID AAH61103 standard; DNA; 19 BP.

XX

AC AAH61103;

XX

XX 10-SEP-2001 (first entry)

XX

XX Cdc25 hs ribozyme binding site SEQ ID NO:3527.

XX

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;

XX recognition site; target; ribozyme binding site; eye disease; vulnary;

XX proliferative disease; skin disease; psoriasis; diabetic retinopathy;

XX cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;

XX matrix metalloproteinase; growth factor; reductase; scarring; cystostatic;

XX antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;

XX antisickling; ophthalmological; keratolytic; gene therapy; viral wart;

XX atopic dermatitis; actinic keratosis; squamous cell carcinoma;

XX basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;

XX sickle cell retinopathy; ss.

XX

OS Homo sapiens.

OS

XX Synthetic.

XX

XX WO200130362-A2.

XX

XX 03-MAY-2001.

XX

XX 26-OCT-2000; 2000WO-US029500.

XX

XX 26-OCT-1999; 99US-0161532P.

XX

XX (IMMU-) IMMUSOL INC.

PA

XX

XX Robbins JM, Tritz R;

PI

XX

XX WPI; 2001-300427/31.

DR

XX

XX Treating proliferative skin or eye diseases and scarring, using ribozymes

PT that cleave RNA encoding cytokines involved in inflammation, matrix

PT metalloproteinases, growth factors and cell-cycle dependent kinases.

PT

XX

XX Example 1; Page 328; 408pp; English.

PS

XX

XX The present invention describes a method for treating a proliferative

XX skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in

CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a

CC nucleic acid molecule (II) comprising a promoter operably linked to a

CC nucleic acid segment encoding (I). (I) can have antipsoriatic,

CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulnary, keratolytic and virucide activities, and

CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin

CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloïd, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAHS7577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;

Query Match 64.5%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 92;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAGAACACC 747
 Db 19 CCAGGAGAAACAAACACC 1

RESULT 24
 AAD30255
 ID AAD30255 standard; DNA; 21 BP.

AC AAD30255;
 XX
 DT 17-MAY-2002 (first entry)

XX Human PKD1 gene mutation detecting nested PCR primer, 5FL.

XX Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;
 KW acquired cystic disease; transgenic animal; PCR primer; ss.

XX Homo sapiens.

XX WO200206529-A2.

XX 24-JAN-2002.

XX 13-JUL-2001; 2001WO-US022035.

XX 13-JUL-2000; 2000US-0218261P.

PR 13-APR-2001; 2001US-0283691P.

PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Germino GG, Watnick TJ, Phakdeekitcharoen B;

XX WPI; 2002-179805/23.

XX Novel primer for diagnosing polycystic kidney disease-associated
 PT disorder, comprises regions having sequence that selectively hybridizes
 PT to polycystic kidney disease gene sequence.

XX Claim 6; Page 100; 192pp; English.

XX The present invention relates to compositions and methods useful for the
 CC identification and detection of polycystic kidney disease (PKD) gene
 CC mutations. The invention also relates to primers comprising a 5' region
 CC having a sequence that selectively hybridizes to a PKD1 gene sequence and
 CC optionally, to a PKD1 homologue sequence and an adjacent 3' region having
 CC a sequence that selectively hybridizes to a PKD1 gene sequence and not to
 CC a PKD1 homologue sequence. Primer pairs of the invention are useful for
 CC detecting the presence or absence of a mutation in a PKD1 polynucleotide
 CC in a sample, for identifying a subject at risk for a PKD1-associated
 CC disorder such as autosomal dominant polycystic kidney disease (ADPKD) or
 CC acquired cystic disease and for diagnosing a PKD1-associated disorder in
 CC a subject. They are useful for selectively amplifying a region of a PKD1
 CC gene. PKD1 DNA fragments are useful detecting the presence of a mutant
 CC PKD1 polynucleotide in a sample, as a probe for an amplification
 CC reaction, in hybridisation or amplification assays of biological samples
 CC to detect abnormalities of PKD1 expression and for engineering transgenic
 CC animals. The present sequence is a PCR primer used to detect mutation in
 CC human PKD1 gene

SQ Sequence 21 BP; 7 A; 6 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 64.5%; Score 14.2; DB 1; Length 21;
 Best Local Similarity 84.2%; Pred. No. 96;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCAGGAGAAACAGAACACC 746
 Db 3 GCAGGAGAGAGAGAACCC 21

RESULT 25
 AAV14110/C
 ID AAV14110 standard; DNA; 18 BP.

XX AAV14110;

XX 27-AUG-2003 (revised)

DT 19-MAY-1998 (first entry)

XX Probe HBP276 for RT pol region of HBV.

XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.

XX Synthetic.

XX Hepatitis B virus.

XX WO9740193-A2.

XX 30-OCT-1997.

XX 21-APR-1997; 97WO-EP002002.

XX 19-APR-1996; 96EP-00870053.

XX (INNO-) INNOGENETICS NV.

XX Stuyver L, Rossau R, Maertens G;

XX WPI; 1997-535867/49.

XX Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.

XX Claim 5; Fig 1; 80pp; English.

XX This sequence represents a probe for the RT pol region of hepatitis b
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (I) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (I) with a combination of at least
 CC 2 nucleotide probes, which are applied to known locations on a solid
 CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 18 BP; 1 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAG 741
Db 18 GCCAGGAGAACAG 5
RESULT 26
AAV02721
ID AAV02721 standard; DNA; 18 BP.
AC AAV02721;
XX 19-MAY-1998 (first entry)
DT Human Class I HLA gene probe GE2-183.
DE Human leukocyte antigen class I gene; allele testing; probe; donor;
KW tissue matching; recipient; graft rejection; class typing; ds.
XX Synthetic.
OS Homo sapiens.
XX WO9723645-A1.
XX 03-JUL-1997.
XX 04-JAN-1996; 96WO-US000362.
XX 04-JAN-1996; 96WO-US000362.
XX (SLOK) SLOAN KETTERING INST CANCER RES.
PA Yang SY, Cereb N;
PI WPI; 1997-351080/32.
DR DNA-based human leukocyte antigen class I gene typing method - useful for
PT tissue matching and prevention of graft versus host disease.
XX Disclosure; Page 10; 89pp; English.
XX AAV02716-V02738 are hybridisation probes used in a novel method for
CC testing tissue samples to determine the allelic type of a human leukocyte
CC antigen (HLA) class I gene in the sample. The HLA Class I gene is
CC selected from among HLA-A, -B and -C genes. The method comprises of
CC treating the tissue sample to obtain nucleic acid polymers suitable for
CC amplification then combining these polymers with a first primer which
CC hybridises with a portion of intron 1 or intron 3 of the HLA Class I gene
CC and a second primer which hybridises with a different portion of the HLA
CC Class I gene under conditions suitable for amplification to obtain an
CC amplified product. The product is then evaluated to determine the allelic
CC type of the HLA-Class I gene. The method is useful for tissue matching
CC HLA class I antigens between donors and recipients and hence for
CC preventing graft versus host disease
XX
SQ Sequence 18 BP; 7 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 62.7%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;
QY 731 AGGAGAACAGAACACC 747
Db 2 AGGAGAACAGAACACC 18
RESULT 27
AA11105
ID AA11105 standard; DNA; 18 BP.
XX AA11105;
AC AA11105;
XX 28-JUL-2000 (first entry)
DT

DE Hybridisation probe GE2-183 for typing HLA Class I genes.
XX Tissue sample testing; allelic typing; human leukocyte antigen;
KW PCR primer; probe; hybridisation; intron; amplification; ss;
KW allelic variation; non-classical HLA class I gene; exon.
XX Homo sapiens.
OS US6030775-A.
XX 29-FEB-2000.
PD 22-DEC-1995; 95US-00577081.
PF 22-DEC-1995; 95US-00577081.
XX 22-DEC-1995; 95US-00577081.
XX (CERE/) CERE B N.
PA (YANG/) YANG S Y.
XX Cereb N, Yang SY;
PI WPI; 2000-223159/19.
DR Testing a tissue sample to determine the allelic type of a human
XX leukocyte antigen class I gene comprises amplification of nucleic acid
PT polymers with primers which flank a region including an allelic variation
PT of the HLA class I gene.
XX Disclosure; Col 8; 90pp; English.
XX The invention relates to a method (I) for testing a tissue sample to
CC determine the allelic type of a human leukocyte antigen (HLA) class I
CC gene in the sample, where the HLA class I gene is selected from HLA-A,
CC HLA-B or HLA-C, by: (a) treating the tissue sample to obtain nucleic acid
CC polymers suitable for amplification; (b) combining the nucleic acid
CC polymers with a primer which hybridizes with a portion of intron 1 or
CC intron 3 of the HLA class I gene, and a second primer which hybridizes
CC with a different portion of the HLA class I gene and performing
CC amplification, where the primers flank a region including at least one
CC site of allelic variation in at least one of exons 2 or 3 of the HLA
CC class I gene and where the first primer is a locus specific primer which
CC hybridizes with intron 1 or 3 of only one of the HLA class I genes; and
CC (c) evaluating the amplified product to determine the allelic type of the
CC HLA class I gene. The method is useful for testing a tissue sample to
CC determine the allelic type of a classical or non-classical HLA class I
CC gene in the sample. The sequences AAA1039-Alt122 represent consensus
CC sequences of introns and exons of the HLA genes and primers and probes
CC used to isolate and analyse the HLA genes
XX
SQ Sequence 18 BP; 7 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 62.7%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;
QY 731 AGGAGAACAGAACACC 747
Db 2 AGGAGAACAGAACACC 18
RESULT 28
AAZ57075/c
ID AAZ57075 standard; DNA; 20 BP.
XX AAZ57075;
AC AAZ57075;
XX 19-MAY-2000 (first entry)
DT Murine melanocortin receptor MC3-R amplifying primer.
DE Medicament; agonist; melanocortin receptor type 3; ACTH; PMN; MC3-R;
XX adrenocorticotrophic hormone; neutrophil chemoattractant; antigen;
KW polymorphonuclear cell; septic shock; skin disorder; antiarthritic;
KW

KW melanocortin receptor; anti-inflammatory; anti-inflammatory; PCR primer; ss.
 OS Mus sp.
 XX WO200005263-A2.
 PN 03-FEB-2000.
 PD 22-JUL-1999; 99WO-GB002392.
 XX 24-JUL-1998; 98GB-00016234.
 XX (HARV-) HARVEY RES LTD WILLIAM.
 PA Perretti M, Getting S, Flower R;
 XX WPI; 2000-182651/16.
 XX Inhibition of neutrophil chemoattractant production, inhibition of
 PT polymorphonuclear cell accumulation or reduction/treatment of
 PT inflammation using compounds comprising the peptide sequence HFRW.
 XX Disclosure; Page 8; 20pp; English.
 PS The invention relates to the use of a compound comprising an amino acid
 CC sequence His-Phe-Arg-Tip (HFRW) in the manufacture of a medicament and/or
 CC an agonist of melanocortin receptor type 3 (MC3-R) where the compound is
 CC not adrenocorticotrophic hormone (ACTH)1-39. The compounds are used to
 CC inhibit neutrophil chemoattractant production, polymorphonuclear cell
 CC (PMN) accumulation or reduction/treatment of inflammation. Especially,
 CC these compounds are agonists of the MC3-R. The inflammatory response/
 CC disease is selected from gout, gouty arthritis, rheumatoid arthritis,
 CC asthma, reperfusion injury or damage, stroke, myocardial infarction,
 CC septic shock, or a skin disorder. Sequences AA257073-80 represent PCR
 CC primers used for amplifying murine melanocortin receptors
 XX
 SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 62.7%; Score 13.8; DB 1; Length 20;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 732 GGAGAAACAGACACCG 748
 DB 19 GGAGAAACAGACAGACAG 3
 RESULT 29
 ID ABT05166/c
 AC ABT05166; standard; DNA; 20 BP.
 XX ABT05166;
 XX 11-OCT-2002 (first entry)
 DE TNFR1 expression modulation related antisense oligo SEQ ID No 196.
 XX Antisense compound; tumour necrosis factor receptor 1; liver disease;
 KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
 KW mouse; murine; ds.
 XX Mus sp.
 OS WO200248168-A1.
 PN 20-JUN-2002.
 PD 22-OCT-2001; 2001WO-US051224.
 XX 24-OCT-2000; 2000US-00695451.
 XX (ISIS-) ISIS PHARM INC.
 PA This sequence represents a probe for the RT pol region of hepatitis b
 CC

PI Baker BF, Cowseert LM, Zhang H, Dean NM;
 XX WPI; 2002-583481/62.
 XX Novel antisense compound targeted to nucleic acid molecule encoding tumor
 PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
 PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
 XX Example 21; Page 61; 121pp; English.
 XX The invention relates to an antisense compound 8 to 30 nucleotides in
 CC length targeted to nucleic acid molecule encoding tumour necrosis factor
 CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
 CC TNFR1. The antisense compound is useful for inhibiting the expression of
 CC TNFR1 in cells or tissues. The antisense compound is also useful for
 CC treating an animal (preferably human) having a disease or condition
 CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
 CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
 CC the expression of TNFR1. The antisense compound is useful for
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
 CC This polynucleotide sequence represents a mouse oligonucleotide relating
 CC to the TNFR1 of the invention
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 61.8%; Score 13.6; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 727 TCCAGGAGAAACAGACAC 746
 DB 20 TGTAGGAGACTCAGACAC 1
 RESULT 30
 ID AAV14107/c
 AC AAV14107; standard; DNA; 18 BP.
 XX AAV14107;
 XX 27-AUG-2003 (revised)
 DT 19-MAY-1998 (first entry)
 XX Probe HBP273 for RT pol region of HBV.
 DE Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.
 XX Synthetic.
 OS Hepatitis B virus.
 XX WO9740193-A2.
 XX 30-OCT-1997.
 XX 21-APR-1997; 97WO-EP002002.
 XX 19-APR-1996; 96EP-00870053.
 XX (INNO-) INNOGENETICS NV.
 XX Stuyver L, Rossau R, Maertens G;
 PI WPI; 1997-535867/49.
 XX Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.
 XX Claim 5; Fig 1; 80pp; English.
 XX This sequence represents a probe for the RT pol region of hepatitis b
 CC

virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polynucleic acids (I) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (I) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV genotype specific target sequences, or their complements or U for T homologues; (c) detecting the hybrids formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the differential hybridisation signal(s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs, e.g. lamivudine and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

SQ Sequence 18 BP; 1 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 60.9%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGA 742
 Db 18 GCCAGGAGAAACGGA 4

RESULT 31
 AAV14104/c
 ID AAV14104 standard; DNA; 18 BP.

XX AAV14104;

AC 27-AUG-2003 (revised)
 DT 19-MAY-1998 (first entry)

DE Probe HBP270 for RT pol region of HBV.

XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 XW mutation detection; ss.

OS Synthetic.
 OS Hepatitis B virus.

PN WO9740193-A2.

XX 30-OCT-1997.

PF 21-APR-1997; 97WO-EP002002.

XX 19-APR-1996; 96EP-00870053.

XX (INNO-) INNOGENETICS NV.

XX Stuyver L, Rossau R, Maertens G;

XX WPI; 1997-535867/49.

XX Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.

PS Claim 5; Fig 1; 80pp; English.

XX This sequence represents a probe for the RT pol region of hepatitis b
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (I) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1

CC suitable primer pair; (b) hybridising (I) with a combination of at least
 CC 2 nucleotide probes, which are applied to known locations on a solid
 CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample.
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

SQ Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 60.9%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGA 742
 Db 18 GCCAGGAGAAACAGA 4

RESULT 32
 AAV14106/c
 ID AAV14106 standard; DNA; 18 BP.

XX AAV14106;

XX 27-AUG-2003 (revised)
 DT 19-MAY-1998 (first entry)

DE Probe HBP272 for RT pol region of HBV.

XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 XW mutation detection; ss.

OS Synthetic.

OS Hepatitis B virus.

PN WO9740193-A2.

XX 30-OCT-1997.

XX 21-APR-1997; 97WO-EP002002.

XX 19-APR-1996; 96EP-00870053.

XX (INNO-) INNOGENETICS NV.

XX Stuyver L, Rossau R, Maertens G;

XX WPI; 1997-535867/49.

XX Detection and/or genetic analysis of hepatitis B virus - specifically
 PI genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.

XX Claim 5; Fig 1; 80pp; English.

XX This sequence represents a probe for the RT pol region of hepatitis b
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (I) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (I) with a combination of at least
 CC 2 nucleotide probes, which are applied to known locations on a solid
 CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T

CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 60.9%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
 DB 18 GCCATGAGAAACAGA 4

RESULT 33
 AAX77255/c
 ID AAX77255 standard; DNA; 20 BP.

XX AC AAX77255;
 XX
 DT 27-AUG-2003 (revised)
 DT 04-AUG-1999 (first entry)
 DE Hepatitis B virus genomic DNA amplifying primer BF108.
 XX
 KW Polymerase chain reaction; nested PCR; viral; mutation detection;
 KW lamivudine resistance; hepatitis B virus; PCR primer; ss.

XX Synthetic.
 XX Hepatitis B virus.
 XX JP11127860-A.
 XX 18-MAY-1999.
 PF 28-OCT-1997; 97JP-00296042.
 PF 28-OCT-1997; 97JP-00296042.
 PR (SAYA/) SAYAMA K.
 DR WPI; 1999-350321/30.

PT A highly sensitive detection method for detecting lamivudine resistant
 PT hepatitis B virus - using nested PCR.

XX Example; Page 6; 11pp; Japanese.
 XX The invention provides a highly sensitive method for detecting variation
 CC of viruses using a 2-step polymerase chain reaction (nested PCR) regime.
 CC The method comprises: (1) amplification of a predetermined region of
 CC viral DNA in the first round of PCR; (2) treatment of the amplified
 CC product with a restriction enzyme capable of cleavage of a product
 CC derived from the wild type virus, (3) amplification of the viral DNA with
 CC a second round of PCR using a primer designed to introduce a mismatch
 CC base, to form a restriction enzyme recognition site in the amplified
 CC product from the viral mutant, (4) treatment of the amplified product
 CC with a restriction enzyme capable of cleavage of the amplified product
 CC derived from the viral mutant, (5) detection of mutation of viruses by
 CC investigation of the restriction pattern. The method allows simple and
 CC highly sensitive detection of mutation in viral genomes using 2-step
 CC nested PCR method in a short period of time. Sequences AAX77255-263
 CC represent PCR primers used for the detection of lamivudine resistant
 CC hepatitis B virus by the method of the invention. (Updated on 27-AUG-2003
 CC to correct OS field.)
 XX
 SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 60.9%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
 DB 17 GCCAGGAGAAACGGA 3

RESULT 34
 AAA85942/c
 ID AAA85942 standard; DNA; 19 BP.

XX AC AAA85942;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Cdc 25 hs ribozyme binding site #50.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX Mammalia.
 XX WO200032765-A2.

XX 08-JUN-2000.

PF 06-DEC-1999; 99WO-US028772.

PR 04-DEC-1998; 98US-0110954P.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.

XX Disclosure; Page 100; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX
 SQ Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAGACAC 746
 DB 18 CCAGGAGAAACAAAC 1

RESULT 35
 AAA85940/c
 ID AAA85940 standard; DNA; 19 BP.

XX AAA85940;

XX 04-DEC-2000 (first entry)

XX Cdc 25 hs ribozyme binding site #48.

XX

KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX PS Disclosure; Page 100; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX SQ Sequence 19 BP; 1 A; 3 C; 4 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 730 CAGGAGAAACAGAACACC 747
DB 19 CAGGAGAAACAAACACC 2
RESULT 36
AAA85679/c
ID AAA85679 standard; DNA; 19 BP.
XX AC AAA85679;
XX DT 04-DEC-2000 (first entry)
XX DE Cyclin B1 ribozyme binding site #8.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves

PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX PS Disclosure; Page 96; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX SQ Sequence 19 BP; 0 A; 8 C; 3 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 1.3e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 728 GCCAGGAGAAACAGAACCA 745
DB 18 GCGGGGAGAGCGAACA 1
RESULT 37
AAH61102/c
ID AAH61102 standard; DNA; 19 BP.
XX AC AAH61102;
XX DT 10-SEP-2001 (first entry)
XX DE Cdc25 hs ribozyme binding site SEQ ID NO:3526.
XX KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200130362-A2.
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029500.
XX PR 26-OCT-1999; 99US-0161532P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Robbins JM, Tritz R;
XX DR WPI; 2001-300427/31.
XX PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX PS Example 1; Page 328; 408pp; English.
XX CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (II). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiscikling,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (II) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 1 A; 3 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 730 CAGGAGAAACAGAACACC 747
 |||||
 Db 19 CAGGAGAAACAAACC 2

RESULT 38
 AAH61104/c
 ID AAH61104 standard; DNA; 19 BP.
 XX
 AC AAH61104;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Cdc25 hs ribozyme binding site SEQ ID NO:3528.
 XX
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antiscikling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US029500.
 XX
 XX 26-OCT-1999; 99US-0161532P.
 XX
 XX (IMMU-) IMMUSOL INC.
 XX
 XX Robbins JM, Tritz R;
 XX
 DR WPI; 2001-300427/31.
 XX
 PT Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 PS Example 1; Page 328; 408pp; English.
 XX
 CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (II). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiscikling,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (II) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;
 Query Match 60.0%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 729 CCAGGAGAAACAGAACAC 746
 |||||
 Db 18 CCAGGAGAAACAAAC 1

RESULT 39
 AAH60841/c
 ID AAH60841 standard; DNA; 19 BP.
 XX
 AC AAH60841;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Cyclin B1 ribozyme binding site SEQ ID NO:3265.
 XX
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antiscikling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US029500.
 XX
 XX 26-OCT-1999; 99US-0161532P.
 XX
 XX (IMMU-) IMMUSOL INC.
 XX
 XX Robbins JM, Tritz R;
 XX
 DR WPI; 2001-300427/31.
 XX
 PT Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 PS Example 1; Page 309; 408pp; English.
 XX

CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulvar, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AA457577 to AA462099 represent sequences used in the
 CC exemplification of the present invention

SQ Sequence 19 BP; 0 A; 8 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGAAC 745
 Db 18 GCGGGGAGAGCAGAAC 1

RESULT 40

AAZ05107

ID AAZ05107 standard; DNA; 20 BP.

XX AC AAZ05107;

XX DT 07-OCT-1999 (first entry)

XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 XX paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
 XX nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 XX bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX OS Synthetic.

XX SS Chlamydia trachomatis.

XX FN WO9928475-A2.

XX PD 10-JUN-1999.

XX XX 27-NOV-1998; 98WO-IB001939.

XX PR 28-NOV-1997; 97FR-00015041.

XX PR 17-DEC-1997; 97FR-00016034.

XX PR 04-NOV-1998; 98US-0107077P.

XX PA (GEST) GENSET.

XX XX Griffais R;

XX DR WPI; 1999-371125/31.

XX PT Genome sequence of Chlamydia trachomatis.

XX PS Disclosure; Page 1743; 1755pp; English.

XX CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY3754-Y3794) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also

CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conjunctivitis; genital diseases such as nongonococcal urethritis;
 CC epididymitis; cervicitis; salpingitis; perihepatitis; bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases

SQ Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 729 CCAGGAGAAACAGAAC 746

Db 1 CCAGGAGAGCTAAGAAC 18

RESULT 41

ABV80008/c

ID ABV80008 standard; DNA; 17 BP.

XX AC ABV80008;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 1254.

XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

XX KW human testis expressed Patched like protein; testis; adrenal; liver;

XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX XX 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX DR WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 XX for identifying agonist and antagonist and specific binding partners, and
 XX for treating subjects having defects in HTPL.

XX PS Example 2; Page 228; 718pp; English.

XX CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
 CC has two isoforms with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was

CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 58.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 727 TGCCAGGAGAAACAGA 742
 ||||| |||||
 Db 17 TGCCAGGTGAACACA 2
 RESULT 42
 ABV80009/c
 ID ABV80009 standard; DNA; 17 BP.
 AC ABV80009;
 XX
 DT 03-JAN-2003 (first entry)
 XX
 DE Human HTPL scanning oligonucleotide SEQ ID 1255.
 XX
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FN EP1229046-A2.
 XX
 PD 07-AUG-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 XX
 PR 30-JAN-2001; 2001WO-US0000663.
 PR 30-JAN-2001; 2001WO-US0000664.
 PR 30-JAN-2001; 2001WO-US0000665.
 PR 30-JAN-2001; 2001WO-US0000667.
 PR 30-JAN-2001; 2001WO-US0000668.
 PR 30-JAN-2001; 2001WO-US0000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX
 PA (AECOM-) ABOMICA INC.
 XX
 PI Zhan J;
 XX
 DR WPI; 2002-676582/73.
 XX
 PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.
 XX
 PS Example 2; Page 228; 718pp; English.
 XX
 CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar

CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 58.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 727 TGCCAGGAGAAACAGA 742
 ||||| |||||
 Db 16 TGCCAGGTGAACACA 1
 RESULT 43
 AAZ88792
 ID AAZ88792 standard; DNA; 19 BP.
 XX
 AC AAZ88792;
 XX
 DT 18-MAY-2000 (first entry)
 XX
 DE Human HLA Cw*07 Gene PCR primer Cw*07 forward.
 XX
 KW Human; HLA; tumor cell; major histocompatibility complex; MHC; vaccine;
 KW prophylaxis; treatment; lymphocyte; HLA; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200004918-A2.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-DE002280.
 XX
 PR 21-JUL-1999; 98DE-01032840.
 XX
 PA (KERK/) KERKMANN-TUCEK A.
 XX
 PI Kerkmann-Tucek A;
 XX
 DR WPI; 2000-182538/16.
 XX
 PT Tumor cells expressing human MHC I and II genes, methods of producing
 PT these and vaccines for immunotherapy of tumors.
 XX
 PS Example 3; Page 8; 17pp; German.
 XX
 CC This invention describes novel tumor cells (I), with a combination of
 CC major histocompatibility (MHC) I and II genes occurring in humans. The
 CC tumor cells, tumor cell library or vaccine described in the invention can
 CC be used for the prophylaxis or treatment of tumor diseases. AAZ88790-
 CC Z88805 represent PCR primers used to amplify the human lymphocyte HLA
 CC molecules described in the method of the invention.
 XX
 SQ Sequence 19 BP; 7 A; 5 C; 7 G; 0 T; 0 U; 0 Other;
 Query Match 58.2%; Score 12.8; DB 1; Length 19;
 Best Local Similarity 87.5%; Pred. No. 1.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 729 CCAGGAGAAACAGAC 744
 ||||| |||||

Db	4	CCGGGAGACAGACAAC	19
RESULT 44			
ABK15585/c			
ID	ABK15585	standard; cDNA; 19 BP.	
XX			
AC	ABK15585;		
XX			
XX	08-MAY-2002	(first entry)	
XX			
DE	Melanocortin 4 receptor (MC4R)	isolation, reverse PCR primer.	
XX			
KW	Melanocortin 4 receptor; MC4R; G-protein coupled receptor; appetite;		
KW	metabolic disorder; cachexia; anorexia; weaning-induced inappetence;		
KW	growth; diabetes; cancer; renal failure; cardiac disease; endotoxaemia;		
KW	fever; hepatic lipidosis; infection; inflammation; post partum sow;		
KW	dairy cow; livestock; poultry; shipping stress; crowding stress; obesity;		
KW	vaccine; PCR; primer; ss.		
XX			
OS	Felidae.		
OS	Canidae.		
XX			
FN	EP1167386-A1.		
XX			
PD	02-JAN-2002.		
XX			
XX	26-JUN-2001; 2001EP-00305509.		
PF			
XX			
PR	26-JUN-2000; 2000US-0213909P.		
XX			
PA	(PF12) PFIZER PROD INC.		
XX			
PI	Hickman MA, Houseknecht KL, Robertson AS;		
PI	WPI; 2002-156598/21.		
DR			
XX			
PT	Novel canine or feline melanocortin 4 receptor polypeptide for screening		
PT	modulator compounds useful for treating cachexia, anorexia, diabetes and		
PT	cancer.		
XX			
PS	Disclosure; Page 10; 73pp; English.		
XX			
CC	The invention describes a substantially pure canine or feline		
CC	melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be		
CC	used in the treatment of appetite-related or metabolic disorders		
CC	including cachexia, anorexia or weaning-induced inappetence and growth		
CC	lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,		
CC	fever, hepatic lipidosis, infection or inflammation, in a post partum		
CC	sow, dairy cow, companion animal, livestock animal, poultry animal,		
CC	animal suffering from shipping or crowding stress, lactating animal,		
CC	obese animal or a gravid animal. (I) is useful in the generation of		
CC	antibodies, as reagents in diagnostic assays, identification of other		
CC	cellular gene products involved in the regulation of appetite in animals,		
CC	as reagents in assays for screening for compounds that can be used in the		
CC	treatment of appetite disorders in animals. A ligand of MC4R is useful		
CC	for elaborating the biological function of MC4R gene product and for		
CC	ameliorating appetite disorders and metabolic disorders, in animals. This		
CC	sequence represents the reverse primer used with primer ABK15584 to		
CC	isolate feline and canine melanocortin 4 receptor (MC4R) clones, a G-		
CC	protein coupled receptor described in the method of the invention		
XX			
SQ	Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;		
Query Match	57.3%;	Score 12.6; DB 1; Length 19;	
Best Local Similarity	78.9%;	Pred. No. 1.6e+02;	
Matches 15; Conservative	0;	Mismatches 4; Indels 0; Gaps 0;	
QY	728	GCACGAGAGAACAGACAAC	746
Db	19	GCAAGAGAGCTACAGATCAC	1

RESULT 46

ABK15582/c
ID ABK15582 standard; cDNA; 19 BP.

XX AC XX
XX ABK15582;

XX DT 08-MAY-2002 (first entry)

XX DE Melanocortin 4 receptor (MC4R) detection, reverse PCR primer.

XX KW Melanocortin 4 receptor; MC4R; G-protein coupled receptor; appetite;
metabolic disorder; cachexia; anorexia; weaning-induced inappetence;
growth; diabetes; cancer; renal failure; cardiac disease; endotoxaemia;
fever; hepatic lipidosis; infection; inflammation; post partum sow;
dairy cow; livestock; poultry; shipping stress; crowding stress; obesity;
vaccine; PCR; primer; ss.

XX OS Felidae.
OS Canidae.

XX PN EP1167386-A1.

XX PD 02-JAN-2002.

XX PF 26-JUN-2001; 2001EP-00305509.

XX PR 26-JUN-2000; 2000US-0213903P.

XX PA (PFIZ) PFIZER PROD INC.

XX PI Hickman MA, Houseknecht KL, Robertson AS;

XX DR WPI; 2002-156598/21.

XX PT Novel canine or feline melanocortin 4 receptor polypeptide for screening
modulator compounds useful for treating cachexia, anorexia, diabetes and
cancer.

XX PS Example 1; Page 27; 73pp; English.

CC The invention describes a substantially pure canine or feline
melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be
used in the treatment of appetite-related or metabolic disorders
including cachexia, anorexia or weaning-induced inappetence and growth
lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,
fever, hepatic lipidosis, infection or inflammation, in a post partum
sow, dairy cow, companion animal, livestock animal, poultry animal,
animal suffering from shipping or crowding stress, lactating animal,
these animal or a gravid animal. (I) is useful in the generation of
antibodies, as reagents in diagnostic assays, identification of other
cellular gene products involved in the regulation of appetite in animals,
as reagents in assays for screening for compounds that can be used in the
treatment of appetite disorders in animals. A ligand of MC4R is useful
for elaborating the biological function of MC4R gene product and for
ameliorating appetite disorders and metabolic disorders, in animals. This
sequence represents the reverse primer used with primer ABK15581 to
isolate feline and canine melanocortin 4 receptor (MC4R) clones, a G-
protein coupled receptor described in the method of the invention

XX SQ Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 57.3%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Fred.No.1.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 728 GCCAGGAGAAACAGAACAC 746
||| ||||| ||||| |||||
DB 19 GCAGGAGCTACAGATCAC 1

RESULT 46

AAS56856/c
ID AAS56856 standard; DNA; 16 BP.

XX AC AAS56856;
 XX XX
 XX DT 16-JAN-2002 (first entry)
 XX XX
 XX DE Validation ribozyme DNA sequence #30.
 XX XX
 XX KW Human; BRCA-1 regulator; ribozyme; BR1; RNA target recognition; probe;
 XX KW cytosolic; RNA cleavage; tumour suppressor; PCR primer; CHLR2; AF6; BR2;
 XX KW inhibitor dominant negative 4; breast basic conserved protein 1; BBC1;
 XX KW BR3; ID4; cancer; proliferative disorder; tumour proliferation; ss.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX FN WO200170982-A2.
 XX XX
 XX PD 27-SEP-2001.
 XX XX
 XX PF 23-MAR-2001; 2001WO-US009559.
 XX XX
 XX PR 23-MAR-2000; 2000US-00536058.
 XX XX
 XX PA (IMMU-) IMMUSOL INC.
 XX PA (BEGE/) BEGER C.
 XX PI Begger C, Barber J, Wong-Staal F;
 XX XX
 XX DR WPI; 2001-611503/70.
 XX XX
 XX PT Novel polypeptides that are the regulators of BRCA-1, useful for treating
 XX PT cancer and diagnosing the presence of neoplastic cells in biological
 XX PT sample.
 XX PS Disclosure; Fig 8; 97pp; English.
 XX XX
 XX CC Sequences AAS56729-AAS56968 represent DNA encoding BRCA-1 regulators,
 XX CC ribozyme target recognition RNA sequences, DNA fragments encoding the RNA
 XX CC and primers used in the methods of the invention. Hybridisation of
 XX CC ribozymes to their targets results in cleavage of the RNA target. The
 XX CC ribozymes can be used to cleave regulators of the tumour suppressor BRCA-
 XX CC 1, resulting in upregulation or downregulation of BRCA-1 in a cell. The
 XX CC mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor
 XX CC dominant negative 4 (ID4), breast basic conserved protein 1 (BBC1),
 XX CC CHLR2, AF6, BR2 and BR3. Regulation of BRCA-1 is useful for treating and
 XX CC diagnosing cancer and other proliferative disorders. The severity of an
 XX CC incidence of cancer can be lessened by regulating tumour proliferation
 XX CC through modulation of BRCA-1 expression. The sequences of the invention
 XX CC are useful in the development of anti-cancer drugs
 XX XX
 XX SQ Sequence 16 BP; 0 A; 2 C; 6 G; 8 T; 0 U; 0 Other;
 XX XX
 XX Query Match 56.4%; Score 12.4; DB 1; Length 16;
 XX Best Local Similarity 92.9%; Pred. No. 1.6e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX XX
 XX QY 734 AGAACACAGACACC 747
 XX Db |||||
 XX 15 AGAACACAGACACC 2
 XX XX
 XX RESULT 47
 XX AAF56034/C
 XX ID AAF56034 standard; DNA; 17 BP.
 XX AC AAF56034;
 XX XX
 XX DT 18-APR-2001 (first entry)
 XX XX
 XX DE HBV DNA polymerase gene L528M mutation probe HBP-293.
 XX XX
 XX KW HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
 XX KW mutation detection; probe; ss.
 XX XX

OS Hepatitis B virus.
 XX XX
 XX FN WO200104358-A2.
 XX XX
 XX PD 18-JAN-2001.
 XX XX
 XX PF 05-JUL-2000; 2000WO-EP006306.
 XX XX
 XX PR 08-JUL-1999; 99EP-00870148.
 XX PR 13-JUL-1999; 99US-0143546P.
 XX XX
 XX PA (INNO-) INNOGENETICS NV.
 XX XX
 XX PI Stuyver L, Maertens G, Van Geyt C;
 XX XX
 XX DR WPI; 2001-138370/14.
 XX XX
 XX PT Monitoring anti-HBV drug resistance by genetic detection of mutations in
 XX PT DNA polymerase of HBV in patient's sample, involves hybridizing the
 XX PT polynucleic acids of the sample with a probe and detecting the hybrid.
 XX XX
 XX PS Claim 2; Page 9; 64pp; English.
 XX XX
 XX CC The present sequence is a probe used in a method for monitoring anti-
 XX CC hepatitis B virus (HBV) drug resistance in a patient by genetic detection
 XX CC of any one of mutations L528M, M552V/I and/or V/L/M551 in HBV DNA
 XX CC polymerase in a biological sample from the patient. The method is useful
 XX CC in the field of genetic detection of anti-HBV drug resistance during HBV
 XX CC therapy. The method is rapid, reliable and precise
 XX XX
 XX SQ Sequence 17 BP; 1 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 XX XX
 XX Query Match 56.4%; Score 12.4; DB 1; Length 17;
 XX Best Local Similarity 92.9%; Pred. No. 1.6e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX XX
 XX QY 728 GCCAGGAGAAACAG 741
 XX Db |||||
 XX 14 GCCAGGAGAAACGG 1
 XX XX
 XX RESULT 48
 XX ABV80011/C
 XX ID ABV80011 standard; DNA; 17 BP.
 XX AC ABV80011;
 XX XX
 XX DT 03-JAN-2003 (first entry)
 XX XX
 XX DE Human HTPL scanning oligonucleotide SEQ ID 1257.
 XX XX
 XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 XX KW human testis expressed Patched like protein; testis; adrenal; liver;
 XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX FN EP1229046-A2.
 XX XX
 XX PD 07-AUG-2002.
 XX XX
 XX PF 28-JAN-2002; 2002EP-00001167.
 XX XX
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 23-MAY-2001; 2001US-00854781.
 XX PR 09-OCT-2001; 2001US-0327898P.
 XX XX

PA (AEOM-) AEOMICA INC.
XX Zhan J;
PI
XX WPI; 2002-676582/73.
DR
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
XX Example 2; Page 228; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
XX Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
SQ

Query Match 56.4%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAACA 740
Db 14 TGCCAGGTGAACA 1
RESULT 49
ABV80010/c
ID ABV80010 standard; DNA; 17 BP.
AC ABV80010;
XX
XX 03-JAN-2003 (first entry)
XX Human HTPL scanning oligonucleotide SEQ ID 1256.
DE
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX human testis expressed Patched like protein; testis; adrenal; liver;
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX Homo sapiens.
XX
XX EPI229046-A2.
XX
XX 07-AUG-2002.
XX
XX 28-JAN-2002; 2002EP-00001167.
XX
XX 30-JAN-2001; 2001WO-US000653.
XX 30-JAN-2001; 2001WO-US000654.
XX 30-JAN-2001; 2001WO-US000655.
XX 30-JAN-2001; 2001WO-US000656.
XX 30-JAN-2001; 2001WO-US000657.
XX 30-JAN-2001; 2001WO-US000658.
XX 30-JAN-2001; 2001WO-US000659.
XX 23-MAY-2001; 2001US-00864761.

PR 09-OCT-2001; 2001US-0327898P.
XX (AEOM-) AEOMICA INC.
PA
XX Zhan J;
PI
XX WPI; 2002-676582/73.
DR
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
XX Example 2; Page 228; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
XX Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
SQ

Query Match 56.4%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAACA 740
Db 15 TGCCAGGTGAACA 2
RESULT 50
AAQ69166/c
ID AAQ69166 standard; DNA; 18 BP.
XX
XX AAQ69166;
AC
XX 25-MAR-2003 (revised)
XX 14-FEB-1995 (first entry)
DE
XX PCR primer LDGF1 UTR-5'.
XX Leucocyte derived growth factor 2; mitogenic; chemotactic; PDGF;
XX receptors; platelet derived growth factor; coagulation; inflammation;
XX immune response; cell growth; coagulation; amplification; ss.
XX Synthetic.
XX
XX WO9416070-A1.
XX
XX 21-JUL-1994.
XX
XX 07-JAN-1994; 94WO-US000300.
XX
XX 07-JAN-1993; 93US-00001177.
XX 07-JAN-1994; 94US-00179656.
XX (UYSF-) UNIV SOUTH FLORIDA.
XX

PI Grotendorst GR, Iida N;
 XX WPI; 1994-249217/30.
 XX
 XX New leukocyte derived growth factor 2 - having mitogenic and/or
 PT chemotactic activity, partic. for connective tissue cells, used esp. for
 PT wound healing.
 XX
 XX Disclosure; Page 24; 58pp; English.
 XX
 XX The sequence is that of a PCR primer used for the amplification of a
 CC leukocyte derived growth factor 2 having mitogenic and/or chemotactic
 CC activity. LDGF2 reacts with PDGF receptors and can be used in wound
 CC healing, coagulation, inflammation, immune responses and cell growth. See
 CC also AAQ69162-73. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 18 BP; 1 A; 4 C; 3 G; 10 T; 0 U; 0 Other;
 Query Match 56.4%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 732 GGAGAAACAGAAC 745
 DB 16 GCAGAAACAGAAC 3
 RESULT 51
 AAV14112/c
 ID AAV14112 standard; DNA; 18 BP.
 XX
 AC AAV14112;
 XX
 XX
 DT 27-AUG-2003 (revised)
 DT 19-MAY-1998 (first entry)
 XX
 DE Probe HBPr278 for RT pol region of HBV.
 XX
 KW Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.
 XX
 OS Synthetic.
 OS Hepatitis B virus.
 XX
 PN WO9740193-A2.
 XX
 PD 30-OCT-1997.
 XX
 PF 21-APR-1997; 97WO-EP002002.
 XX
 PR 19-APR-1996; 96EP-00870053.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Stuyver L, Rossau R, Maertens G;
 XX
 DR WPI; 1997-535867/49.
 XX
 XX Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.
 XX
 PS Claim 5; Fig 1; 80pp; English.
 XX
 XX This sequence represents a probe for the RT pol region of hepatitis b
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (i) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (i) with a combination of at least
 CC 2 nucleotide probes, which are applied to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC suitable primer pair; (b) hybridising (i) with a combination of at least
 CC 2 nucleotide probes, which are applied to known locations on a solid

CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 18 BP; 2 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 56.4%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAACAG 741
 DB 18 GCCATGAGAACAG 5
 RESULT 52
 AAV14109/c
 ID AAV14109 standard; DNA; 18 BP.
 XX
 AC AAV14109;
 XX
 DT 27-AUG-2003 (revised)
 DT 19-MAY-1998 (first entry)
 XX
 DE Probe HBPr275 for RT pol region of HBV.
 XX
 KW Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.
 XX
 OS Synthetic.
 OS Hepatitis B virus.
 XX
 PN WO9740193-A2.
 XX
 PD 30-OCT-1997.
 XX
 PF 21-APR-1997; 97WO-EP002002.
 XX
 PR 19-APR-1996; 96EP-00870053.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Stuyver L, Rossau R, Maertens G;
 XX
 DR WPI; 1997-535867/49.
 XX
 XX Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.
 XX
 PS Claim 5; Fig 1; 80pp; English.
 XX
 XX This sequence represents a probe for the RT pol region of hepatitis b
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (i) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (i) with a combination of at least
 CC 2 nucleotide probes, which are applied to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC suitable primer pair; (b) hybridising (i) with a combination of at least
 CC 2 nucleotide probes, which are applied to known locations on a solid

CC differential hybridisation signal(s). The composition can be used to
CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC specifically genotype, preCore mutations, vaccine escape mutations and RT
CC gene mutations selected by treatment with drugs, e.g. lamivudine and
CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 18 BP; 1 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAG 741
|||||
Db 18 GCCAGGAGAAACGG 5

RESULT 53
ABT11223/c
ID ABT11223 standard; DNA; 19 BP.
XX
AC ABT11223;
XX
DT 12-DEC-2002 (first entry)
XX
TRC8 related PCR primer SEQ ID No 28.
XX
TRC8; Translocation in Renal cancer from Chromosome 8; fused DNA; 3.2;
KW FHIT/TRC8 fusion DNA; sporadic renal cell carcinoma; TRC8/FHIT; TRC8FHIT;
KW human chromosomal translocation; PCR; primer; ss.
XX
OS Homo sapiens.
XX
US2002106656-A1.
XX
08-AUG-2002.
XX
02-JUL-2001; 2001US-00899833.
XX
12-MAR-1998; 98US-0077723P.
PR
12-MAR-1999; 99US-00268140.
XX
(GEMM/) GEMMILL R M.
PA (DRAB/) DRABKIN H A.
XX
Gemmill RM, Drabkin HA;
XX
WPI; 2002-712395/77.
XX

Novel Translocation in Renal cancer from Chromosome 8 genes, useful for
PT detection of tumors, comprises rearrangements in the t(3;8)(p14.2;q24.1)
PT chromosomal translocation which occurs in renal and thyroid carcinomas.
XX
Claim 9; Page 10; 49pp; English.
XX
The invention relates to an isolated TRC8 (Translocation in Renal cancer
CC from Chromosome 8) nucleic acid molecule, encoding a polypeptide
CC comprising a sequence of 664 amino acids fully defined in the
CC specification and comprising a sequence located in the 5' flanking region
CC to the coding region of TRC8 and a sequence which occurs in certain
CC sporadic renal cell carcinomas. The methods are useful for detecting the
CC presence of the TRC8 gene in a biological sample, detecting alterations
CC to the gene, such as a 3;2 human chromosomal translocation, and fused DNA
CC containing the fused site of TRC8/FHIT. A nucleic acid probe is useful
CC for detecting the 3;8 human chromosomal translocation, by contacting the
CC nucleic acid probe with a biological sample to be tested, and determining
CC whether the nucleic acid probe specifically hybridises to the TRC8FHIT or
CC FHIT/TRC8 fusion DNA. This polynucleotide sequence represents a TRC8
CC related PCR primer of the invention
XX

Sequence 19 BP; 2 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 56.4%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TCCAGGAGAAACA 740
|||||
Db 16 TCCAGGAGAAACA 3

RESULT 55
AAZ70293/c

Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 727 TCCAGGAGAAACA 740
|||||
Db 16 TCCAGGAGAAACA 3

RESULT 54
ABK10445/c
ID ABK10445 standard; DNA; 19 BP.
XX
AC ABK10445;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human TRC8 coding region SSCP PCR primer 4F.

XX
KW Human; ss; translocation in renal cancer from chromosome 8; 4F; TRC8;
KW fragile histidine triad; FHIT; renal cell carcinoma; t(3; 8);
KW single-stranded conformational polymorphism; thyroid tumour; PCR; primer;
KW SSCP.
XX
OS Homo sapiens.
XX
US6268176-B1.
PN
31-JUL-2001.
XX
12-MAR-1999; 99US-00268140.
PF
12-MAR-1998; 98US-0077723P.
PR
(UYTE-) UNIV TECHNOLOGY CORP.
XX
Gemmill RM, Drabkin HA;
XX
WPI; 2002-224110/28.
XX
New TRC8 (Translocation in Renal Cancer from Chromosome 8) polypeptide,
PT useful for diagnosing tumors, particularly for determining TRC8 gene
PT expression in samples.
XX
Example 5; Col 17; 45pp; English.
XX

The invention relates to a polypeptide (which is the product of the
CC expression in a host cell of a DNA) TRC8 (Translocation in Renal Cancer
CC from Chromosome 8). Also included are a polypeptide product of the
CC expression in a host cell of a DNA, comprising (a) culturing a host cell
CC containing a vector comprising a nucleic acid molecule encoding the
CC polypeptide comprising TRC8 and (b) recovering the polypeptide. The gene
CC encoding TRC8 is located in the chromosomal translocation region t(3;8),
CC resulting in a fusion with the fragile histidine triad gene, FHIT. This
CC region is associated with renal and thyroid tumors (especially renal
CC cell carcinoma, RCC). The polypeptide is useful for diagnosing tumors,
CC particularly for determining if the TRC8 gene is expressed in samples.
CC The present sequence is an single-stranded conformational polymorphism
CC (SSCP) PCR primer used to identify tumour specific mutations in TRC8 in
CC sporadic renal cell carcinoma samples
XX

Sequence 19 BP; 2 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 56.4%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ID AAZ70293 standard; DNA; 18 BP.
 AC AAZ70293;
 XX
 XX 10-SEP-2001 (first entry)
 XX
 XX Human biallelic marker upstream amplification primer SEQ ID NO:4649.
 DE
 DE Human genome; biallelic marker; high density disequilibrium map;
 XX
 XX Genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW
 KW haplotyping; hybridisation; identification; characterisation;
 KW
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW
 KW diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9954500-A2.
 PN
 XX 28-OCT-1999.
 XX
 XX 21-APR-1999; 99WO-IB000822.
 PF
 XX 21-APR-1998; 98US-0082614P.
 PR
 XX 23-NOV-1998; 98US-0109732P.
 PR
 XX (GEST) GENSET.
 PA
 XX Cohen D, Blumenfeld M, Chumakov I;
 PI
 XX WPI; 2000-013267/01.
 DR
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 PT
 XX
 XX Claim 8; Page 1222; 2745pp; English.
 PS
 CC AA65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 XX Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 55.5%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 731 AGGAGAAACAGACACC 747
 DE |||||
 DB 17 AGGAGAAACAGAGGAC 1
 RESULT 56
 AAZ36131/C
 ID AAZ36131 standard; DNA; 17 BP.
 XX
 XX AAZ36131;
 AC
 XX 26-JUL-2000 (first entry)
 DT
 DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:188.
 XX

KW Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
 KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
 KW genomic classification; identification; DNA fingerprinting;
 KW tumour characterisation; hybridisation; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200018960-A2.
 PN
 XX 06-APR-2000.
 PD
 XX 24-SEP-1999; 99WO-US022283.
 PF
 XX 25-SEP-1998; 98US-0101757P.
 PR
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA
 XX Landers JE, Jordan B, Housman DE, Charest A;
 PI
 XX WPI; 2000-293181/25.
 DR
 XX Detection of single nucleotide polymorphisms in genomes by preparation
 PT and analysis of reduced complexity genomes, useful for genotyping,
 PT fingerprinting and determining allele frequency of SNPs.
 PT
 XX Disclosure; Page 59; 111pp; English.
 PS
 XX A method has been developed for detecting the presence or absence of a
 CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
 CC method comprises preparing a reduced complexity genome (RCG) from the
 CC genomic sample and analysing the RCG for the presence or absence of a SNP
 CC allele. The method can be used to characterise a tumour, to generate a
 CC genomic pattern for an individual genome or to generate a genomic
 CC classification code for a genome. The method can be used to assess
 CC whether a subject is at risk for developing a disease or to identify a
 CC set of SNP alleles associated with a disease. The method can also be used
 CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences
 CC used in the exemplification of the present invention. AAA35948 to
 CC AAA36632 represent nucleotide sequences containing SNPs
 XX
 SQ Sequence 17 BP; 1 A; 2 C; 5 G; 9 T; 0 U; 0 Other;
 Query Match 54.5%; Score 12; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 736 AAACAGACACC 747
 DE |||||
 DB 13 AAACAGACACC 2
 RESULT 57
 AAF16608
 ID AAF16608 standard; DNA; 17 BP.
 XX
 XX AAF16608;
 AC
 XX 13-MAR-2001 (first entry)
 DT
 XX Gastric acid production inhibiting oligonucleotide SEQ ID NO: 95.
 DE
 XX Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
 KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antitense;
 KW DNA-RNA hybrid; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200071164-A1.
 PN
 XX 30-NOV-2000.
 PD
 XX 24-MAY-2000; 2000WO-AU000498.
 PF
 XX

PR 24-MAY-1999; 99AU-00000510.
XX (TACH/) TACHAS G.
XX Tachas G;
XX WPI; 2001-025093/03.
XX Treating gastric acid disturbance by administering an oligonucleotide
PT which modulates the activity of a polypeptide involved in gastric acid
PT production or secretion.
XX Example 3; Page 149; 164pp; English.
XX The present invention provides oligonucleotides, and methods for their
CC use, which are useful in modulating the action of proteins involved in
CC gastric acid production. The target protein is preferably the histamine
CC H2 receptor or one of the proteins which form part of the gastric proton
CC pump. The sequences and methods of the invention are useful in the
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC duodenal ulcers and other gastric acid disturbances, most of which are
CC caused by Helicobacter pylori.
XX Sequence 17 BP; 10 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
SQ Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAGACGACACCG 748
Db ||||| ||||| |||||
3 AGGAACAGACACAG 17
RESULT 59
ABV80007/c
ID ABV80007 standard; DNA; 17 BP.
XX AC ABV80007;
XX 03-JAN-2003 (first entry)
XX Human HTPL scanning oligonucleotide SEQ ID 1253.
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX Homo sapiens.
XX EP1229046-A2.
XX 07-AUG-2002.
XX 28-JAN-2002; 2002EP-00001167.
XX 30-JAN-2001; 2001WO-US0000663.
XX 30-JAN-2001; 2001WO-US0000664.
XX 30-JAN-2001; 2001WO-US0000665.
XX 30-JAN-2001; 2001WO-US0000667.
XX 30-JAN-2001; 2001WO-US0000668.
XX 30-JAN-2001; 2001WO-US0000669.
XX 23-MAY-2001; 2001US-00864761.
XX 09-OCT-2001; 2001US-0327898P.
XX (AEOM-) ASOMICA INC.
XX Zhan J;
XX WPI; 2002-676582/73.
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX Example 2; Page 228; 718pp; English.
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX Sequence 17 BP; 1 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
SQ Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGA 742
Db ||||| ||||| |||||
17 GCCAGGTGAACACA 3
RESULT 59
ACC54250/c
ID ACC54250 standard; DNA; 17 BP.
XX AC ACC54250;
XX 27-JUN-2003 (first entry)
XX Human tumour suppressor sequence #3017.
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX Homo sapiens.
XX FR2826373-A1.
XX 27-DEC-2002.
XX 20-JUN-2001; 2001FR-00008139.
XX 20-JUN-2001; 2001FR-00008139.
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX Tuijnder M, Telerman A, Amson R;
XX WPI; 2003-250498/25.
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX Claim 1; Page 737; 798pp; French.
XX This sequence represents an isolated nucleic acid sequence associated

CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAAC 744
 |||||
 Db 15 CTGGAGAAACAGATC 1

RESULT 60
 ABT35836/c
 ID ABT35836 standard; DNA; 17 BP.

XX ACD50569;

XX 23-SEP-2003 (first entry)

DE HBV hammerhead ribozyme substrate sequence #137.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 XX RNA stability; RNA expression; RNA synthesis; antisense;
 XX enzymatic; G-cleaver ribozyme; hammerhead ribozyme; DNase; zymase;
 XX ambrzyme; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004208.

XX 17-SEP-2001; 2001FR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumours and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.

XX Disclosure; Page 205; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and

CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX

SQ Sequence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAAC 744
 |||||
 Db 15 CAGGAGACACAGATC 1

RESULT 61

ACD50569/c
 ID ACD50569 standard; RNA; 17 BP.

XX ACD50569;

XX 23-SEP-2003 (first entry)

DE HBV hammerhead ribozyme substrate sequence #137.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 XX RNA stability; RNA expression; RNA synthesis; antisense;
 XX enzymatic; G-cleaver ribozyme; hammerhead ribozyme; DNase; zymase;
 XX ambrzyme; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.

XX Homo sapiens.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296878P.

XX 24-OCT-2001; 2001US-0330599P.

XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MACE/) MACEJAK D.

XX (MCSW/) MCSWIGGEN J.

XX (MORR/) MORRISSEY D.

XX (PAVC/) PAVCO P.

XX (LEEP/) LEE P.

XX (DRAP/) DRAPER K.

XX (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Example 1; Page 138; 387pp; English.
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

DR WFI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX

XX Example 1; Page 138; 387pp; English.

XX

XX The present invention relates to nucleic acid molecules which modulate

CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

CC as oligonucleotides that specifically bind the Enhancer I region of HBV

CC DNA. The nucleic acids may be used to modulate the expression of HBV

CC genes and HBV viral replication. Also disclosed is a method for screening

CC compounds and/or potential therapies directed against HBV, and compounds

CC that modulate the expression and/or replication of HCV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and

CC disease states related to HBV and HCV infection, replication and gene

CC expression such as cirrhosis, liver failure, and hepatocellular

CC carcinoma. The present sequence represents a substrate for one of the HBV

CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences

CC disclosed in the present invention

XX

XX Sequence 17 BP; 1 A; 5 C; 4 G; 0 T; 7 U; 0 Other;

SQ

Query Match 53.6%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. NO. 2e-02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742

DB 17 GCCAAGAGAAACCGA 3

RESULT 63

ACD51996/c

ID ACD51996 standard; RNA; 17 BP.

XX ACD51996;

XX 24-SEP-2003 (first entry)

XX HBV inozyme substrate sequence #177.

XX

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;

KW RNA stability; RNA expression; RNA synthesis; antisense;

KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;

KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;

KW HBV reverse transcriptase; Enhancer I region; viral replication;

KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;

KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

XX virucide; antiinflammatory; substrate; ss.

XX

XX Hepatitis B virus.

XX

XX WO200281494-A1.

XX

XX 17-OCT-2002.

XX

XX 26-MAR-2002; 2002WO-US009187.

XX

XX 26-MAR-2001; 2001US-00817879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-0335059P.

XX 05-DEC-2001; 2001US-0337055P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA

PI Stuyver L, Rossau R, Maertens G;
DR WPI; 1997-535867/49.
XX
XX Detection and/or genetic analysis of hepatitis B virus - specifically
PT genotype, preCore mutations, vaccine escape mutations and RT gene
PT mutations selected by treatment with drugs.
XX
XX
PS Claim 5; Page 32; 80pp; English.
XX
XX This sequence represents a probe for the RT pol region of hepatitis b
CC virus (HBV). This sequence can be used in the method of the invention for
CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleic acids (I) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1
CC suitable primer pair; (b) hybridising (I) with a combination of at least
CC 2 nucleotide probes, which are applied to mutant target sequences chosen from
CC support and hybridise specifically to mutant target sequences on a solid
CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC genotype specific target sequences, or their complements or U for T
CC homologues; (c) detecting the hybrids formed in step (b), and inferring
CC the HBV genotype and/or mutants present in the sample from the
CC differential hybridisation signal(s). The composition can be used to
CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC specifically genotype, preCore mutations, vaccine escape mutations and RT
CC gene mutations selected by treatment with drugs, e.g. lamivudine and
CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 18 BP; 1 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACGGA 4
|||||
AAV14105;
AC AAV14105;
XX
XX
XX 27-AUG-2003 (revised)
DT 19-MAY-1998 (first entry)
XX
XX Probe HBPz271 for RT pol region of HBV.
XX
XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
KW preCore region; HBsAg region; genotype specific target;
KW mutation detection; ss.
XX
XX Synthetic.
OS Hepatitis B virus.
FN WO9740193-A2.
XX
XX 30-OCT-1997.
PD
XX 21-APR-1997; 97WO-EP002002.
PF
XX 19-APR-1996; 96EP-00870053.
PR
XX (INNO-) INNOGENETICS NV.
PA
XX Stuyver L, Rossau R, Maertens G;
PI
XX WPI; 1997-535867/49.
DR
XX Detection and/or genetic analysis of hepatitis B virus - specifically

PT genotype, preCore mutations, vaccine escape mutations and RT gene
XX mutations selected by treatment with drugs.
XX
PS Claim 5; Fig 1; 80pp; English.
XX
XX This sequence represents a probe for the RT pol region of hepatitis b
CC virus (HBV). This sequence can be used in the method of the invention for
CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleic acids (I) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1
CC suitable primer pair; (b) hybridising (I) with a combination of at least
CC 2 nucleotide probes, which are applied to mutant target sequences on a solid
CC support and hybridise specifically to mutant target sequences chosen from
CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC genotype specific target sequences, or their complements or U for T
CC homologues; (c) detecting the hybrids formed in step (b), and inferring
CC the HBV genotype and/or mutants present in the sample from the
CC differential hybridisation signal(s). The composition can be used to
CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC specifically genotype, preCore mutations, vaccine escape mutations and RT
CC gene mutations selected by treatment with drugs, e.g. lamivudine and
CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 18 BP; 2 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACGGA 4
|||||
AAV14105;
AC AAV14105;
XX
XX
XX 15-JUL-1999 (first entry)
DT
XX
XX HIV-1 Group O env PCR primer SEQ ID NO:42.
DE
XX
XX HIV; human immunodeficiency virus; antigen; detection; antibody;
KW differentiation; Group O; env; immunogen; immunoassay; ss.
XX
XX Synthetic.
OS Human immunodeficiency virus 1.
XX
XX WO9909179-A2.
PN
XX 25-FEB-1999.
PD
XX 17-AUG-1998; 98WO-US017014.
PF
XX 15-AUG-1997; 97US-00911824.
PR
XX (ABBO) ABBOTT LAB.
PA
XX Hackett JR, Yamaguchi J, Golden AM, Brennan CA, Hickman RK;
PI
XX WPI; 1999-190167/16.
DR
XX New isolated HIV-1 Group O env polypeptides - used for the detection of
PT anti-HIV antibodies and for the production of antibodies for use in
PT detection, purification and therapy.
XX
XX Example 3; Page 69; 138pp; English.
PS
XX The present invention describes (A) an isolated HIV-1 Group O env
CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env

CC polypeptide comprising an immunoreactive portion of a polypeptide as in (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) an
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a
 CC second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as
 CC in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a
 CC host cell transformed by an expression vector as in (8); and (10) an
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an
 CC antigen construct as in (3)-(6). The antigen constructs can be used for
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be
 CC used as immunogens to produce antibodies. The antibodies can be used to
 CC purify HIV polypeptides, for therapy and for detection of HIV
 CC polypeptides
 XX
 SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 2.1e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAAC 744
 |||||
 DB 3 CAGCAGGAACAGAAC 17

RESULT 68
 AAX37184
 ID AAX37184 standard; DNA; 18 BP.
 XX
 AC AAX37184;
 XX
 XX 06-JUL-1999 (first entry)
 DT PCR primer Seq ID No: 42.
 DE
 DE HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;
 KW antibody; assay; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO9909410-A2.
 PN
 XX 25-FEB-1999.
 PD
 XX 07-AUG-1999; 98WO-US016506.
 PF
 XX 15-AUG-1997; 97US-00912129.
 PR
 XX (ABBO) ABBOTT LAB.
 PA
 XX Vallari AS, Hackett JR, Hickman RK, Varitek V, Necklaws EC;
 PI Golden AM, Brennan CA, Devare SG;
 PI WPI; 1999-190224/16.
 DR
 XX New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 - can
 XX be used in field assay, requiring no electricity and less specialised
 XX equipment.
 PT
 PS Example; Page 50; 104pp; English.

CC The invention relates to a rapid assay for simultaneous detection and
 CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
 CC method comprises (a) contacting the sample with a strip containing at
 CC least one immobilised capture reagent per analyte and on which the sample
 CC moves from the proximal to the distal end by capillary action, under
 CC conditions sufficient to form capture reagent/analyte complexes, and (b)
 CC determining the presence of analyte(s) by detecting a visible colour

CC change at the capture reagent site on the strip wherein the capture
 CC reagent for HIV-1 group O comprises a polypeptide shown in AA06977-80
 CC and AA06983-84; and that for HIV-1 group M comprises a polypeptide shown
 CC in AA06982; and that for HIV-2 comprises the polypeptide shown in
 CC AA06981. The invention is used to screen patients for antibodies to HIV-
 CC 1 types O and M, and HIV-2. The invention will be particularly useful in
 CC places and situation where equipment and/or electricity is not available.
 CC The invention provides a screening method which is faster and requires
 CC less equipment than prior art methods
 XX
 SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 2.1e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAAC 744
 |||||
 DB 3 CAGCAGGAACAGAAC 17

RESULT 69
 AAF73900/C
 ID AAF73900 standard; DNA; 15 BP.
 XX
 AC AAF73900;
 XX
 DT 30-APR-2001 (first entry)
 XX
 XX Human SLC6A4 allele-specific oligonucleotide primer #20.
 DE
 XX Solute carrier family 6 neurotransmitter transporter; seotonin 4; SLC6A4;
 KW genotyping; allele specific oligonucleotide; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200109161-A1.
 PN
 XX 08-FEB-2001.
 PD
 XX 31-JUL-2000; 2000WO-US020638.
 PF
 XX 29-JUL-1999; 99US-0146290P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
 PI WPI; 2001-123317/13.
 DR
 XX New isolated polynucleotide comprising a polymorphic variant for the
 XX solute carrier family 6 neurotransmitter transporter, serotonin member 4
 XX gene for identifying drugs for treating disorders related to expression
 XX of the protein.

CC Claim 12; Page 21; 152pp; English.
 PS
 XX The present invention relates to a polymorphic variant of a reference
 CC sequence for the solute carrier family 6 neurotransmitter transporter,
 CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence
 CC complementary to the first sequence. The invention is used in producing a
 CC recombinant organism that can be used to express SLC6A4 for protein
 CC structure analysis and binding studies. A composition comprising a
 CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
 CC gene
 XX
 SQ Sequence 15 BP; 1 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 51.8%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 2.2e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAG 741

50K-cellulase; endoglucanase; bio-stoning; bio-washing; denim; detergent;
 KW textile; pulp; paper; Melanocarpus albomyces; Myriococcus albomyces;
 KW
 xx

PR 11-JAN-1996;

PR 11-JAN-1996; 96US-00584040.

```

XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX DR WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 128; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate the
XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more
XX CC receptors of vascular endothelial growth factor (VEGF). A patient
XX CC (preferably human) having a condition associated with the level of the
XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX CC treated by administering the nucleic acid molecule or the expression
XX CC vector to the patient. AA67275 to AA75752 represent specific examples
XX CC of nucleic acid molecules from the present invention
XX SQ Sequence 17 BP; 9 A; 1 C; 3 G; 0 T; 4 U; 0 Other;
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAAC 745
DB 2 GAGAAAUAGAAC 14
RESULT 73
ABV80012/c
ID ABV80012 standard; DNA; 17 BP.
XX AC ABV80012;
XX DT 03-JAN-2003 (first entry)
XX DE Human HTPL scanning oligonucleotide SEQ ID 1258.
XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX KW human testis expressed Patched like protein; testis; adrenal; liver;
XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX OS Homo sapiens.
XX PN EP1229046-A2.
XX PD 07-AUG-2002.
XX PF 28-JAN-2002; 2002EP-00001167.
XX PR 30-JAN-2001; 2001WO-US000653.
XX PR 30-JAN-2001; 2001WO-US000654.
XX PR 30-JAN-2001; 2001WO-US000655.
XX PR 30-JAN-2001; 2001WO-US000656.
XX PR 30-JAN-2001; 2001WO-US000657.
XX PR 30-JAN-2001; 2001WO-US000658.
XX PR 30-JAN-2001; 2001WO-US000659.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 09-OCT-2001; 2001US-0327898P.
XX PA (ABOM-) ABOMICA INC.
XX PI Zhan J;
XX DR WPI; 2002-676582/73.
XX XX
XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
XX PT for identifying agonist and antagonist and specific binding partners, and
XX PT for treating subjects having defects in HTPL.
XX PS Example 2; Page 228; 718pp; English.
XX CC The present invention relates to human testis expressed Patched like
XX CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
XX CC has two isoforms, with a few single base pair differences between the
XX CC two. One of the single base pair changes introduces a premature stop
XX CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX CC shares an overall structure organisation with the Patched protein. The
XX CC shared structural features strongly imply that HTPL plays a role similar
XX CC to that of Patched, and is a potential tumour suppressor. HTPL is
XX CC important in regulating male germ cell development, and the HTPL gene was
XX CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX CC useful for diagnosing a disorder caused by mutation in HTPL, and in
XX CC therapy and manufacture of a medicament for treatment or prevention of
XX CC such disorder associated with decreased expression or activity of human
XX CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX CC clinically useful diagnostic markers and potential therapeutic agents for
XX CC male infertility and cancer. The present oligonucleotide was used in an
XX CC example from the invention
XX SQ Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAC 739
DB 13 TGCCAGGTGAAC 1
RESULT 74
ACC53821/c
ID ACC53821 standard; DNA; 17 BP.
XX AC ACC53821;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #2588.
XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX KW tumour regression; apoptosis; virus resistance; diagnosis;
XX KW cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (WOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Anson R;
XX DR WPI; 2003-250498/25.
XX XX
XX PT New nucleic acid sequences associated with tumor suppression, regression,
XX PT apoptosis or virus resistance are useful to diagnose and treat viral
XX PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 638; 798pp; French.

```

XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX

SQ Sequence 17 BP; 1 A; 4 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGCA 742
| | | | | | | | | |
Db 17 CAGGAGAAACAGCA 5

RESULT 75
ABT38554/c
ID ABT38554 standard; DNA; 17 BP.
XX
AC ABT38554;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4191.
XX
KW Cytostatic; viricide; neuroprotective; nootropic; neuroleptic; gene chip;
KW anisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 523; 720pp; French.
XX
SQ The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in

CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX

SQ Sequence 17 BP; 2 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAGCA 745
| | | | | | | | | |
Db 17 GTGAAACAGCA 5

RESULT 76
AAI64977
ID AAI64977 standard; DNA; 16 BP.
XX
AC AAI64977;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human Creml protein coding sequence exon 25/intron 25 junction.
XX
KW Human; Creml; repeat; transcriptional control factor; Rb;
KW retinoblastoma protein; intron-exon junction; ds.
XX
OS Homo sapiens.
XX
PN CN1303861-A.
XX
PD 18-JUL-2001.
XX
PF 07-JAN-2000; 2000CN-00111426.
XX
PR 07-JAN-2000; 2000CN-00111426.
XX
PA (SHAN-) SHANGHAI INST CYTOBIOLOGY CHINESE ACAD.
XX
PI Zhu X, Yan X, Qian M;
XX
DR WPI; 2001-566148/64.
XX
PT New retinoblastoma protein binding protein, its preparation and
PT application.
XX
PS Disclosure; Fig 3B; 35pp; Chinese.
XX
SQ The present invention relates to the coding sequence of human Creml,
CC which is a protein containing a repetitive 96 amino acid motif. The
CC protein is a transcriptional control factor, and is a conjugate of
CC retinoblastoma protein (Rb). The present sequence is the an intron-exon
CC junction in the coding sequence of the invention
XX

SQ Sequence 16 BP; 4 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 50.9%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 727 TGCAGGAGAAACAGCA 742
| | | | | | | | | |
Db 1 TGCAGGAGAGTCAGA 16

RESULT 77
AAT16993
ID AAT16993 standard; DNA; 17 BP.
XX

```

AC AAT16993;
XX
DT 10-JUL-1996 (first entry)
XX
DE E-Dex integrin inhibitor 1 PCR primer No. 1771.
XX
KW Integrin inhibitor; E-Dex; neutrophil; leukocyte; trans-migration;
XX cell adhesion; tick-derived anti-inflammatory protein; Ixodes pacificus;
XX Amblyomma americanum; polymerase chain reaction; PCR; primer; ss.
XX
OS Synthetic.
XX
FN WO9605304-A1.
XX
PD 22-FEB-1996.
XX
PF 08-AUG-1995; 95WO-US010138.
XX
PR 09-AUG-1994; 94US-00287730.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bard F, Yednock TA, Keim PS, Basi GS;
XX
DR WPI; 1996-139700/14.
XX
PT Tick derived anti-inflammatory proteins E-Dex and Y/A-Dex - used to
PT inhibit leukocyte trans-migration and in the treatment of inflammatory
PT disease.
PS Example; Fig 3A; 76pp; English.
XX
CC Degenerate sense PCR primers (AAT16990-94) are based on the 5' end of a
CC anti-inflammatory protein E-Dex (see also AAR81794). They were used with
CC antisense primers (AAT16995-99) complementary to the 3' end of the
CC sequence for the RT-PCR amplification of tick salivary gland mRNA.
CC Partial cDNA clones were obtd. and used to screen a cDNA library to
CC obtain a full-length cDNA clone (AAT16988) coding for E-Dex
XX
SQ Sequence 17 BP; 8 A; 1 C; 4 G; 1 T; 0 U; 3 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAAC 744
DB 2 ARGARARAGAAC 15

RESULT 78
AAX73286/c
ID AAX73286 standard; RNA; 17 BP.
XX
AC AAX73286;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #719.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
FN WO9715662-A2.
XX
PD 01-MAY-1997.
XX

```

```

PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-000584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 146; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 1 A; 6 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGAGAACAGAA 743
DB 16 GCCAGAGACACGTAA 1

RESULT 79
AAX73641/c
ID AAX73641 standard; DNA; 17 BP.
XX
AC AAX73641;
XX
DT 02-FEB-2001 (first entry)
XX
DE Forward primer #143 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
FN WO200058516-A2.
XX
PD 05-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US008069.
XX
PR 26-MAR-1999; 99US-0126473P.
PR 23-JUN-1999; 99US-0140359P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX
DR WPI; 2000-656171/63.
XX
PT Universal array of oligonucleotides tags attached to a solid substrate
PT

```

PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
PS Example 7; Page 63; 70pp; English.
XX
CC The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one of the primers used in
CC the method of the present invention to amplify a polymorphic sample. The
CC amplified nucleic acid product is then used as a template in a SBE
CC reaction with an extension primer. The SBE reaction products are used to
CC form the oligonucleotide array
XX
SQ Sequence 17 BP; 1 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGAGAGAACAGAA 743
Db 16 GCCATGAGAGCAGGA 1

RESULT 80
AAH95688
XX ID AAH95688 standard; RNA; 17 BP.
XX AC AAH95688;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human Chk1 ribozyme substrate SEQ ID NO: 1113.
XX
KW Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
KW RNA cleavage; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157206-A2.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US003504.
XX
PR 03-FEB-2000; 2000US-0179983P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (FATT/) FATTAEY A R.
XX
PI Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;
XX WPI; 2001-496922/54.
DR
XX
PT Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
PT molecules, which downregulates expression of a checkpoint kinase-1 gene,
PT useful for treating colorectal, lung, breast or prostate cancers.
XX
PS Claim 4; Page 80; 115pp; English.
XX
CC The present invention provides nucleic acid molecules capable of
CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
CC gene. These may be antisense or ribozyme sequences, and are useful in the
CC treatment of diseases associated with conditions affected by Chk1 levels,
CC including cancer. The present sequence is an oligonucleotide described in
CC the exemplification of the invention
XX
SQ Sequence 17 BP; 10 A; 2 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 731 AGGAGAGAACAGAACAC 746
Db 2 AGGAGAGAACAUUAAAC 17

RESULT 81
AAH45387/c
XX ID AAH45387 standard; DNA; 17 BP.
XX AC AAH45387;
XX
DT 11-SEP-2001 (first entry)
XX
DE Corynebacterium thermoaminogenes lysa PCR primer #2.
XX
KW Heat-resistant; lysin biosynthesis; enzyme; coryneform;
KW aspartate-semialdehyde dehydrogenase; lysa; PCR primer; ss.
XX
OS Corynebacterium thermoaminogenes.
XX
PN JP2001120270-A.
XX
PD 08-MAY-2001.
XX
PF 01-NOV-1999; 99JP-00311148.
XX
PR 01-NOV-1999; 99JP-00311148.
XX
PA (AJIN) AJINOMOTO KK.
XX
DR WPI; 2001-364760/38.
XX
PT A heat-resistant lysin biosynthetic system enzyme gene of a high
PT temperature-resistant coryneform microbe.
XX
PS Example 2; Page 7; 27pp; Japanese.
XX
CC The invention relates to a gene from a high temperature-resistant
CC coryneform microbe that encodes a heat-resistant lysin biosynthetic
CC enzyme. The enzyme has aspartate-semialdehyde dehydrogenase activity and
CC can be used for growing amino acid-producing microbes. The present
CC sequence is a primer which was used to amplify DNA encoding a heat-
CC resistant lysin biosynthetic enzyme of the invention
XX
SQ Sequence 17 BP; 1 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGAGAGAACAGAA 743
Db 17 GCCACGAGGATCAGAA 2

RESULT 82
ABL31707
XX ID ABL31707 standard; DNA; 17 BP.
XX AC ABL31707;
XX
DT 21-MAR-2002 (first entry)
XX
DE Human HLA genotyping oligonucleotide SEQ ID NO 1196.
XX
KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
XX
OS Homo sapiens.
XX

PN W0200192572-A1.
 XX 06-DEC-2001.
 XX 01-JUN-2001; 2001WO-JP004662.
 XX 01-JUN-2000; 2000JP-00164798.
 XX (NISHIN) NISSHINBO IND INC.
 XX (SYST-) SYSTEM RES INC.
 XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 XX WPI; 2002-122074/16.
 XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 PT individuals e.g. by determining immunogenetic differences when
 PT transplanting between them.
 XX Claim 10; Page 320; 345pp; Japanese.
 XX The invention relates to a typing kit for judging human leukocyte antigen
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
 CC oligonucleotides (ASL30512-ABL31809) originating in the sequences of
 CC genes e.g. belonging to HLA class I antigens on human genome and
 CC containing gene polymorphisms as alloantigens have been immobilised as
 CC primers for amplification of cleaved nucleic acids relating to gene
 CC polymorphisms. The method is useful for judging HLA genotypes of
 CC individuals by determining immunogenetic differences before transplanting
 CC between them, providing genetic information to decide compatibility of
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
 CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
 CC diagnosis of genetic diseases and identifying individuals
 XX Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 50.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAACAGAC 744
 |||||
 Db 1 CCGGAGATACAGATC 16

RESULT 83
 ADB03778/c
 ID ADB03778 standard; DNA; 17 BP.
 XX ADB03778;
 AC ADB03778;
 DT 20-NOV-2003 (first entry)
 XX Human MD27 scanning oligonucleotide SEQ ID 4764.
 DE
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS
 XX EP1281758-A2.
 PN
 XX 05-FEB-2003.
 PD
 XX 30-JUL-2002; 2002EP-00016874.
 PF
 XX 02-AUG-2001; 2001US-00922181.
 PR
 XX (AEOM-) AEOMICA INC.
 PA
 XX Shannon M, Gu Y, Nguyen C;
 PI
 XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MDZ12, e.g. cancer.

XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MDZ12, e.g. cancer.
 XX Example 8; SEQ ID NO 4764; 103pp; English.
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MDZ12. MD23 is
 CC encoded at chromosome 7q22.1. MD24 is encoded at chromosome 6p21.3-22.2.
 CC MD27 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX Sequence 17 BP; 0 A; 8 C; 2 G; 7 T; 0 U; 0 Other;
 SQ

Query Match 50.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAGAA 743
 |||||
 Db 16 GCCAGGAGAGAGGGA 1

RESULT 84
 ADB03777/c
 ID ADB03777 standard; DNA; 17 BP.
 XX ADB03777;
 AC ADB03777;
 DT 20-NOV-2003 (first entry)
 XX Human MD27 scanning oligonucleotide SEQ ID 4763.
 DE
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS
 XX EP1281758-A2.
 PN
 XX 05-FEB-2003.
 PD
 XX 30-JUL-2002; 2002EP-00016874.
 PF
 XX 02-AUG-2001; 2001US-00922181.
 PR
 XX (AEOM-) AEOMICA INC.
 PA
 XX Shannon M, Gu Y, Nguyen C;
 PI
 XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MDZ12, e.g. cancer.


```

PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, McSwiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 225; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the
CC nucleotide base position indicated in the DE line. The relA gene product
CC is a subunit of the transcriptional regulator NF-kappaB and is implicated
CC specifically in the induction of inflammatory responses. Regions of the
CC mRNA that do not form secondary folding structures and that contain
CC potential hammerhead and hairpin ribozyme cleavage sites were identified
CC by computer analysis. Ribozymes directed against these mRNA sequences
CC were designed and synthesised with modifications that improve their
CC nuclease resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit relA expression, making them potentially
CC useful for treating rheumatoid arthritis, restenosis and asthma as well
CC as for increasing tolerance to transplanted tissues. The potential
CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means
CC that uses are limited to local delivery, acute indications or ex vivo
CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 15 BP; 1 A; 6 C; 2 G; 0 T; 6 U; 0 Other;
SQ
Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAAC 744
DB 14 AGGGGAAACAGATC 1

RESULT 87
AAZ63818/c
ID AAZ63818 standard; RNA; 15 BP.
XX
XX AAZ63818;
XX
XX 28-MAR-2000 (first entry)
XX
XX Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 1861.
XX
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
XX cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX autoimmune disease; ss.
XX
XX Hepatitis C virus.
XX
XX WO9955847-A2.
XX
XX 04-NOV-1999.
XX
XX 26-APR-1999; 99WO-US009027.
XX
XX 27-APR-1998; 98US-0083217P.
XX
XX 18-SEP-1998; 98US-0100842P.
XX
XX 25-FEB-1999; 99US-00257608.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
XX Claim 1; Page 71; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
XX Sequence 15 BP; 2 A; 4 C; 3 G; 0 T; 6 U; 0 Other;
SQ
Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGACACCG 748
DB 15 GAAACAGTACACTG 2

RESULT 88
AAZ50111/c
ID AAF50111 standard; DNA; 15 BP.
XX
XX AAF50111;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #1071.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT

```


PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.

XX Example 8; Page 67; 201pp; English.

PS The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

XX Sequence 15 BP; 1 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

QY 730 CAGGAGAAACAGAA 743
DB 14 CAGAGGTAACAGAA 1

RESULT 89
AAF50110/c
ID AAF50110 standard; DNA; 15 BP.
XX
XX
AC AAF50110;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #1070.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cycostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.

OS Homo sapiens.
XX
XX WO200078341-A1.
XX
PD 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.

PS Example 8; Page 67; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

XX Sequence 15 BP; 2 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

QY 730 CAGGAGAAACAGAA 743
DB 15 CAGAGGTAACAGAA 2

RESULT 90
ABX00871/c
ID ABX00871 standard; RNA; 15 BP.
XX
XX
AC ABX00871;
XX
XX 23-DEC-2002 (first entry)
XX
XX Hepatitis C virus substrate #853 for HCV hammerhead ribozyme #653.
XX
XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
XX liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX type I interferon; interferon alpha; interferon beta; cytosstatic;
XX interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX substrate; hammerhead ribozyme; HH ribozyme; ss.

OS Hepatitis C virus.
XX
XX US2002082225-A1.
XX
XX 27-JUN-2002.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (ROBE/) ROBERTS B.
XX (PVC/) PAVCO P A.
XX (MACE/) MACEJACK D.
XX
XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
XX WPI; 2002-617759/66.
XX
XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX replication and are useful to treat hepatitis C virus infections and
XX cirrhosis, liver failure or hepatocellular carcinoma.

PS Claim 1; Page 40; 80pp; English.

XX The present invention relates to enzymatic nucleic acids which

CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
 CC (HP) motif where the binding arms comprise sequences complementary to one
 CC of the substrate sequences defined in the specification. The HCV
 CC ribozymes are useful for modulating the expression and/or replication of
 CC HCV. They can be used to treat cirrhosis, liver failure and/or
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
 CC a condition associated with HCV infection in conjunction with one or more
 CC other drug therapies, particularly type I interferon, especially
 CC interferon alpha, beta or gamma or consensus interferon. The present
 CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
 CC Some of the sequence data for this patent did not form part of the
 CC printed specification. The complete sequence data for this patent was
 CC obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/paipsDIDEntry.html
 XX seqdata.uspto.gov/paipsDIDEntry.html
 XX

SQ Sequence 15 BP; 2 A; 4 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 49.1%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGTACACTG 748
 Db 15 GAAACAGTACACTG 2

RESULT 91
 ABV72560/C
 ID ABV72560 standard; DNA; 15 BP.
 XX
 AC ABV72560;
 XX
 DT 12-FEB-2003 (first entry)
 XX
 DE Consensus sequence of methanol regulated promoters of yeast.
 XX
 KW Yeast; alcohol oxidase 1; AOX1; AOX2; promoter; formaldehyde; methanol;
 KW protein production; peroxisome biogenesis; ss.
 XX
 OS Synthetic.
 XX
 PN WO200281650-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 05-APR-2002; 2002WO-US012851.
 XX
 PR 05-APR-2001; 2001US-0281861P.
 XX
 PA (UNNE-) UNIV NEBRASKA.
 XX
 PI Inan M, Meagher MM, Benson AK;
 XX
 DR WPI; 2003-058528/05.
 XX

PT Novel alcohol oxidase 1 regulatory nucleotide sequences useful for
 PT enhancing expression of genes of interest in a variety of host cells,
 PT especially yeast cells.
 XX

PS Disclosure; Fig 6; 66pp; English.

XX The present sequence represents a consensus sequence of methanol
 CC regulated promoters of methylotrophic yeast. The specification describes
 CC 5' regulatory sequences within the alcohol oxidase 1 (AOX1) promoter
 CC region. AOX1 catalyzes the oxidation of methanol to formaldehyde. The
 CC AOX1 promoter is an inducible promoter, primarily induced by methanol and
 CC starvation, and repressed in response to glucose and ethanol. The AOX1 5'
 CC regulatory sequences can be used to produce expression cassettes and
 CC vectors, which are useful for protein production. The regulatory
 CC sequences are useful to increase expression of genes of interest in a
 CC variety of host cells, in a research setting to further characterize
 CC promoter function and to study peroxisome biogenesis. They are also

CC useful as probes
 XX
 SQ Sequence 15 BP; 1 A; 6 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 49.1%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAACAG 741
 Db 15 GCCAGGAGAACAG 2
 RESULT 92
 AAF56033/C
 ID AAF56033 standard; DNA; 16 BP.
 XX
 AC AAF56033;
 XX
 DT 18-APR-2001 (first entry)
 XX
 DE HBV DNA polymerase gene L528M mutation probe HBPr270.
 XX
 KW HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
 KW mutation detection; probe; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200104358-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 05-JUL-2000; 2000WO-EP006306.
 XX
 PR 08-JUL-1999; 99EP-00870148.
 PR 13-JUL-1999; 99US-0143546P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Stuyver L, Maertens G, Van Geyt C;
 XX
 DR WPI; 2001-138370/14.
 XX
 PT Monitoring anti-HBV drug resistance by genetic detection of mutations in
 PT DNA polymerase of HBV in patient's sample, involves hybridizing the
 PT polynucleic acids of the sample with a probe and detecting the hybrid.
 XX
 PS Claim 2; Page 9; 64pp; English.
 XX
 CC The present sequence is a probe used in a method for monitoring anti-
 CC hepatitis B virus (HBV) drug resistance in a patient by genetic detection
 CC of any one of mutations L528M, M552V/I and/or V/L/M555I in HBV DNA
 CC polymerase in a biological sample from the patient. The method is useful
 CC in the field of genetic detection of anti-HBV drug resistance during HBV
 CC therapy. The method is rapid, reliable and precise
 XX
 SQ Sequence 16 BP; 0 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 49.1%; Score 10.8; DB 1; Length 16;
 Best Local Similarity 85.7%; Pred. No. 2.8e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAACAG 741
 Db 14 GCCAGGAGAACAG 1
 RESULT 93
 AAS98698
 ID AAS98698 standard; DNA; 15 BP.
 XX
 AC AAS98698;
 XX

26-MAR-2002 (first entry)
Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #64.
Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
cytostatic; gene therapy; malignant histiocytosis; isogene;
myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
genotype; human; allele specific oligonucleotide; ASO; primer; ss.
Homo sapiens.
WO200179225-A2.
25-OCT-2001.
12-APR-2001; 2001WO-US012044.
12-APR-2000; 2000US-0196411P.
(GENA-) GENAISSANCE PHARM INC.
Chew A, Choi JY, Koshy B;
WPI; 2002-075058/10.
Novel polymorphic variants of colony stimulating factor 1 receptor useful
in studying expression and function of the protein, useful for screening
candidate drugs to treat diseases e.g. inflammatory disorders.
Claim 15; Page 16; 164pp; English.
The invention describes a novel isolated polynucleotide (I) comprising a
sequence which is a polymorphic variant (PV) of a reference sequence for
colony stimulating factor 1 receptor (CSF1R) gene, found on the
polypeptide are useful for improving the discovery and development of
drugs for treating diseases associated with CSF1R activity e.g. disorders
malignant histiocytosis, myeloid malignancies, and inflammatory disorders
and the haplotypes can be used to validate CSF1R as a candidate target
for treating a specific condition or disease predicted to be associated
with CSF1R activity. Genotyping the CSF1R gene of an individual can also
be used in developing diagnostic tests and therapeutic treatments. (I) is
useful in studying the expression and function of CSF1R, and in
expressing CSF1R protein for use in screening for candidate drugs to
treat diseases related to CSF1R activity and in studying the effect of
the variation on the biological activity of CSF1R as well as on the
binding affinity of candidate drugs targeting CSF1R. Antibodies are
useful in a variety of diagnostic and prognostic formats and therapeutic
methods. A transgenic animal is useful in studying expression of the
CSF1R isogenes in vivo, for in vivo screening and testing of drugs
targeted against CSF1R protein, and for testing the efficacy of
therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
are useful as probes and primers, and for assaying a polymorphism in the
target region. Without requiring any a priori knowledge of the phenotypic
effect of any particular CSF1R or haplotype the invention provides a
method for identifying lead compounds that are more likely to show
efficacy in clinical trials. This sequence is an allele specific
oligonucleotide primer used for detecting CSF1R gene polymorphisms,
described in the method of the invention
Sequence 15 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 1 Other;
Query Match 48.2%; Score 10.6; DB 1; Length 15;
Best Local Similarity 90.9%; Pred. No. 2.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
|||||||
Db 5 AGGAGAAACRG 15
RESULT 94
ABI99104/c
ID ABI99104 standard; DNA; 15 BP.

26-MAR-2002 (first entry)
Human PCDH2 ASO PCR primer SEQ ID NO 61.
Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;
single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31;
allele-specific oligonucleotide; ASO; PCR primer; ss.
Homo sapiens.
WO200194361-A2.
13-DEC-2001.
06-JUN-2001; 2001WO-US019321.
06-JUN-2000; 2000US-0209564P.
(GENA-) GENAISSANCE PHARM INC.
Kliem SE, Koshy B, Tanguay DA;
WPI; 2002-097928/13.
New protocadherin 2 (PCDH2) polymorphic variants and encoding genes,
PT useful in expressing PCDH2 protein for screening candidate drugs to treat
PT diseases related to PCDH2 activity.
Claim 16; Page 14; 127pp; English.
The invention relates to haplotyping the protocadherin 2 (PCDH2) gene,
comprising determining which of the haplotypes given in the specification
defines one or both copies of the individual's PCDH2 gene. The
polymorphisms are within a 30244 base pair sequence (ABA05413), fully
defined in the specification. The polymorphic variants are useful in
studying the expression and function of PCDH2, in expressing PCDH2
protein for use in screening for candidate drugs to treat diseases such
as cancer, related to PCDH2 activity, in studying the effect of the
variation on the biological activity of PCDH2 and the binding affinity of
candidate drugs targeting PCDH2. The haplotyping methods are useful in
validating PCDH2 as a candidate target for treating a specific condition
or disease predicted to be associated with PCDH2 activity or in the
design of clinical trials of candidate drugs for treating a specific
condition or disease associated with PCDH2 activity. The present sequence
is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of
the invention
Sequence 15 BP; 0 A; 3 C; 2 G; 9 T; 0 U; 1 Other;
Query Match 48.2%; Score 10.6; DB 1; Length 15;
Best Local Similarity 90.9%; Pred. No. 2.9e+02;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
|||||||
Db 15 GAGAAACAGAA 5
RESULT 95
AA556920
ID AA556920 standard; DNA; 12 BP.
XX
AC AA556920;
XX
DT 16-OCT-2003 (revised)
DT 15-JUL-1999 (first entry)
XX
DE HIV-1 proviral DNA fragment 3.
XX
KW DNA-targeting conjugate; anticancer drug; viral DNA-cleaving agent;

KW vital DNA-binding agent; solid support; primer; ss.

OS Human immunodeficiency virus 1.

XX WO9531434-A1.

XX 23-NOV-1995.

XX 12-MAY-1995; 95WO-US006379.

XX 13-MAY-1994; 94US-00242664.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX (ZWBI-) ZW BIOMEDICAL RES AG.

XX Watanabe KA, Ren W, Weil R;

XX WPI; 1996-010846/01.

XX Derivatized solid supports and reagents for oligonucleotide synthesis -
PT and new oligo:nucleotide phosphoramidate conjugates.

PS Disclosure; Page 43; 68pp; English.

XX This invention describes novel derivatised solid supports of formula S'-L
CC -Z-CH₂CH₂-R, where: S' = a solid support; L = a bond or an (in)organic
CC linker; Z = SO₂ or S-S; R = OH, an H-phosphate, alkanephosphonate,
CC phosphotriester, phosphite diester, phosphite diester, phosphorothioate,
CC phosphorodithioate, phosphoramidate or phosphoramidite group, OR₁, SR₁,
CC an optionally substituted or modified nucleotide (N'), or an
CC oligonucleotide of formula (N')GR₂; G = 1-200; R₁ = a protecting group;
CC R₂ = an H-phosphate, alkanephosphonate, phosphotriester, phosphite
CC triester, phosphite diester, phosphorothioate, phosphorodithioate,
CC phosphoramidate or phosphoramidite group, OH, OR₁, SR₁ or
CC OP(OCH₂CH₂CN)OCH₂CH₂CH₂CH₂OR₁. Also mentioned are compounds of formula
CC R₃CH₂CH₂CH₂CH₂CH₂OR₄, where: R₃ = a protecting group; and R₄ = OH or an H-
CC phosphate, alkanephosphonate, phosphotriester, phosphite triester,
CC phosphite diester, phosphorothioate, phosphorodithioate, phosphoramidate
CC or phosphoramidite group. Also claimed are new phosphoramidates, a
CC process for preparing an oligonucleotide 5'-phosphate, a process for
CC preparing a solid support useful for preparation of an oligonucleotide 3'-
CC phosphate, a process for preparing an oligonucleotide 3'-phosphate and a
CC process for preparing an oligonucleotide 3',5'-diphosphate. The
CC oligonucleotide 3'- and/or 5'-phosphates may be used to prepare DNA-
CC targeting conjugates, e.g. with anticancer drugs or viral (e.g. HIV) DNA-
CC cleaving or -binding agents. The process for preparing oligonucleotide
CC 3',5'-diphosphates is simple and suitable for use in automatic DNA
CC synthesizers. This sequence represents a fragment of the HIV-1 provirus
CC genome, used to describe the method of the invention. (Updated on 16-OCT-
CC 2003 to standardise OS field)

XX Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 12;

Best Local Similarity 91.7%; Pred. No. 2.8e+02;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742

Db 1 AGGAGAAACAGA 12

RESULT 96

ABI03318

ID ABI03318 standard; DNA; 12 BP.

XX ABI03318;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 303291 for detecting SNP TSC0020423.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 303291; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 12;

Best Local Similarity 91.7%; Pred. No. 2.8e+02;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGACACC 747

Db 1 AAACATACACC 12

RESULT 97

ABI54034

ID ABI54034 standard; DNA; 12 BP.

XX ABI54034;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 354007 for detecting SNP TSC0006126.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 354007; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 1 C; 4 G; 0 T; 0 U; 0 Other;
SQ

Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 2.8e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACGAGAAC 744
DB 1 GAGAAAGAGAAC 12
|||||
|||||

RESULT 98
ABH94559/C
ID ABH94559 standard; DNA; 12 BP.
XX
XX ABH94559;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 294552 for detecting SNP TSC0016175.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
FN
XX
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PP
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 294552; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;
SQ

Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 2.8e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACGAGAAC 746
DB 12 GAAACAAACAC 1
|||||
|||||

RESULT 99
ABH40265
ID ABH40265 standard; DNA; 13 BP.
XX
XX ABH40265;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 240242 for detecting SNP TSC0058589.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
FN
XX
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PP
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 240242; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 6 C; 1 G; 0 T; 0 U; 0 Other;
SQ

Query Match	47.3%;	Score 10.4;	DB 1;	Length 13;
Best Local Similarity	91.7%;	Pred. No. 2.9e+02;		
Matches 11;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	736	AAACAGAACACC 747		
DB	2	AAACCGAACACC 13		
RESULT 100				
ABF73171				
ID	ABF73171	standard;	DNA; 13 BP.	
XX	AC			
XX	ABF73171;			
XX				
DT	22-FEB-2002	(first entry)		
XX				
DE	Oligonucleotide SEQ ID NO 173168	for detecting SNP TSC0006888.		
XX				
XX	SNP; single nucleotide polymorphism; human; cancer; CNS;			
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;			
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.			
XX				
OS	Homo sapiens.			
XX				
FN	WO200177384-A2.			
XX				
PD	18-OCT-2001.			
XX				
PF	06-APR-2001; 2001WO-IB000713.			
XX				
PR	07-APR-2000; 2000DE-01019173.			
XX				
PA	(EPIG-) EPIGENOMICS AG.			
XX				
PI	Olek A, Piepenbrock C, Berlin K;			
XX				
DR	WPI; 2001-657177/75.			
XX				
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is			
PT	designed to detect single-nucleotide polymorphisms and cytosine			
PT	methylation status.			
XX				
PS	Claim 1; SEQ ID NO 173168; 29pp + Sequence Listing; German.			
XX				
CC	This invention describes novel oligonucleotide primers or peptide nucleic			
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)			
CC	and cytosine methylation status in chemically pretreated genomic DNA. The			
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a			
CC	range of diseases including immune system, gastrointestinal, respiratory,			
CC	central nervous system, cardiovascular and metabolic disorders. The			
CC	oligoners are also used for detecting cell type differentiation. ABC00010			
CC	-ABF9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073			
CC	represent the oligomers described in the invention. NOTE: The sequence			
CC	data for this patent did not form part of the printed specification, but			
CC	was obtained in electronic format from WIPO at			
CC	ftp.wipo.int/pub/published_pct_sequences			
XX				
SQ	Sequence 13 BP; 7 A; 5 C; 0 G; 1 T; 0 U; 0 Other;			
Query Match	47.3%;	Score 10.4;	DB 1;	Length 13;
Best Local Similarity	91.7%;	Pred. No. 2.9e+02;		
Matches 11;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	736	AAACAGAACACC 747		
DB	2	AAACATACACC 13		
RESULT 101				
ABF73170/c				
ID	ABF73170	standard;	DNA; 13 BP.	

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Gaps 0;
 Matches 10; Conservative 0; Indels 2; Indels 0; Gaps 0;
 QY 736 AAACAGAACACC 747
 Db 13 AAACAAACATC 2
 RESULT 561
 ABF56045/c
 ID ABF56045 standard; DNA; 13 BP.
 XX AC ABF56045;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 156042 for detecting SNP TSC0039372.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 156042; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 13 BP; 1 A; 5 C; 0 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Gaps 0;
 Matches 10; Conservative 0; Indels 2; Indels 0; Gaps 0;
 QY 734 AGAAACAGAACCA 745
 Db 2 AGAAACGGAAGA 13
 RESULT 563
 ABH34756/c
 ID ABH34756 standard; DNA; 13 BP.
 XX AC ABH34756;
 XX

Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Gaps 0;
 Matches 10; Conservative 0; Indels 2; Indels 0; Gaps 0;
 QY 731 AGGACAAACAGA 742
 Db 12 AGGACAATGAGA 1
 RESULT 562
 ABH33790
 ID ABH33790 standard; DNA; 13 BP.
 XX AC ABH33790;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 233767 for detecting SNP TSC0057055.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 233767; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 13 BP; 7 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Gaps 0;
 Matches 10; Conservative 0; Indels 2; Indels 0; Gaps 0;
 QY 734 AGAAACAGAACCA 745
 Db 2 AGAAACGGAAGA 13
 RESULT 563
 ABH34756/c
 ID ABH34756 standard; DNA; 13 BP.
 XX AC ABH34756;
 XX

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XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 87428; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0;
XX
QY 734 AGAAACAGAACCA 745
Db 2 AAAAAACACACCA 13
|||||
RESULT 559
ABH24319
ID ABH24319 standard; DNA; 13 BP.
XX AC ABH24319;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 224296 for detecting SNP TSC0054650.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 224296; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
XX XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0;
XX
QY 736 AAACAGACACAC 747
Db 1 AAACCCACACAC 12
|||||
RESULT 560
ABF49924/C
ID ABF49924 standard; DNA; 13 BP.
XX AC ABF49924;
XX XX
XX DT 21-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 149921 for detecting SNP TSC0037827.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 149921; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX

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CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 734 AGAACAGAACCA 745
Db 2 AAAACACAAACA 13

RESULT 556
ABC07303
ID ABC07303 standard; DNA; 13 BP.
XX
AC ABC07303;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 7294 for detecting SNP TSC0002134.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 7294; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 11 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAACAGAACCA 745
Db 2 AAAACACAAACA 13

RESULT 557
ABC09300/c
ID ABC09300 standard; DNA; 13 BP.
XX
AC ABC09300;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 9291 for detecting SNP TSC0002459.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 9291; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
Db 12 AAACATAAACCC 1

RESULT 558
ABC87411
ID ABC87411 standard; DNA; 13 BP.
XX
AC ABC87411;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 87428 for detecting SNP TSC0021983.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

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QY 736 AATACAGAACACC 747
DB 1 AATACAGAACACC 12
RESULT 551
ABH48475
ID ABH48475 standard; DNA; 13 BP.
XX AC ABH48475;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 248452 for detecting SNP TSC0060719.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 248452; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB00010-ABF99989, ABH0010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -AB00010-ABF99989, ABH0010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 53.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AATACAGAACACC 747
DB 1 AATACAGAACACC 12
RESULT 552
ABH54080/C
ID ABH54080 standard; DNA; 13 BP.
XX AC ABH54080;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 1509 for detecting SNP TSC0000521.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.

DE Oligonucleotide SEQ ID NO 254057 for detecting SNP TSC0061944.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 254057; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB00010-ABF99989, ABH0010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 2 A; 1 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 735 GAATACAGAACACC 746
DB 12 GAATACATATATAC 1
RESULT 553
ABC01518/C
ID ABC01518 standard; DNA; 13 BP.
XX AC ABC01518;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 1509 for detecting SNP TSC0000521.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 32973; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAACAGACA 745
 DB 13 ATAAACATACAA 2

RESULT 549
 ABC87410/C
 ID ABC87410 standard; DNA; 13 BP.
 XX
 AC ABC87410;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 87427 for detecting SNP TSC0021983.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 87427; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAACAGACA 745
 DB 12 AAAACACACAA 1

RESULT 550
 ABH42939
 ID ABH42939 standard; DNA; 13 BP.
 XX
 AC ABH42939;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 242916 for detecting SNP TSC0000966.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 242916; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX ABH42938;
AC
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 242915 for detecting SNP TSC0000966.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPFIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 242915; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
PS Claim 1; SEQ ID NO 242915; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACGACACCC 747
Db 13 AACACACACACCC 2
RESULT 547
ABH48474/c
ID ABH48474 standard; DNA; 13 BP.
XX
AC ABH48474;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 248451 for detecting SNP TSC0060719.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX

PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPFIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 248451; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACGACACCC 747
Db 13 AACACACACACCC 2
RESULT 548
ABC32956/c
ID ABC32956 standard; DNA; 13 BP.
XX
AC ABC32956;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 32973 for detecting SNP TSC0010416.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPFIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;

QY 736 AAACAGAACACC 747
 Db 2 AAACAGAACACC 13
 ||||| |||||

RESULT 544
 ABH02515
 ID ABH02515 standard; DNA; 13 BP.
 XX AC ABH02515;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 202492 for detecting SNP TSC0049770.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 202492; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;

QY 736 AAACAGAACACC 747
 Db 2 AAACAGAACACC 13
 ||||| |||||

RESULT 545
 ABH42937
 ID ABH42937 standard; DNA; 13 BP.
 XX AC ABH42937;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 242914 for detecting SNP TSC0000966.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 242914; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;

QY 736 AAACAGAACACC 747
 Db 1 AAACAGAACACC 12
 ||||| |||||

RESULT 546
 ABH42938/C
 ID ABH42938 standard; DNA; 13 BP.

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 82397; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGACACC 747
DB 12 AAACCGAAACC 1
RESULT 542
ABF30658/C
ID ABF30658 standard; DNA; 13 BP.
XX AC ABF30658;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 130655 for detecting SNP TSC0032625.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX This invention describes novel oligonucleotide primers or peptide nucleic

PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 130655; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAACCA 745
DB 12 ACAACCAAAACA 1
RESULT 543
ABH19407
ID ABH19407 standard; DNA; 13 BP.
XX AC ABH19407;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 219384 for detecting SNP TSC0008134.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 219384; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAGACAGACACC 747

Db 2 AAGACATCACC 13

RESULT 539

ABC23145

ID ABC23145 standard; DNA; 13 BP.

XX AC

XX AC ABC23145;

XX DT

XX 20-FEB-2002 (first entry)

XX DE

XX Oligonucleotide SEQ ID NO 23162 for detecting SNP TSC0004665.

XX KW

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS

XX Homo sapiens.

XX XX

XX WO200177384-A2.

XX XX

XX 18-OCT-2001.

XX XX

XX 06-APR-2001; 2001WO-IB000713.

XX PR

XX 07-APR-2000; 2000DE-01019173.

XX XX

XX (EPIG-) EPIGENOMICS AG.

XX PA

XX Olek A, Piepenbrock C, Berlin K;

XX PI

XX WPI; 2001-657177/75.

XX DR

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX XX

XX Claim 1; SEQ ID NO 23162; 29pp + Sequence Listing; German.

XX SQ

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 9 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 40.0%; Score 8.8; DB 1; Length 13;

XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGACACA 745

Db 2 ACAACACACACA 13

RESULT 540

ABC06154/c

ID ABC06154 standard; DNA; 13 BP.

XX AC

XX AC ABC06154;

XX XX

XX 20-FEB-2002 (first entry)

XX DT

XX DE

XX Oligonucleotide SEQ ID NO 6145 for detecting SNP TSC0001931.

XX XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS

XX Homo sapiens.

XX XX

XX WO200177384-A2.

XX PN

XX 18-OCT-2001.

XX PD

XX XX

XX 06-APR-2001; 2001WO-IB000713.

XX PF

XX 07-APR-2000; 2000DE-01019173.

XX PR

XX (EPIG-) EPIGENOMICS AG.

XX PA

XX Olek A, Piepenbrock C, Berlin K;

XX PI

XX WPI; 2001-657177/75.

XX DR

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX XX

XX Claim 1; SEQ ID NO 6145; 29pp + Sequence Listing; German.

XX PS

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX XX

SQ Sequence 13 BP; 1 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 40.0%; Score 8.8; DB 1; Length 13;

XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGACACA 745

Db 13 AAAACACATAACA 2

RESULT 541

ABC82380/c

ID ABC82380 standard; DNA; 13 BP.

XX AC

XX ABC82380;

XX XX

XX 21-FEB-2002 (first entry)

XX DT

XX DE

XX Oligonucleotide SEQ ID NO 82397 for detecting SNP TSC0020796.

XX KW

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;


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XX PF 06-APR-2001; 2001WO-IB000713.
XX PS 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 253818; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 736 AAACAGAACACC 747
XX DB 1 AAAAAAACACC 12
XX
XX RESULT 537
XX ABH54081
XX ID ABH54081 standard; DNA; 13 BP.
XX AC ABH54081;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 254058 for detecting SNP TSC0061944.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

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XX PT methylation status.
XX PS Claim 1; SEQ ID NO 254058; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 7 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 735 GAACAGAACACC 746
XX DB 2 GAACATATATAC 13
XX
XX RESULT 538
XX ABC94297
XX ID ABC94297 standard; DNA; 13 BP.
XX AC ABC94297;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 94314 for detecting SNP TSC0023541.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 94314; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence

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Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAGAACCA 745
 Db 1 ATAAACATAACA 12
 ||||| |||||
 ||||| |||||

RESULT 534
 ABH42798/C
 ID ABH42798 standard; DNA; 13 BP.
 AC AC
 XX ABH42798;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 242775 for detecting SNP TSC0059232.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 242775; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
 Db 12 AAACAAAAAAC 1
 ||||| |||||
 ||||| |||||

RESULT 535
 ABH43252/C
 ID ABH43252 standard; DNA; 13 BP.
 AC AC
 XX ABH43252;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 253818 for detecting SNP TSC0061853.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX

DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 243229 for detecting SNP TSC0059331.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 243229; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

Sequence 13 BP; 0 A; 1 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
 Db 12 AAACCGAACAC 1
 ||||| |||||
 ||||| |||||

RESULT 536
 ABH53841
 ID ABH53841 standard; DNA; 13 BP.
 AC AC
 XX ABH53841;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 253818 for detecting SNP TSC0061853.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX

XX WIPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 202493; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACGACACC 747
Db 12 AAAAAAACACC 1
|||||
RESULT 532
ABF82674/C
ID ABF82674 standard; DNA; 13 BP.
XX
AC ABF82674;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 182671 for detecting SNP TSC0045147.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WIPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 182671; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 0 C; 4 G; 9 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACGACACC 747
Db 12 AAAAAAACACC 1
|||||
RESULT 533
ABH34757
ID ABH34757 standard; DNA; 13 BP.
XX
AC ABH34757;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 234734 for detecting SNP TSC0057297.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WIPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 234734; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;

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ABF39592/c
ID ABF39592 standard; DNA; 13 BP.
XX AC ABF39592;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 139589 for detecting SNP TSC0034952.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 139589; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 0 A; 2 C; 5 G; 6 T; 0 U; 0 Other;
XX CC Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX CC Best Local Similarity 83.3%; Pred. No. 5e+02;
XX CC Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 CCAGGAGAAACA 740
DB 13 CCAGCGGAAACA 2
|||||
RESULT 530
ABH25372/c
ID ABH25372 standard; DNA; 13 BP.
XX AC ABH25372;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 225349 for detecting SNP TSC0054939.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

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OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 225349; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
XX CC Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX CC Best Local Similarity 83.3%; Pred. No. 5e+02;
XX CC Mismatches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAAACA 745
DB 13 ATAAACAAACA 2
|||||
RESULT 531
ABH02516/c
ID ABH02516 standard; DNA; 13 BP.
XX AC ABH02516;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 202493 for detecting SNP TSC0049770.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;

```

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAACAGACAA 745
Db 1 ATRACATAACA 12
|||||

RESULT 527
ABC37924
ID ABC37924 standard; DNA; 13 BP.
AC ABC37924;
XX 20-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 37941 for detecting SNP TSC0011780.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 37941; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 6 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAACAGAA 743
Db 2 GGAGAGGAGAA 13
|||||

RESULT 528
ABF27769
ID ABF27769 standard; DNA; 13 BP.
XX AC ABF27769;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 127766 for detecting SNP TSC0031989.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 127766; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 735 GAACAGAACAC 746
Db 2 GAACCGAAAC 13
|||||

RESULT 529

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 240239; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 736 AACACAGACACC 747
 Db ||||| |||||
 12 AACCAACACACC 1
 XX
 RESULT 525
 ABC48960
 ID ABC48960 standard; DNA; 13 BP.
 XX
 AC ABC48960;
 XX
 XX 21-FEB-2002 (first entry)
 DT
 XX
 DE Oligonucleotide SEQ ID NO 48977 for detecting SNP TSC0013898.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 OS
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX

PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 48977; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 5 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 733 GAGAAACAGAAC 744
 Db ||||| |||||
 1 GAGAAACGTAC 12
 XX
 RESULT 526
 ABC32957
 ID ABC32957 standard; DNA; 13 BP.
 XX
 AC ABC32957;
 XX
 XX 20-FEB-2002 (first entry)
 DT
 XX
 DE Oligonucleotide SEQ ID NO 32974 for detecting SNP TSC0010416.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 OS
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 32974; 29pp + Sequence Listing; German.


```

XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 29871; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAACCA 745
DB 12 AAAACACAAACA 1
RESULT 521
ABH29482/c
ID ABH29482 standard; DNA; 13 BP.
XX AC ABH29482;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 229459 for detecting SNP TSC0055973.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 05-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 229459; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAACCA 745
DB 12 AAAACACAAACA 1
RESULT 520
ABF23388/c
ID ABF23388 standard; DNA; 13 BP.
XX AC ABF23388;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 123385 for detecting SNP TSC0030855.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.

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Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAGAGAAACACC 747
   ||||| |||||
Db 2 AAGAGAAACACC 13

RESULT 517
ABH41118
ID ABH41118 standard; DNA; 13 BP.
XX AC
XX ABH41118;
XX XX
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide SEQ ID NO 241095 for detecting SNP TSC0058805.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN
XX WO200177384-A2.
XX PD
XX 18-OCT-2001.
XX PF
XX 06-APR-2001; 2001WO-IB000713.
XX PR
XX 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 241095; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match      40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
   ||||| |||||
Db 2 AAGAGAAAGAGA 13

RESULT 518
ABC24673
ID ABC24673 standard; DNA; 13 BP.
XX AC
XX ABC24673
```

```
AC ABC24673;
XX 20-FEB-2002 (first entry)
DT XX
XX Oligonucleotide SEQ ID NO 24690 for detecting SNP TSC0005920.
DE XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN
XX WO200177384-A2.
XX PD
XX 18-OCT-2001.
XX PF
XX 06-APR-2001; 2001WO-IB000713.
XX PR
XX 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 24690; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match      40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGACA 745
   ||||| |||||
Db 2 AAAAACAATAACA 13

RESULT 519
ABC29854/c
ID ABC29854 standard; DNA; 13 BP.
XX AC
XX ABC29854;
XX XX
XX 20-FEB-2002 (first entry)
DT XX
XX Oligonucleotide SEQ ID NO 29871 for detecting SNP TSC0008971.
DE XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN
XX WO200177384-A2.
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XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX CC Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX CC Claim 1; SEQ ID NO 173769; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 13 BP; 9 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 734 AGAACAAGAACCA 745
XX Db 1 AGAATAAGAAAA 12
XX
XX RESULT 515
XX ABF82673
XX ID ABF82673 standard; DNA; 13 BP.
XX AC ABF82673;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 182670 for detecting SNP TSC0045147.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX CC Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX CC Claim 1; SEQ ID NO 182670; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 13 BP; 9 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 734 AGAACAAGAACCA 745
XX Db 1 AGAATAAGAAAA 12
XX
XX RESULT 516
XX ABH40261
XX ID ABH40261 standard; DNA; 13 BP.
XX AC ABH40261;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 240238 for detecting SNP TSC0058589.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX CC Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX CC Claim 1; SEQ ID NO 240238; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 13 BP; 6 A; 7 C; 0 G; 0 T; 0 U; 0 Other;
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 736 AAACAGAACACC 747
XX Db 2 AAACATAAACCC 13
XX

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```
RESULT 512
ABH19990/C
ID ABH19990 standard; DNA; 13 BP.
XX AC
XX ABH19990;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 219967 for detecting SNP TSC0053525.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 219967; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 1 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 737 AACAGAACACCG 748
XX
XX Db 12 AACACAACTCCG 1
XX
XX
XX RESULT 513
ABF48664/C
ID ABF48664 standard; DNA; 13 BP.
XX AC
XX ABF48664;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 148661 for detecting SNP TSC0037536.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
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KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 148661; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 734 AGAAACAGAACCA 745
XX
XX Db 13 AAAACATAACA 2
XX
XX
XX RESULT 514
ABF73772
ID ABF73772 standard; DNA; 13 BP.
XX AC
XX ABF73772;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 173769 for detecting SNP TSC0043273.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
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PS Claim 1; SEQ ID NO 37942; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 7 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAA 743
DB 12 GGAGAGGAGAA 1
RESULT 510
ID ABC64865
XX ABC64865 standard; DNA; 13 BP.
XX
AC ABC64865;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 64882 for detecting SNP TSC0017098.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
DT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 64882; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 7 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAA 743
DB 12 GGAGAGGAGAA 1
RESULT 510
ID ABC64865
XX ABC64865 standard; DNA; 13 BP.
XX
AC ABC64865;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 64882 for detecting SNP TSC0017098.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
DT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 64882; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 7 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAA 745
DB 2 ACACACACATC 13

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGACACC 747
DB 2 AAACACACATC 13
RESULT 511
ID ABF23389 standard; DNA; 13 BP.
XX
AC ABF23389;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 123386 for detecting SNP TSC0030855.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
DT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 123386; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAA 745
DB 2 ACACACACATC 13

XX Oligonucleotide SEQ ID NO 107386 for detecting SNP TSC0026896.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 107386; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAACAGACACA 745
DB 2 ATAAACAAAACA 13
RESULT 508
ABC82381
ID ABC82381 standard; DNA; 13 BP.
XX
XX ABC82381;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 82398 for detecting SNP TSC0020796.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX

PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 82398; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGACACC 747
DB 2 AAACGAAACC 13
RESULT 509
ABC37925/c
ID ABC37925 standard; DNA; 13 BP.
XX
XX ABC37925;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 37942 for detecting SNP TSC0011780.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PF (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 20494; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e-02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AACAGAACACC 747
 DB 2 AAAAAAACACC 13
 RESULT 503
 ABC48961/c
 ID ABC48961 standard; DNA; 13 BP.
 XX AC ABC48961;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 49978 for detecting SNP TSC0013898.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PF (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 24689; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e-02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AACAGAACACC 747
 DB 2 AAAAAAACACC 13
 RESULT 504
 ABC24672/c
 ID ABC24672 standard; DNA; 13 BP.
 XX AC ABC24672;
 XX 20-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 24689 for detecting SNP TSC0005920.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PF (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 24689; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 1 A; 5 C; 2 G; 5 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e-02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 733 GAGAAACGATAC 744
 DB 13 GAGAAACGATAC 2

DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 48978; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 1 A; 5 C; 2 G; 5 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e-02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 733 GAGAAACGATAC 744
 DB 13 GAGAAACGATAC 2
 RESULT 504
 ABC24672/c
 ID ABC24672 standard; DNA; 13 BP.
 XX AC ABC24672;
 XX 20-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 24689 for detecting SNP TSC0005920.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PF (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 24689; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 1 A; 5 C; 2 G; 5 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e-02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 733 GAGAAACGATAC 744
 DB 13 GAGAAACGATAC 2

XX (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 9290; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACAGAACACC 747
Db 2 AACACACAAACCC 13
|||||
RESULT 498
ABC64866/C
ID ABC64866 standard; DNA; 13 BP.
XX
AC ABC64866;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 64883 for detecting SNP TSC0017098.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 64883; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACAGAACACC 747
Db 12 AACACACAAACATC 1
|||||
RESULT 499
ABF24769
ID ABF24769 standard; DNA; 13 BP.
XX
AC ABF24769;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 124766 for detecting SNP TSC0031192.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 124766; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

DB 13 AGAAGCAGCACA 2

RESULT 495
ABC76054/C
ID ABC76054 standard; DNA; 13 BP.
XX AC ABC76054;
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 76071 for detecting SNP TSC0019478.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 76071; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
SQ
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 736 AAACGACACACC 747
XX 12 AAACCTAACACC 1
XX
XX RESULT 496
ABC09298/C
ID ABC09298 standard; DNA; 13 BP.
XX AC ABC09298;
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 9289 for detecting SNP TSC0002459.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 19-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 9289; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 0 C; 5 G; 8 T; 0 U; 0 Other;
SQ
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 736 AAACGACACACC 747
XX 12 AAACACAAACC 1
XX
XX RESULT 497
ABC09299
ID ABC09299 standard; DNA; 13 BP.
XX AC ABC09299;
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 9290 for detecting SNP TSC0002459.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 19-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
XX

AA56496 standard; DNA; 13 BP.
AA56496;
27-JUL-1999 (first entry)
Locked nucleoside analogue oligomer.
Locked nucleoside analogue; LNA; bicyclic; tricyclic; diagnosis;
PCR application; strand displacement oligomer; polymerase; substrate;
nucleotide based drug; diagnostic probe; antisense therapy; antiviral;
antitumour; ss.
Synthetic.
WO9914226-A2.
25-MAR-1999.
14-SEP-1998; 98WO-DK000393.
12-SEP-1997; 97DK-00001054.
19-DEC-1997; 97DK-00001492.
16-JAN-1998; 98DK-00000061.
03-MAR-1998; 98DK-00000286.
29-APR-1998; 98DK-00000585.
05-JUN-1998; 98US-0008309P.
08-JUN-1998; 98DK-00000750.
28-JUL-1998; 98DK-00000982.
(EXIQ-) EXIQON AS.
Wengel J, Nielsen P;
WPI; 1999-337376/28.
New oligonucleotides containing polycyclic, locked nucleoside analogs,
useful e.g. as diagnostic probes or in antisense therapy.
Example 161; Page 186; 269pp; English.
The present invention describes novel modified oligonucleotides (I)
containing at least one locked nucleoside analog (LNA). Monomeric LNA's
(II) are also described. (I) are used: (i) to bind to target sequences in
double-stranded DNA or RNA (by strand displacement or triplex formation);
(ii) as ribozymes; (iii) as therapeutic antisense, antigene or gene
activating agents, specifically for recruitment of RNase H; (iv)
diagnostically for isolation, purification, detection, identification,
quantitation or capture of (synthetic) nucleic acid, e.g. as probes or
primers; (v) as aptamers for therapy, diagnosis, RNA-mediated catalytic
processes and for specific binding to antibodies, drugs etc., including
resolution of enantiomers; (vi) for labeling, then separating, cells; and
(vii) to hybridize to non-coding RNA. LNA are used in synthesis of (I);
as therapeutic and diagnostic agents; to equalize the melting point of;
unmodified reference oligonucleotides and as enzyme substrates. Typical
therapeutic applications are as antiviral and antitumour agents. (I) have
increased specificity and/or affinity, i.e. higher melting point (Tm),
for complementary RNA or DNA than oligomers not containing LNA, and are
more resistant to nuclease. The present sequence represents an oligomer
used in an example from the present invention
Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACGACACC 747
|||||
12 AACACGACACC 1

RESULT 494

AAA62335/c
ID AAA62335 standard; cDNA; 13 BP.
XX
AC AAA62335;
XX
DT 06-NOV-2000 (first entry)
XX
DE Mouse wild-type agouti cDNA exon junction.
XX
KW Mouse; agouti; chromosome 2; coat colour; diabetes; hyperamylinaemia;
KW tumour; obesity; bulimia; anorexia; transgenic mouse; lethal yellow; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT exon 1..7
FT FT /*tag= a
FT FT /number= 1
FT FT 8..13
FT FT /*tag= b
FT FT /number= 2
XX
PN US6080550-A.
XX
PD 27-JUN-2000.
XX
PF 22-JUN-1998; 98US-00102977.
PR 21-MAY-1993; 93US-00064385.
PR 05-JUN-1995; 95US-00462732.
PR 23-JUL-1997; 97US-00899134.
XX
PA (LOCK) LOCKHEED MARTIN ENERGY RES CORP.
XX
PI Woychik RP;
XX
DR WPI; 2000-451204/39.
XX
PT Detecting Agouti protein, useful for screening for the risk of developing
PT e.g. diabetes or obesity in animals, by contacting a biological sample
PT with antibodies specific for the protein and detecting the resulting
PT immune complex.
XX
PS Example 10; Fig 9B; 28pp; English.
XX
CC The present sequence is the junction between the first and second exons
CC of the wild-type agouti cDNA. The agouti locus is located on mouse
CC chromosome 2. It regulates the differential production of black and
CC yellow pigment granules which give rise to the agouti coat colour of the
CC mouse. The cDNA sequence of the lethal yellow allele, which confers an
CC all-yellow phenotype in the heterozygous condition, diverges from the
CC wild-type sequence at the junction between the first and second exons.
CC The agouti locus also contributes to essential developmental processes
CC unrelated to pigmentation. For example, the lethal yellow allele is
CC associated with obesity, diabetes and the development of tumours in a
CC wide variety of tissues. Embryonic lethality and hyperamylinaemia may
CC also be associated with certain agouti alleles. The agouti gene may
CC therefore be used to produce transgenic mice which can be used as animal
CC models for the study of such disorders. Potential therapeutic agents to
CC treat these disorders and others, such as bulimia or anorexia, may be
CC tested using the animal models. Oligonucleotide probes derived from the
CC agouti cDNA sequence may be used for the detection of the agouti gene and
CC mutations in the gene. Antibodies to the agouti gene product may be used
CC as therapeutic and diagnostic agents
XX
SQ Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGACA 745
|||||

SQ Sequence 13 BP; 4 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 729 CCAGGAGAAACA 740
 || |||||
 Db 2 CCTGGAGAGACA 13

RESULT 491
 AAV81348/c
 ID AAV81348 standard; cDNA; 13 BP.
 XX
 AC AAV81348;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE Mouse agouti wild type exon 1/2 junction.
 XX
 KW Mouse; agouti; locus; neonatal skin cell; mutant; inversion; deletion;
 KW mutation; alternative splicing; breakpoint; detection; amplification;
 KW hybridisation; ss.
 XX
 OS Mus sp.
 XX
 FN US5843652-A.
 XX
 PD 01-DEC-1998.
 XX
 PF 05-JUN-1995; 95US-00463387.
 XX
 PR 21-MAY-1993; 93US-00064385.
 XX
 PA (LOCK) LOCKHEED MARTIN ENERGY SYSTEMS INC.
 XX
 PI Woychik RP;
 XX
 DR WPI; 1999-044565/04.
 XX
 PT Detection of Agouti gene by amplification or hybridisation assay - for
 PT diagnosis of diabetes or obesity.
 XX
 PS Claim 10; Fig 9B; 31pp; English.
 XX
 CC The inversion relates to the isolation of the mouse agouti locus cDNA
 CC sequence (AAV81341) from neonatal skin cells. Several mutant sequences
 CC were also isolated: the ISI-Gso and a (SMNU) mutations. The ISI-Gso
 CC mutation contains an inversion which causes the 3' half of the gene to be
 CC juxtaposed with the 1d gene in the opposite transcriptional orientation. Also
 CC the a(SMNU) mutation contains an intragenic 2.8 kb genomic deletion. Also
 CC isolated was a lethal yellow mutant A(y) which contains an alternatively
 CC splice 1st exon sequence (see AAV81342-V81350 for the sequences around
 CC the mutation breakpoints). This sequence represents the wild type
 CC sequence across the exon I and exon II junction. The agouti cDNA is
 CC claimed to be useful in method for detecting the agouti gene by
 CC amplification or hybridisation
 XX
 SQ Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGACA 745
 |||||
 Db 13 AGAAGACAGACA 2

RESULT 492
 AAX56464/c
 ID AAX56464 standard; DNA; 13 BP.

XX AAX56464;
 AC
 XX 27-JUL-1999 (first entry)
 DT
 XX Locked nucleoside analogue oligomer FP2.
 DE
 XX Locked nucleoside analogue; LNA; bicyclic; tricyclic; diagnosis;
 KW PCR application; strand displacement oligomer; polymerase; substrate;
 KW nucleotide based drug; diagnostic probe; antisense therapy; antiviral;
 KW antitumor; ss.
 XX
 OS Synthetic.
 XX
 FN WO9914226-A2.
 XX
 PD 25-MAR-1999.
 XX
 PF 14-SEP-1998; 98WO-DK000393.
 XX
 PR 12-SEP-1997; 97DK-00001054.
 PR 19-DEC-1997; 97DK-00001492.
 PR 16-JAN-1998; 98DK-00000061.
 PR 03-MAR-1998; 98DK-00000286.
 PR 29-APR-1998; 98DK-00000585.
 PR 05-JUN-1998; 98US-0088309P.
 PR 08-JUN-1998; 98DK-00000750.
 PR 28-JUL-1998; 98DK-00000982.
 XX
 PA (EXIQ-) EXIQON AS.
 XX
 PI Wengel J, Nielsen P;
 XX
 DR WPI; 1999-337376/28.
 XX
 PT New oligonucleotides containing polycyclic, locked nucleoside analogs,
 PT useful e.g. as diagnostic probes or in antisense therapy.
 XX
 XX Example 137; Page 152; 269pp; English.
 XX
 CC The present invention describes novel modified oligonucleotides (I)
 CC containing at least one locked nucleoside analog (LNA). Monomeric LNA's
 CC (II) are also described. (I) are used: (i) to bind to target sequences in
 CC double-stranded DNA or RNA (by strand displacement or triplex formation);
 CC (ii) as ribozymes; (iii) as therapeutic antisense, antigene or gene
 CC activating agents, specifically for recruitment of RNase H; (iv)
 CC diagnostically for isolation, purification, detection, identification,
 CC quantitation or capture of (synthetic) nucleic acid, e.g. as probes or
 CC primers; (v) as aptamers for therapy, diagnosis, RNA-mediated catalytic
 CC processes and for specific binding to antibodies, drugs etc., including
 CC resolution of enantiomers; (vi) for labeling, then separating, cells; and
 CC (vii) to hybridize to non-coding RNA. LNA are used in synthesis of (I);
 CC as therapeutic and diagnostic agents; to equalize the melting point of
 CC unmodified reference oligonucleotides and as enzyme substrates. Typical
 CC therapeutic applications are as antiviral and antitumor agents. (I) have
 CC increased specificity and/or affinity, i.e. higher melting point (Tm).
 CC for complementary RNA or DNA than oligomers not containing LNA, and are
 CC more resistant to nuclease. The present sequence represents an oligomer
 CC used in an example from the present invention
 XX
 SQ Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
 |||||
 Db 12 AAACAGAACACC 1

RESULT 493
 AAX56496/c

XX PI Kool ET;

XX WPI; 1997-245044/22.

XX New C-5 thiol-substituted nucleoside derivatives - whose presence in

PT oligonucleotide(s) allows formation of covalent cross-links between non-

PT complementary DNA domains.

XX Example 11; Page 101; 122pp; English.

XX PS

XX The present sequence represents a complementary target sequence for a

CC bridged oligonucleotide derivative (AAV06762). The invention relates to C

CC -5 thiol-substituted nucleoside derivatives which can be incorporated

CC into an RNA or DNA strand during synthesis of oligonucleotides. These

CC compounds can be in the form of cross-linked linear, cross-linked hairpin

CC or bridged circular oligonucleotides. The oligonucleotides may be used

CC for detection and isolation of target nucleic acids, or for targeting

CC drugs to specific cell types (e.g. for treatment of Alzheimer's disease,

CC beta-thalassemia, osteogenesis imperfecta, arthritis, sickle cell anaemia

CC or viral infections). The presence of the nucleoside derivatives in a

CC linear oligonucleotide allows the formation of covalent crosslinks

CC between non-complementary DNA domains

XX SQ Sequence 13 BP; 9 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;

Best Local Similarity 83.3%; Pred. No. 5e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 743

|||||

DB 1 GAAGAAAAGAA 12

RESULT 489

AAV42361/C

ID AAV42361 standard; cDNA; 13 BP.

XX AC AAV42361;

XX 02-OCT-1998 (first entry)

XX Transition point of exon 1 from exon 2 in agouti locus of chromosome 2.

XX Agouti locus; mouse chromosome 2; hair colour; embryonic lethality;

KW Obesity; diabetes; tumour development; transgenic mouse model; ss.

XX OS Mus sp.

XX US5789651-A.

XX 04-AUG-1998.

XX 05-JUN-1995; 95US-00465293.

XX 21-MAY-1993; 93US-00064385.

XX (WARM) MARTIN MARIETTA ENERGY SYSTEMS.

XX Woychik RP;

XX WPI; 1998-446202/38.

XX Transgenic mouse containing agouti gene - exhibiting diabetes, obesity,

PT hyperamylinemia or tumours.

XX Disclosure; Fig 9B; 30pp; English.

XX AAV42361-62 represent the transition point of exon 1 from exon 2 in

CC agouti locus of chromosome 2 of mice (see AAV42361 for wild type

CC sequence). The mutations for homozygous lethal yellow (AAV42362) and

CC heterozygous lethal yellow (AAV42362) occur here. The agouti gene is

CC responsible for hair colour in mice, as well as embryonic lethality,

CC obesity, diabetes, and the development of tumours in a wide variety of

CC tissues. A transgene encoding the agouti gene product is used to

CC transform the germ and somatic cells to produce a transgenic mouse. The

CC transgene includes an operable linkage a promoter necessary for

CC transcription of the transgene in the mouse, and where the agouti gene

CC product is ectopically expressed in the mouse at levels sufficient for

CC the mouse to exhibit insulin-independent diabetes, obesity,

CC hyperamylinemia or tumours. The mouse is used in animal models for the

CC study of diabetes, obesity and tumours, and for the testing of potential

CC therapeutic agents against these diseases

XX SQ Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;

Best Local Similarity 83.3%; Pred. No. 5e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGACACA 745

|||||

DB 13 AGAAGCAGACACA 2

RESULT 490

AAV16594

ID AAV16594 standard; DNA; 13 BP.

XX AC AAV16594;

XX 12-JUN-1998 (first entry)

XX Probe H30 used to identify HLA-DR sequences.

XX DR region; major histocompatibility complex; HLA-DR; HLA-typing;

KW HLA-DR beta consensus sequence; allelic polymorphism;

XX HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant; ss.

XX Synthetic.

OS Homo sapiens.

XX US5702885-A.

XX 30-DEC-1997.

XX 08-APR-1993; 93US-00057957.

XX 27-JUN-1990; 90US-00544218.

XX (BLOO-) BLOOD CENT RES FOUND INC.

XX Gorski JA, Baxter-Lowe LA;

XX WPI; 1998-076408/07.

XX Disclosure; Col 20; 20pp; English.

XX Probes AAV1651-624 are used to identify differences in the DR region of

CC human major histocompatibility complex (HLA-DR). The specification

CC describes a method for HLA-typing, which includes an oligonucleotide

CC probe which undergoes sequence-specific hybridisation with an HLA-DR beta

CC consensus sequence at positions 61-64. The probe contains a labelling

CC substance other than a nucleotide sequence, which facilitates detection

CC of the probe. The HLA sequence of a subject is PCR amplified, and a probe

CC that recognises an allelic polymorphism at a selected HLA locus is

CC contacted with the amplified product. This first probe recognises a HLA-

CC DR beta-allelic polymorphism. A second (different) probe is brought into

CC contact with a second sample of the amplified DNA in a separate reaction,

CC and hybridisation detected. The probes and primers are used for HLA

CC typing, e.g. for tissue, especially bone marrow, transplants

KW glaucoma related disorder; motif; repeat element; regulatory region.
 XX Homo sapiens.
 OS
 XX
 XX
 PN US2003190617-A1.
 XX
 PD 09-OCT-2003.
 XX
 XX
 PF 06-MAR-2002; 2002US-00091281.
 XX
 PR 06-MAR-2002; 2002US-00091281.
 XX
 XX
 PA (SIE/) SI E.
 PA (RAYM/) RAYMOND V.
 PA (MORI/) MORISSETTE J.
 XX
 XX Raymond V, Morissette J, Si E;
 PI
 XX
 XX WPI; 2003-864168/80.
 DR
 XX
 XX New nucleic acid sequences of the optineurin gene are useful to detect
 PT polymorphisms particularly single nucleotide polymorphisms in the
 PT optineurin promoter to diagnose, prognosis and treat glaucoma and related
 PT disorders.
 XX
 XX Claim 11; SEQ ID NO 393; 159pp; English.
 PS
 XX
 CC The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADE13890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient (or the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 CC capable of detecting a SNP located within an optineurin promoter, and
 CC detecting the polymorphism). The invention is used to diagnose and
 CC prognose glaucoma and also to treat glaucoma related disorders. The
 CC present sequence is an optineurin promoter motif, repeat element or
 CC putative regulatory region.
 XX
 XX Sequence 12 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACAGAGACA 745
 Db 1 AAAAAACAGAGACA 12
 |||||
 RESULT 487
 AAX79398
 ID AAX79398 standard; DNA; 13 BP.
 XX
 XX
 AC AAX79398;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE HLA-DR typing probe H30.
 XX
 XX

KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
 KW major histocompatibility complex; bone marrow transplant; primer;
 KW amplification; polymerase chain reaction; probe; polymorphism;
 KW sequence-specific oligonucleotide probe hybridisation; ss.
 XX
 XX Synthetic.
 OS
 XX
 XX US5468611-A.
 PN
 XX
 XX 21-NOV-1995.
 PD
 XX
 PF 08-APR-1993; 93US-00045530.
 XX
 PR 27-JUN-1990; 90US-00544218.
 XX
 XX (BLOO-) BLOOD CENT RES FOUND INC.
 PA
 XX Gorski JA, Baxter-Lowe LA;
 PI
 XX
 XX WPI; 1996-010091/01.
 DR
 XX
 XX Improved method for HLA typing - by DNA amplification and sequence-
 PT specific oligonucleotide hybridisation, used to select bone marrow
 PT donors.
 PT
 XX
 XX Disclosure; Col 19-20; 20pp; English.
 PS
 XX
 CC A novel method of typing the human leukocyte antigen (HLA) of the major
 CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
 CC transplants, involves determining if the donor tissue HLA-DR alleles are
 CC selected from the gp.: HLA-DRW52C, DR12a.b, DR3a.n, DR5a.e, DRNew1, DR6a,
 CC DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and DR1a-
 CC c. The method uses PCR to amplify these regions followed by sequence-
 CC specific oligonucleotide probe hybridisation (SSOPH) using the probes-
 CC AAX79365-X79429. SSOPH allows detection of polymorphisms that predict
 CC differences at a single amino acid level thus reducing errors and
 CC improving the chance of successfully matching tissues
 XX
 XX Sequence 13 BP; 4 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 729 CCAGGAGAGACA 740
 Db 2 CCTGGAGAGACA 13
 |||||
 RESULT 488
 AAV06763
 ID AAV06763 standard; DNA; 13 BP.
 XX
 XX
 AC AAV06763;
 XX
 DT 02-JUN-1998 (first entry)
 XX
 XX Target oligonucleotide for bridged DNA ligand.
 DE
 KW Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
 KW circular; bridged; hairpin; detection; target sequence; ss.
 XX
 XX Synthetic.
 OS
 XX
 XX WO9714708-A1.
 PN
 XX
 XX 24-APR-1997.
 PD
 XX
 PF 29-MAR-1996; 96WO-US004525.
 XX
 XX 04-OCT-1995; 95US-0004778P.
 PR
 XX
 XX (RESE) RESEARCH CORP TECHNOLOGIES INC.
 PA

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 736 AACACAGAACACC 747
|||||
DB 1 AACCTAACACC 12

RESULT 484

AAS20481/C
ID AAS20481 standard; DNA; 12 BP.

XX AAS20481;

XX 20-MAR-2002 (first entry)

XX Oligonucleotide used to prepare a DNA triplex affinity gel.

XX ss; DNA purification; triple helix; plasmid purification;

XX DNA triplex affinity chromatography.

XX Synthetic.

XX WO200192511-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US017122.

XX 26-MAY-2000; 2000US-00580923.

XX (AVET) AVENTIS PHARMA SA.

XX Crouzet J, Scherman D, Wils P, Blanche F, Cameron B;

XX WPI; 2002-097772/13.

XX Purifying double-stranded (ds) DNA from a solution containing dsDNA and
XX other components, comprises passing the solution through a support
XX comprising a covalently coupled oligonucleotide able to form a triple
XX helix with the dsDNA.

XX Claim 1; Page 25; 40pp; English.

XX This invention comprises a method of purifying double-stranded DNA from a
XX solution containing the double-stranded DNA mixed with other components,
XX comprising passing the solution through a support comprising a covalently
XX coupled oligonucleotide capable of forming a triple helix with the double
XX -stranded DNA by hybridisation with a specific sequence present in the
XX double-stranded DNA. The method is useful for purifying double-stranded
XX DNA contained in a solution and mixed with other components. The new
XX method is a simple, rapid and effective method for DNA purification, and
XX makes it possible to obtain especially high purities with high yields.
XX The method enables DNA to be purified from complex mixtures comprising
XX other nucleic acids, proteins, endotoxins, nucleases and the like. The
XX supports may be readily recycled, and the DNAs obtained display improved
XX properties to pharmaceutical safety. Further, the method entails only one
XX step contrary to prior art. The present sequence represents an
XX oligonucleotide which can be used to prepare a DNA triplex affinity gel
XX used to purify ColEI derived plasmids by triple-helix affinity
XX chromatography

XX Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 731 AGGAGAAACAGA 742
|||||
DB 12 AGGAAAAAAGA 1

RESULT 485

ADD71434/C
ID ADD71434 standard; DNA; 12 BP.

XX ADD71434;

XX 15-JAN-2004 (first entry)

XX Stimulus-responsive DNA organization oligonucleotide #4.

XX ss; stimulus-responsive DNA organization; supercoil; rotation;
XX external stimulus; medical micromachines; artificial muscle.

XX Synthetic.

XX WO2003072772-A1.

XX 04-SEP-2003.

XX 28-AUG-2002; 2002WO-JP008656.

XX 27-FEB-2002; 2002JP-00051927.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Yui N, Ootani T;

XX WPI; 2003-679952/64.

XX Stimulus-responsive DNA organization of highly compatible functional
XX material undergoing reversible formation/dissociation of supercoil or
XX rotation in response to external stimulus, useful as e.g. artificial
XX muscles.

XX Example 3; SEQ ID NO 5; 29pp; Japanese.

XX The invention relates to a stimulus-responsive DNA organization
XX undergoing formation/dissociation of a supercoil or rotation in response
XX to an external stimulus and comprises a number of plasmid DNAs ligated in
XX it. The DNA organization is applicable in various materials and body
XX parts or medical micromachines e.g. artificial muscles. This sequence
XX represents an oligonucleotide used in the method of the invention.

XX Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 731 AGGAGAAACAGA 742
|||||
DB 12 AGGAAAAAAGA 1

RESULT 486

ADE14282
ID ADE14282 standard; DNA; 12 BP.

XX ADE14282;

XX 29-JAN-2004 (first entry)

XX Optineurin promoter motif, repeat element or regulatory region #391.

XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX SNP; glaucoma; progressive ocular hypertensive disorder;

XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 281819; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AAACAGACACACC 747
 Db 12 AAACAAATACC 1
 RESULT 482
 AB108687
 ID AB108687 standard; DNA; 12 BP.
 AC AB108687;
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 308660 for detecting SNP TSC0023145.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 308660 for detecting SNP TSC0023145.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD
 DT 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PT methylation status.
 XX Claim 1; SEQ ID NO 308660; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AAACAGACACACC 747
 Db 1 AAACACACACACC 12
 RESULT 483
 AB115833
 ID AB115833 standard; DNA; 12 BP.
 AC AB115833;
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 315806 for detecting SNP TSC0027111.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD
 DT 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 315806; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence


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Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAA 743
DB 12 GGAGAAATAGAA 1
RESULT 479
ABI26708/c
ID ABI26708 standard; DNA; 12 BP.
AC ABI26708;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 326681 for detecting SNP TSC0033222.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 326681; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGAACACC 747
DB 12 AAACAATCACC 1
RESULT 480
ABH81408
ID ABH81408 standard; DNA; 12 BP.
XX
AC ABH81408;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 281819 for detecting SNP TSC0010087.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
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DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 281401 for detecting SNP TSC0009722.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 281401; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGAACACC 747
DB 1 AAATAAACACC 12
RESULT 481
ABH81826/c
ID ABH81826 standard; DNA; 12 BP.
XX
AC ABH81826;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 281819 for detecting SNP TSC0010087.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
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XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 365188; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACGAGACA 745
 Db 1 ACAACCGAGACA 12
 | | | | | | | | | |
 | | | | | | | | | |
 RESULT 477
 AB123702
 ID AB123702 standard; DNA; 12 BP.
 AC AB123702;
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 323675 for detecting SNP TSC0031537.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 323675; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACGAGACA 745
 Db 1 ACAACCGAGACA 12
 | | | | | | | | | |
 | | | | | | | | | |
 RESULT 477
 AB123702
 ID AB123702 standard; DNA; 12 BP.
 AC AB123702;
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 323675 for detecting SNP TSC0031537.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 323675; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 8 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACGAGACA 745
 Db 1 ATAACATACCA 12
 | | | | | | | | | |
 | | | | | | | | | |
 RESULT 478
 AB147510/C
 ID AB147510 standard; DNA; 12 BP.
 AC AB147510;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 347483 for detecting SNP TSC0045131.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 347483; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;

ABI46968
ID ABI46968 standard; DNA; 12 BP.
XX AC ABI46968;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 346941 for detecting SNP TSC0044842.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 346941; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB09989, AB00010-ABF99989, ABH0010-ABH99989 and ABT00010-ABT2073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB09989, ABF0010-ABF99989, ABH0010-ABH99989 and ABT00010-ABT2073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGAACACC 747
DB 1 AAACAGAACACC 12
RESULT 475
ABI67539
ID ABI67539 standard; DNA; 12 BP.
XX AC ABI67539;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 367512 for detecting SNP TSC0056383.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;

OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 367512; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB09989, ABF0010-ABF99989, ABH0010-ABH99989 and ABT00010-ABT2073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGAACACC 747
DB 1 AAACAGAACACC 12
RESULT 476
ABI65215
ID ABI65215 standard; DNA; 12 BP.
XX AC ABI65215;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 365188 for detecting SNP TSC0054956.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 271109; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAGA 742
Db 1 AGGAGAGAGAGA 12
RESULT 470
ABI44609
ID ABI44609 standard; DNA; 12 BP.
XX AC ABI44609;
XX DT 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 344582 for detecting SNP TSC0043623.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 344582; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAGA 742
Db 1 AGGAGAAAAA 12
RESULT 471
ABI77488
ID ABI77488 standard; DNA; 12 BP.
XX AC ABI77488;
XX DT 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 377461 for detecting SNP TSC0062342.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 377461; 29pp + Sequence Listing; German.

```

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
  Query Match 40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Mismatches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAA 738
Db 1 TGAGAGGAGAAA 12
  |||||
  |||||

RESULT 467
ABIS8619/c
ID ABI58619 standard; DNA; 12 BP.
XX
AC ABI58619;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 358592 for detecting SNP TSC0051195.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 358592; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
  Query Match 40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Mismatches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAGACGAAA 743

```

```

Db 12 GGAGAGAGATAA 1
  |||||
  |||||

RESULT 468
ABH70467
ID ABH70467 standard; DNA; 12 BP.
XX
AC ABH70467;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 270444 for detecting SNP TSC0002139.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 270444; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
  Query Match 40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Mismatches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACACCC 747
Db 1 AAACAGACACCTCC 12
  |||||
  |||||

RESULT 469
ABH71132
ID ABH71132 standard; DNA; 12 BP.
XX
AC ABH71132;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 271109 for detecting SNP TSC0002401.

```

XX 18-OCT-2001.
XX
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX FA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 298959; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 736 AAACAGACACC 747
Db 1 AAACATAAACC 12
RESULT 465
ABI08983/C
ID ABI08983 standard; DNA; 12 BP.
XX
XX AC ABI08983;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 308956 for detecting SNP TSC0023294.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 308956; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 732 GGAGAAACAGAA 743
Db 12 GGATAAACAGAA 1
RESULT 466
ABI47139
ID ABI47139 standard; DNA; 12 BP.
XX
XX AC ABI47139;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 347112 for detecting SNP TSC0044915.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 347112; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

```

Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 745
Db 12 AGAAACAGAAC 1

RESULT 462
ABH97184
ID ABH97184 standard; DNA; 12 BP.
XX
AC ABH97184;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 269724 for detecting SNP TSC0001860.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DE 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 269724; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 1 A; 1 C; 3 G; 7 T; 0 U; 0 Other;
XX
Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAC 744
Db 12 GATAAACCAAC 1

RESULT 463
ABH97184
ID ABH97184 standard; DNA; 12 BP.
XX
AC ABH97184;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 298959 for detecting SNP TSC0018363.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX

```


XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 330934; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, cardiovascular and metabolic disorders. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAGAGAGACA 745
 Db 1 AGAAGAGAGAAA 12
 |||||
 RESULT 460
 ABH86305
 ID ABH86305 standard; DNA; 12 BP.
 XX
 AC ABH86305;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 286298 for detecting SNP TSC0012661.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 286298; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AACACAGAACAC 747
 Db 1 AACACAAACCCC 12
 |||||
 RESULT 461
 AB172010/C
 ID AB172010 standard; DNA; 12 BP.
 XX
 AC AB172010;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 371983 for detecting SNP TSC0059099.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 371983; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;
 SQ

```

RESULT 457
ABI25965
ID ABI25965 standard; DNA; 12 BP.
XX
AC ABI25965;
XX
DT 22-FEB-2002 (first entry)
XX
DZ Oligonucleotide primer SEQ ID NO 325938 for detecting SNP TSC0032808.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 325938; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: the sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: the sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 737 AACAGAACACCG 748
DB 1 AACAAAAAACCG 12
|||||
|||||

RESULT 458
ABI48399
ID ABI48399 standard; DNA; 12 BP.
XX
AC ABI48399;
XX
DT 22-FEB-2002 (first entry)
XX
DZ Oligonucleotide primer SEQ ID NO 348372 for detecting SNP TSC0045565.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 325938; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: the sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 737 AACAGAACACCG 748
DB 1 AACAAAAAACCG 12
|||||
|||||

RESULT 459
ABI30861
ID ABI30861 standard; DNA; 12 BP.
XX
AC ABI30861;
XX
DT 22-FEB-2002 (first entry)
XX
DZ Oligonucleotide primer SEQ ID NO 330834 for detecting SNP TSC0035783.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.

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KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 348372; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACCG 747
DB 1 AACATTACACCG 12
|||||
|||||

RESULT 459
ABI30861
ID ABI30861 standard; DNA; 12 BP.
XX
AC ABI30861;
XX
DT 22-FEB-2002 (first entry)
XX
DZ Oligonucleotide primer SEQ ID NO 330834 for detecting SNP TSC0035783.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.

```

XX Claim 1; SEQ ID NO 270303; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAACACA 745
Db 1 AAAAAACAGAACACA 12

RESULT 455
ABI11213/c
ID ABI11213 standard; DNA; 12 BP.
XX
AC ABI11213;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 311186 for detecting SNP TSC0024345.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
PT
XX
XX Claim 1; SEQ ID NO 311186; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAACACA 745
Db 1 AAAAAACAGAACACA 12

RESULT 455
ABI11213/c
ID ABI11213 standard; DNA; 12 BP.
XX
AC ABI11213;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 311186 for detecting SNP TSC0024345.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
PT
XX
XX Claim 1; SEQ ID NO 311186; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAACACA 745
Db 1 AAAAAACAGAACACA 12

RESULT 456
ABI22547/c
ID ABI22547 standard; DNA; 12 BP.
XX
AC ABI22547;
XX
XX 22-FEB-2002 (first entry)
DT
XX
DE Oligonucleotide primer SEQ ID NO 322520 for detecting SNP TSC0030916.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
PT
XX
XX Claim 1; SEQ ID NO 322520; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAACACA 745
Db 12 ATAAACAGAACACA 1

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 2 C; 3 G; 7 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACA 746
Db 12 GAAACAGAACACA 1

RESULT 456
ABI22547/c
ID ABI22547 standard; DNA; 12 BP.
XX
AC ABI22547;
XX
XX 22-FEB-2002 (first entry)
DT
XX
DE Oligonucleotide primer SEQ ID NO 322520 for detecting SNP TSC0030916.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
PT
XX
XX Claim 1; SEQ ID NO 322520; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAACACA 745
Db 12 ATAAACAGAACACA 1

XX Oligonucleotide primer SEQ ID NO 316187 for detecting SNP TSC0027326.
DE
DE
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 316187; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: the sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 736 AAACAGAACACC 747
XX ||||| |||||
XX 1 AAACAAAAACC 12
XX
XX RESULT 453
XX AB117624
XX ID AB117624 standard; DNA; 12 BP.
XX AC AB117624;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 317597 for detecting SNP TSC0028131.
DE
DE
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 316187; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: the sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 736 AAACAGAACACC 747
XX ||||| |||||
XX 1 AAACAAAAACC 12
XX
XX RESULT 453
XX AB117624
XX ID AB117624 standard; DNA; 12 BP.
XX AC AB117624;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 317597 for detecting SNP TSC0028131.
DE
DE
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 317597; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 731 AGGAGAAACAGA 742
XX ||||| |||||
XX 1 AGGAGAGATAGA 12
XX
XX Db
XX
XX RESULT 454
XX ABH70326
XX ID ABH70326 standard; DNA; 12 BP.
XX AC ABH70326;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 270303 for detecting SNP TSC0002082.
DE
DE
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAA 738
DB 1 TGTTAGGAGAAA 12

RESULT 450
ABI03566/c
ID ABI03566 standard; DNA; 12 BP.
XX
AC ABI03566;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 303539 for detecting SNP TSC0020522.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 303539; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACGAGACACC 747
DB 12 AAACGAGACCCC 1

RESULT 451
ABH84329/c
ID ABH84329 standard; DNA; 12 BP.
XX
AC ABH84329;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 284322 for detecting SNP TSC0011780.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 284322; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 6 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 743
DB 12 GGAGAGGAGAAA 1

RESULT 452
ABI16214
ID ABI16214 standard; DNA; 12 BP.
XX
AC ABI16214;
XX
DT 22-FEB-2002 (first entry)

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XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 353314; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 736 AAGACAGACACC 747
Db |||||
1 AAGACAGACACC 12

RESULT 448
ABI53341
ID ABI53341 standard; DNA; 12 BP.
XX AC ABI53341;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide primer SEQ ID NO 353314 for detecting SNP TSC0048447.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 353314; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 10 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 734 AGAAGACAGACA 745
Db |||||
1 AGAAGACAGAAA 12

RESULT 448
ABI53341
ID ABI53341 standard; DNA; 12 BP.
XX AC ABI53341;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide primer SEQ ID NO 353314 for detecting SNP TSC0048447.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX

```

SQ Sequence 12 BP; 6 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAACAGAACAC 746
 ||||| |||||
 Db 1 GAACAGAACACC 12

RESULT 445
 ABH79549
 ID ABH79549 standard; DNA; 12 BP.
 AC ABH79549;
 XX
 XX
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 279542 for detecting SNP TSC0007468.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 279542 for detecting SNP TSC0007468.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 DT 06-APR-2001; 2001WO-IB000713.
 XX
 DE 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 279542; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
 ||||| |||||
 Db 1 AAAAACACACC 12

RESULT 446
 ABI07767
 ID ABI07767 standard; DNA; 12 BP.
 AC ABI07767;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 333457 for detecting SNP TSC0037554.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.

ID ABI07767 standard; DNA; 12 BP.
 XX
 AC ABI07767;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 307740 for detecting SNP TSC0022659.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 DT 06-APR-2001; 2001WO-IB000713.
 XX
 DE 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 307740; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 8 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 743
 ||||| |||||
 Db 1 GGAGAAATAAAA 12

RESULT 447
 ABI33484
 ID ABI33484 standard; DNA; 12 BP.
 XX
 AC ABI33484;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 333457 for detecting SNP TSC0037554.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.

XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 301683; 29pp + Sequence Listing; German.
 PS
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGA 742
 DB 12 AGGAGAAACAAA 1
 RESULT 443
 ABH73881/c
 ID ABH73881 standard; DNA; 12 BP.
 XX
 AC ABH73881;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 273866 for detecting SNP TSC0003339.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 273866; 29pp + Sequence Listing; German.
 PS
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGA 742
 DB 12 AGGAGAAACAAA 1
 RESULT 444
 ABI04383
 ID ABI04383 standard; DNA; 12 BP.
 XX
 AC ABI04383;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 304356 for detecting SNP TSC0020884.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 304356; 29pp + Sequence Listing; German.
 PS
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAACAACAGAA 745
 DB 12 AAAAAACAAACA 1
 RESULT 444
 ABI04383
 ID ABI04383 standard; DNA; 12 BP.
 XX
 AC ABI04383;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 304356 for detecting SNP TSC0020884.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 304356; 29pp + Sequence Listing; German.
 PS
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAACAACAGAA 745
 DB 12 AAAAAACAAACA 1

Db 1 GGAGAAAAGGAA 12

RESULT 440

AB122903/C

ID AB122903 standard; DNA; 12 BP.

XX AC AB122903;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 322876 for detecting SNP TSC0031092.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PI WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 322876; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 0 A; 1 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGACAC 746

Db 12 GAAACAAAAC 1

RESULT 441

ABH76378

ID ABH76378 standard; DNA; 12 BP.

XX AC ABH76378;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 276371 for detecting SNP TSC0004169.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PI WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 276371; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 GAAACAGACAC 745

Db 1 AAAAAAACA 12

RESULT 442

ABI01710/C

ID ABI01710 standard; DNA; 12 BP.

XX AC ABI01710;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 301683 for detecting SNP TSC0019609.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 367441; 29pp + Sequence Listing; German.

XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747

DB 12 AAAAAAACACC 1

RESULT 438

ABI75557
ID ABI75557 standard; DNA; 12 BP.

XX ABI75557;

XX
XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 375530 for detecting SNP TSC0061310.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 375530; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747

DB 1 AAAAAAACACC 12

RESULT 439

ABI80821
ID ABI80821 standard; DNA; 12 BP.

XX ABI80821;

XX
XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 380794 for detecting SNP TSC0000528.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 380794; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAACAGAA 743

|||||


```

Best Local Similarity 83.3%; Pred No. 4. 9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
    |||||
Db 12 AGGAGAGAGAGA 1

RESULT 434
ABH74521/C
ID ABH74521 standard; DNA; 12 BP.

```

XX	ABH74521;	
AC		
XX		
XX		
DT	22-FEB-2002	(first entry)
XX		
XX		
XX		
DE	Oligonucleotide primer	SEQ ID NO 274506 for detecting SNP TSC0003574.
XX		
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;	
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;	
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.	
XX		
XX	Homo sapiens.	
OS		
XX		
XX		
PN	WO200177384-A2.	
XX		
XX		
PD	18-OCT-2001.	
XX		

```

XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 274506; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

```

```

SQ      Sequence 12 BP; 0 A; 1 C; 2 G; 9 T; 0 U; 0 Other;

Query Match          40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      733 GAGAAACGAAAC 744
        |||||
Db       12 GAAACACAAAC 1

RESULT 435
ABH75098/c
ID      ABH75098 standard; DNA; 12 BP.
XX
AC      ABH75098;

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```

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match      40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAAGAAC 745
Db 12 AAAAAACATAACA 1

RESULT 428
ABI43959/c
ID ABI43959 standard; DNA; 12 BP.
XX
AC ABI43959;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 343932 for detecting SNP TSC0005420.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 343932; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match      40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAAGAAC 745
Db 12 AAAAAACATAACA 1

RESULT 428
ABI43959/c
ID ABI43959 standard; DNA; 12 BP.
XX
AC ABI43959;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 343932 for detecting SNP TSC0005420.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 343932; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match      40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAAGAAC 745
Db 12 AAAAAACATAACA 1

RESULT 428
ABI43959/c
ID ABI43959 standard; DNA; 12 BP.
XX
AC ABI43959;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 343932 for detecting SNP TSC0005420.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 343932; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match      40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAGAACATC 1

RESULT 430
ABH68614
ID ABH68614 standard; DNA; 12 BP.
XX
AC ABH68614;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 268591 for detecting SNP TSC0001238.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

```

XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 347162; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGAACACC 747
Db 1 AAACCCAACACC 12
|||||
RESULT 426
ABI52196
ID ABI52196 standard; DNA; 12 BP.
XX AC ABI52196;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352169 for detecting SNP TSC0047706.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

PS Claim 1; SEQ ID NO 352169; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAACCA 745
Db 1 ACAAAACAAACCA 12
|||||
RESULT 427
ABH81189/c
ID ABH81189 standard; DNA; 12 BP.
XX AC ABH81189;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 281182 for detecting SNP TSC0009516.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 281182; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at

```

QY      736 AATACAGACACC 747
Db      1 AATACAGACACC 12

RESULT 423
ABI31059
ID ABI31059 standard; DNA; 12 BP.
XX
XX
AC ABI31059;
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 331032 for detecting SNP TSC0035932.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 331032; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB099989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Claim 1; SEQ ID NO 331032; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB099989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AATACAGACACC 747
Db      1 AATACAGACACC 12

RESULT 424
ABI12029
ID ABI12029 standard; DNA; 12 BP.
XX
XX
AC ABI12029;
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 331032 for detecting SNP TSC0044938.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 331032; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB099989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AATACAGACACC 747
Db      1 AATACAGACACC 12

RESULT 425
ABI47189
ID ABI47189 standard; DNA; 12 BP.
XX
XX
AC ABI47189;
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 347162 for detecting SNP TSC0044938.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
PF 06-APR-2001; 2001WO-IB000713.
XX

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DE Oligonucleotide primer SEQ ID NO 312002 for detecting SNP TSC0024799.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 312002; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB099989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAACACAGACA 745
Db      1 ATAAACACACA 12

RESULT 425
ABI47189
ID ABI47189 standard; DNA; 12 BP.
XX
XX
AC ABI47189;
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 347162 for detecting SNP TSC0044938.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
PF 06-APR-2001; 2001WO-IB000713.
XX

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XX SQ Sequence 12 BP; 9 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 734 AGAAACAGAGACA 745
Db 1 AAAAAGAGAGACA 12
RESULT 421
AAA06946/C
ID AAA06946 standard; RNA; 12 BP.
XX AC AAA06946;
XX DT 03-JUL-2000 (first entry)
XX DE Human XIAP IRES wild-type polypyrimidine tract.
XX KW X-linked inhibitor of apoptosis protein; XIAP; IRES;
XX KW internal ribosome entry site; human; cap-independent translation;
XX KW drug screening; cancer; autoimmune disease; degenerative disease;
XX KW immunorejection; gene therapy; polypyrimidine tract; ss.
XX OS Homo sapiens.
XX FN WO200005366-A2.
XX PD 03-FEB-2000.
XX PF 22-JUL-1999; 99WO-IB001415.
XX PR 24-JUL-1998; 98US-00121979.
XX PA (UYOT-) UNIV OTTAWA.
XX PI Korneluk RG, Holcik M, Liston P;
XX WPI; 2000-338644/29.
XX New isolated X-linked inhibitor of apoptosis internal ribosome entry
XX site, used to develop agents for treating, e.g. cancer.
XX Example IV; Fig 5A; 87pp; English.
XX The invention relates to the identification of modulators of cap-
XX independent translation and apoptosis. The method comprises exposing a
XX test compound to an X-linked inhibitor of apoptosis protein (XIAP)
XX internal ribosome entry site (IRES) reporter cistron, and determining the
XX amount of translation from the XIAP IRES reporter cistron exposed to the
XX compound relative to the translation from the unexposed XIAP IRES
XX reporter cistron. A relative increase in translation from the exposed
XX XIAP IRES reporter cistron indicates a compound that increases XIAP IRES-
XX dependent (cap independent) translation. XIAP protein plays a critical
XX role in the regulation of apoptosis by suppressing activation of
XX downstream caspase-3 and caspase-7. Compounds identified by the method
XX which decrease XIAP IRES-dependent translation (thus leading to reduced
XX expression of XIAP and hence increasing apoptosis) can be used for
XX treating cancer. The methods can also be used for the identification of
XX agents that upregulate XIAP translation and hence inhibit apoptosis,
XX which can be used to treat autoimmune diseases, degenerative diseases or
XX immunorejection. Such agents may, for example, be used to inhibit
XX apoptosis of neurons in conditions such as Alzheimer's disease; islet
XX cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis
XX pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial
XX infarction. They can also be used to enhance the survival of cell or
XX organ transplants. XIAP IRES elements can also be incorporated into
XX expression constructs which encode XIAP or other IAPs (inhibitor of
XX apoptosis proteins, e.g., XIAP; AAY81440). Such constructs may be used in

CC gene therapy to inhibit apoptosis in a cell. The present sequence
CC represents the RNA sequence of the wild-type human XIAP IRES
CC polypyrimidine tract which, along with mutant polypyrimidine tracts
CC (AAA06947-A06954), was used in an exemplification of the present
CC invention to determine whether the polypyrimidine tract is important for
CC XIAP IRES function
XX Sequence 12 BP; 0 A; 2 C; 1 G; 0 T; 9 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 734 AGAAACAGAGACA 745
Db 12 AAAAAGAGAGACA 1
RESULT 422
ABH75798
ID ABH75798 standard; DNA; 12 BP.
XX AC ABH75798;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 275791 for detecting SNP TSC0004001.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 275791; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABQ0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 745
:|||||
Db 13 RAAACACACA 3

RESULT 419
AAA06941/C
ID AAA06941 standard; DNA; 12 BP.
XX
AC AAA06941;
DT 03-JUL-2000 (first entry)
XX
DE Human XIAP IRES polypyrimidine tract.
XX
KW X-linked inhibitor of apoptosis protein; XIAP; IRES;
KW internal ribosome entry site; human; cap-independent translation;
KW drug screening; cancer; autoimmune disease; degenerative disease;
KW immunorejection; gene therapy; polypyrimidine tract; ds.
XX
OS Homo sapiens.
XX
PN WO200005366-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-IB001415.
XX
PR 24-JUL-1998; 98US-00121979.
PR 14-JUN-1999; 99US-00332319.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Holcik M, Liston P;
XX
DR WPI; 2000-338644/29.
XX
PT New isolated X-linked inhibitor of apoptosis internal ribosome entry
PT site, used to develop agents for treating, e.g. cancer.
XX
PS Disclosure; Page 31; 87pp; English.

CC The invention relates to the identification of modulators of cap-
CC independent translation and apoptosis. The method comprises exposing a
CC test compound to an X-linked inhibitor of apoptosis protein (XIAP)
CC internal ribosome entry site (IRES) reporter cistron, and determining the
CC amount of translation from the XIAP IRES reporter cistron exposed to the
CC compound relative to the translation from the unexposed XIAP IRES
CC reporter cistron. A relative increase in translation that increases XIAP IRES-
CC dependent (cap independent) translation. XIAP protein plays a critical
CC role in the regulation of apoptosis by suppressing activation of
CC downstream caspase-3 and caspase-7. Compounds identified by the method
CC which decrease XIAP IRES-dependent translation (thus leading to reduced
CC expression of XIAP and hence increasing apoptosis) can be used for
CC treating cancer. The methods can also be used for the identification of
CC agents that upregulate XIAP translation and hence inhibit apoptosis,
CC which can be used to treat autoimmune diseases, degenerative diseases or
CC immunorejection. Such agents may, for example, be used to inhibit
CC apoptosis of neurons in conditions such as Alzheimer's disease; islet
CC cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis
CC pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial
CC infarction. They can also be used to enhance the survival of cell or
CC organ transplants. XIAP IRES elements can also be incorporated into
CC expression constructs which encode XIAP or other IAPs (inhibitor of
CC apoptosis proteins, e.g., TIAP: AAY81440). Such constructs may be used in
CC gene therapy to inhibit apoptosis in a cell. The present sequence
CC represents the polypyrimidine tract of human XIAP IRES, which is
CC necessary for IRES-dependent translation of XIAP

QY 734 AGAACAGAAC 745
:|||||
Db 12 AAAAGAGAAC 1

RESULT 420
AAA06942
ID AAA06942 standard; DNA; 12 BP.
XX
AC AAA06942;
DT 03-JUL-2000 (first entry)
XX
DE Human XIAP IRES polypyrimidine tract antisense oligonucleotide.
XX
KW X-linked inhibitor of apoptosis protein; XIAP; IRES;
KW internal ribosome entry site; human; cap-independent translation;
KW drug screening; cancer; autoimmune disease; degenerative disease;
KW immunorejection; gene therapy; polypyrimidine tract; antisense; ss.
XX
OS Homo sapiens.
XX
PN WO200005366-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-IB001415.
XX
PR 24-JUL-1998; 98US-00121979.
PR 14-JUN-1999; 99US-00332319.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Holcik M, Liston P;
XX
DR WPI; 2000-338644/29.
XX
PT New isolated X-linked inhibitor of apoptosis internal ribosome entry
PT site, used to develop agents for treating, e.g. cancer.
XX
PS Disclosure; Page 31; 87pp; English.

CC The invention relates to the identification of modulators of cap-
CC independent translation and apoptosis. The method comprises exposing a
CC test compound to an X-linked inhibitor of apoptosis protein (XIAP)
CC internal ribosome entry site (IRES) reporter cistron, and determining the
CC amount of translation from the XIAP IRES reporter cistron exposed to the
CC compound relative to the translation from the unexposed XIAP IRES
CC reporter cistron. A relative increase in translation that increases XIAP IRES-
CC dependent (cap independent) translation. XIAP protein plays a critical
CC role in the regulation of apoptosis by suppressing activation of
CC downstream caspase-3 and caspase-7. Compounds identified by the method
CC which decrease XIAP IRES-dependent translation (thus leading to reduced
CC expression of XIAP and hence increasing apoptosis) can be used for
CC treating cancer. The methods can also be used for the identification of
CC agents that upregulate XIAP translation and hence inhibit apoptosis,
CC which can be used to treat autoimmune diseases, degenerative diseases or
CC immunorejection. Such agents may, for example, be used to inhibit
CC apoptosis of neurons in conditions such as Alzheimer's disease; islet
CC cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis
CC pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial
CC infarction. They can also be used to enhance the survival of cell or
CC organ transplants. XIAP IRES elements can also be incorporated into
CC expression constructs which encode XIAP or other IAPs (inhibitor of
CC apoptosis proteins, e.g., TIAP: AAY81440). Such constructs may be used in
CC gene therapy to inhibit apoptosis in a cell. The present sequence
CC represents the polypyrimidine tract of human XIAP IRES, which is
CC necessary for IRES-dependent translation of XIAP

Sequence 12 BP; 0 A; 2 C; 1 G; 9 T; 0 U; 0 Other;

DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 68284; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 5 C; 1 G; 5 T; 0 U; 1 Other;
SQ
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 731 AGGAGAAAC 739
Db 11 AGGAGAAAC 3
RESULT 417
ABH65495/c
ID ABH65495 standard; DNA; 13 BP.
XX
XX ABH65495;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 265472 for detecting SNP TSC0064332.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 265472; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 1 Other;
SQ
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 734 AGAAACAGAAC 744
Db 11 AGAAACAGAA 1
RESULT 418
ABF34136/c
ID ABF34136 standard; DNA; 13 BP.
XX
XX ABF34136;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 134133 for detecting SNP TSC0033441.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 134133; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 1 Other;
SQ
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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ID ABF34137 standard; DNA; 13 BP.
XX AC ABF34137;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 134134 for detecting SNP TSC0033441.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 134134; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF0010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 1 Other;
XX Query Match 40.9%; Score 9; DB 1; Length 13;
XX Best Local Similarity 81.8%; Pred. NO. 4.7e+02;
XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX QY 735 GAACACAGAAC 745
XX Db 1 RAAACACACA 11
XX RESULT 415
XX ABF81153
XX ID ABF81153 standard; DNA; 13 BP.
XX AC ABF81153;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 181150 for detecting SNP TSC0004966.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.

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XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 181150; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF0010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 1 Other;
XX Query Match 40.9%; Score 9; DB 1; Length 13;
XX Best Local Similarity 81.8%; Pred. NO. 4.7e+02;
XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX QY 735 GAACACAGAAC 745
XX Db 1 RAAACACACA 11
XX RESULT 416
XX ABC68267/c
XX ID ABC68267 standard; DNA; 13 BP.
XX AC ABC68267;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 68284 for detecting SNP TSC0017813.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX

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CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 1 Other;
XX
XX Query Match 40.9%; Score 9; DB 1; Length 13;
XX Best Local Similarity 81.8%; Pred. No. 4.7e+02;
XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAAAC 745
DB 1 RAAACATAACA 11
:|||||

RESULT 412
ABH65494
ID ABH65494 standard; DNA; 13 BP.
XX AC ABH65494;
XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 265471 for detecting SNP TSC0064332.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 265471; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 7 A; 0 C; 3 G; 2 T; 0 U; 1 Other;
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGAAAC 744
DB 3 AGAAGAGAAAY 13
:|||||

RESULT 413
ABC68266
ID ABC68266 standard; DNA; 13 BP.
XX AC ABC68266;
XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 68283 for detecting SNP TSC0017813.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 68283; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 1 C; 5 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 40.9%; Score 9; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 4.7e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAAC 739
DB 3 AGGAGAAAC 11
:|||||

RESULT 414
ABF34137

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 1 Other;
SQ Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
Db 1 RACACACACC 11
RESULT 407
ABF24041
ID ABF24041 standard; DNA; 13 BP.
AC ABF24041;
XX 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 124038 for detecting SNP TSC0031015.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 124038 for detecting SNP TSC0031015.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 124038; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 1 Other;
SQ Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAACCA 745
Db 1 RACACACACC 11
RESULT 407
ABF24041
ID ABF24041 standard; DNA; 13 BP.
AC ABF24041;
XX 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 124038 for detecting SNP TSC0031015.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 124038; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 1 Other;
SQ Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
Db 1 RACACACACC 3
RESULT 409
ABF81152/C
ID ABF81152 standard; DNA; 13 BP.
AC ABF81152;
XX 22-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 181149 for detecting SNP TSC0004966.
XX

Db 1 RACACACACC 11
RESULT 408
ABC80016/C
ID ABC80016 standard; DNA; 13 BP.
XX ABC80016;
XX 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 80033 for detecting SNP TSC0020318.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 80033; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

PT	designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX	Claim 1; SEQ ID NO 124037; 29pp + Sequence Listing; German.
XX	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
XX	-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
XX	ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 13 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 1 Other;
XX	Query Match 40.9%; Score 9; DB 1; Length 13;
XX	Best Local Similarity 81.8%; Pred. No. 4.7e+02;
XX	Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY	735 GAAACAGAACCA 745
DB	13 RAAACCGAACCA 3
RESULT 406	
ABC80017	
ID	ABC80017 standard; DNA; 13 BP.
XX	AC ABC80017;
XX	21-FEB-2002 (first entry)
XX	Oligonucleotide SEQ ID NO 80034 for detecting SNP TSC0020318.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
XX	WO200177384-A2.
XX	18-OCT-2001.
XX	06-APR-2001; 2001WO-IB000713.
XX	07-APR-2000; 2000DE-01019173.
XX	(EPIG-) EPIGENOMICS AG.
XX	Olek A, Piepenbrock C, Berlin K;
XX	WPI; 2001-657177/75.
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX	Claim 1; SEQ ID NO 134132; 29pp + Sequence Listing; German.
XX	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
XX	-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
XX	ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 13 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
XX	Query Match 40.9%; Score 9; DB 1; Length 13;
XX	Best Local Similarity 81.8%; Pred. No. 4.7e+02;
XX	Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	735 GAAACAGAACCA 745
DB	1 RAAACATAACA 11
RESULT 405	
ABF24040/C	
ID	ABF24040 standard; DNA; 13 BP.
XX	AC ABC24040;
XX	21-FEB-2002 (first entry)
XX	Oligonucleotide SEQ ID NO 124037 for detecting SNP TSC0031015.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
XX	WO200177384-A2.
XX	18-OCT-2001.
XX	06-APR-2001; 2001WO-IB000713.
XX	07-APR-2000; 2000DE-01019173.
XX	(EPIG-) EPIGENOMICS AG.
XX	Olek A, Piepenbrock C, Berlin K;
XX	WPI; 2001-657177/75.
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX	Claim 1; SEQ ID NO 80034; 29pp + Sequence Listing; German.
XX	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
XX	-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
XX	ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 13 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 1 Other;
XX	Query Match 40.9%; Score 9; DB 1; Length 13;
XX	Best Local Similarity 81.8%; Pred. No. 4.7e+02;
XX	Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	735 GAAACAGAACCA 745
DB	1 RAAACATAACA 11
RESULT 405	
ABF24040/C	
ID	ABF24040 standard; DNA; 13 BP.
XX	AC ABC24040;
XX	21-FEB-2002 (first entry)
XX	Oligonucleotide SEQ ID NO 124037 for detecting SNP TSC0031015.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
XX	WO200177384-A2.
XX	18-OCT-2001.
XX	06-APR-2001; 2001WO-IB000713.
XX	07-APR-2000; 2000DE-01019173.
XX	(EPIG-) EPIGENOMICS AG.
XX	Olek A, Piepenbrock C, Berlin K;
XX	WPI; 2001-657177/75.
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX	Claim 1; SEQ ID NO 80034; 29pp + Sequence Listing; German.
XX	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
XX	-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
XX	ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 13 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 1 Other;
XX	Query Match 40.9%; Score 9; DB 1; Length 13;
XX	Best Local Similarity 81.8%; Pred. No. 4.7e+02;
XX	Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	735 GAAACAGAACCA 745
DB	1 RAAACCGAACCA 3
RESULT 406	
ABC80017	
ID	ABC80017 standard; DNA; 13 BP.
XX	AC ABC80017;
XX	21-FEB-2002 (first entry)
XX	Oligonucleotide SEQ ID NO 80034 for detecting SNP TSC0020318.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
XX	WO200177384-A2.

PD 22-MAY-2003.
XX
XX 19-MAR-2002; 2002US-00100957.
XX
XX 27-FEB-1997; 97US-00810983.
XX 27-FEB-1998; 98US-00631271.
XX 28-FEB-1999; 99US-0122152P.
XX 08-MAR-1999; 99US-0123399P.
XX 12-JUL-1999; 99US-00352171.
XX 31-AUG-1999; 99US-0151797P.
XX 17-SEP-1999; 99US-00398965.
XX 29-OCT-1999; 99US-00430656.
XX 01-DEC-1999; 99US-0168408P.
XX 25-FEB-2000; 2000US-00513783.
XX (CELL-) CELLOMICS INC.
XX
XX Giuliano X, Kapur R;
XX
XX WPI; 2003-786988/74.
XX P-PSDB; ADC18388.
XX
XX Cell based toxin characterization method for e.g. in drug discovery
XX paradigm, involves treating cells possessing luminescent reporter
XX molecules with fluorescence based molecules reagents to detect presence
XX of toxins.
XX
XX Example 10; SEQ ID NO 75; 98pp; English.
XX
XX The invention relates to characterising cell based toxins, where the cell
XX possessing luminescent reporter molecules (biosensors) are provided on a
XX microchip, and are treated with fluorescence based molecular reagents.
XX The cells are photographed with fluorescence optics, and the optical
XX information is converted into digital data. The presence of the toxin in
XX a reagent, is detected using the digital data, based on changes in the
XX localisation, distribution structure of identifier, detector and
XX classifier in each cell. Also included are a computer readable storage
XX medium storing a cell based toxin characterisation program, and a kit for
XX detecting a biological cell based toxin that affect particular biological
XX functions and for preparing molecular biochemical arrays for new drug
XX discovery paradigm. It is also used in automated DNA sequencing, PCR
XX application, positional cloning, hybridisation arrays and bioinformatics
XX using cell based scanning and screening system. The method improves the
XX target validation and candidate optimisation by combining many cell
XX screening formats with fluorescence based molecular reagents, thereby
XX resulting in increased quantity and speed of data collection, shortened
XX cycle times and faster evaluation of promising drug candidates. The
XX method also provides increased throughput while decreasing the volumes of
XX reagent and test compounds required in each assay. The biosensor
XX comprises a signal component (fluorescent protein (fused e.g. MAP4,
XX tethering it to microtubules) or detectable signal (epitope or affinity
XX tag)), a protease recognition site (e.g. for a caspase protein) and a
XX target domain (localising the biosensor to a particular cellular
XX compartment). The present sequence encodes a protease recognition site
XX for a biosensor of the invention.
XX
XX Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query March 40.9%; Score 9; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 734 AGAACAACA 742
XX |||||
XX 3 AGAACAACA 11
XX
XX RESULT 403
XX ABF34134/c
XX ID ABF34134 standard; DNA; 13 BP.
XX
XX AC ABF34134;

XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 134131 for detecting SNP TSC0033441.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 134131; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 1 Other;
XX
XX Query Match 40.9%; Score 9; DB 1; Length 13;
XX Best Local Similarity 81.8%; Pred. No. 4.7e+02;
XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 735 GAACAGACA 745
XX :|||||
XX 13 RAACATAACA 3
XX
XX RESULT 404
XX ABF34135
XX ID ABF34135 standard; DNA; 13 BP.
XX
XX AC ABF34135;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 134132 for detecting SNP TSC0033441.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX

PR 31-AUG-1999; 99US-0151797P.
PR 17-SEP-1999; 99US-00398965.
PR 29-OCT-1999; 99US-00430656.
PR 01-DEC-1999; 99US-0168408P.
XX
PA (GIUL/) GIULIANO K.
PA (KAPU/) KAPUR R.
XX
PI Giuliano K, Kapur R;
XX
DR WPI; 2002-634730/68.
DR P-PSDB; ABG94459.
XX
XX Automated cell-based toxin detection, classification, and/or
PT identification by treating cells involves use of three classes of
PT luminescent reporter molecules such as detectors, classifiers or
PT identifiers.
XX
PS Example 10; Fig 29B; 214pp; English.
XX
CC The invention describes methods of automated detection, classification
CC and identification comprising treating cells containing luminescent
CC reporter molecules (I) in array of locations with a test substance, where
CC (I) are detectors, classifiers or identifiers, imaging cells in each
CC location to obtain luminescent signals and converting optical information
CC into digital data to interpret presence of toxins in the test substance.
CC The method are useful for detection of toxins chosen from proteases, ADP-
CC ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
CC Three classes of cell-based luminescent reporter molecules such as
CC detectors, classifiers and identifiers are described and serve as
CC reporters of toxic threat agents. The first two levels of
CC characterisation ensure a rapid readout of toxin class without
CC sacrificing the ability to detect many new mutant toxins or dissect
CC several complex mixtures of known toxins. This sequence encodes a
CC protease biosensor recognition site used in the cell-based screening
CC system
XX
SQ Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 734 AGAAACAGA 742
DB 3 AGAAACAGA 11
|||||
RESULT 399
ABS71493
ID ABS71499 standard; DNA; 12 BP.
XX
AC ABS71499;
XX
DT 27-NOV-2002 (first entry)
XX
DE DNA encoding protease biosensor recognition site #5.
XX
KW Detection; classification; identification; toxin detection; protease;
KW ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
KW toxic threat agent; ds.
XX
OS Synthetic.
XX
FN US6416959-B1.
XX
PD 09-JUL-2002.
XX
XX 25-FEB-2000; 2000US-00513783.
PF
XX
PR 27-FEB-1997; 97US-00810983.
PR 27-FEB-1998; 98US-00031271.
PR 26-FEB-1999; 99US-0122152P.

PR 08-MAR-1999; 99US-0123399P.
PR 12-JUL-1999; 99US-00352171.
PR 31-AUG-1999; 99US-0151797P.
PR 17-SEP-1999; 99US-00398965.
PR 29-OCT-1999; 99US-00430656.
PR 01-DEC-1999; 99US-0168408P.
XX
PA (GIUL/) GIULIANO K.
PA (KAPU/) KAPUR R.
XX
PI Giuliano K, Kapur R;
XX
DR WPI; 2002-634730/68.
DR P-PSDB; ABG94452.
XX
XX Automated cell-based toxin detection, classification, and/or
PT identification by treating cells involves use of three classes of
PT luminescent reporter molecules such as detectors, classifiers or
PT identifiers.
XX
PS Example 10; Fig 29B; 214pp; English.
XX
CC The invention describes methods of automated detection, classification
CC and identification comprising treating cells containing luminescent
CC reporter molecules (I) in array of locations with a test substance, where
CC (I) are detectors, classifiers or identifiers, imaging cells in each
CC location to obtain luminescent signals and converting optical information
CC into digital data to interpret presence of toxins in the test substance.
CC The method are useful for detection of toxins chosen from proteases, ADP-
CC ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
CC Three classes of cell-based luminescent reporter molecules such as
CC detectors, classifiers and identifiers are described and serve as
CC reporters of toxic threat agents. The first two levels of
CC characterisation ensure a rapid readout of toxin class without
CC sacrificing the ability to detect many new mutant toxins or dissect
CC several complex mixtures of known toxins. This sequence encodes a
CC protease biosensor recognition site used in the cell-based screening
CC system
XX
SQ Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 734 AGAAACAGA 742
DB 3 AGAAACAGA 11
|||||
RESULT 400
AAL46301/C
ID AAL46301 standard; DNA; 12 BP.
XX
AC AAL46301;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human M33 protein coding sequence intron 1 fragment.
XX
KW Neurodegenerative disease; M30; M31; M32; M33; stroke;
KW fragile X syndrome; Huntington's disease; Parkinson's disease;
KW Alzheimer's disease; multiple sclerosis; ovarian cancer;
KW neurodegeneration; immune disorder; autoimmune disease; allergy;
KW infection; leukaemia; inflammation; neuroprotective; cerebroprotective;
KW immunosuppressive; cytostatic; nootropic; antiparkinsonian; antiallergic;
KW virucide; antiinflammatory; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200221138-A2.
XX
PD 14-MAR-2002.

PR 30-OCT-1998; 98US-0106308P.
 PR 26-MAY-1999; 99US-0136078P.
 PA (CELL-) CELLOMICS INC.
 PI Guiliano KA, Bright G, Olson K, Burroughs-Tencza S;
 XX WPI; 2000-365644/31.
 DR P-PSDB; AAY79592.
 XX Recombinant nucleic acid encoding a protease biosensor useful for
 PT fluorescence based cell and molecular biochemical assays for drug
 PT discovery comprising three operably linked nucleic acid sequences.
 PS Claim 6; Fig 29B; 218pp; English.

XX The present sequence is that of DNA encoding the substrate recognition
 CC sequence (see AAY79592) of procaspase-3. The DNA is used in a claimed
 CC recombinant nucleic acid encoding a protease biosensor. The nucleic acid
 CC (see AA227627-43) comprises: (1) a sequence (see AAA27568-76) encoding at
 CC least 1 detectable signal polypeptide; (2) a sequence (see AAA27577-611)
 CC that encodes at least 1 protease recognition site, such as the present
 CC sequence; and (3) a sequence (see AAA27611-26) that encodes at least 1
 CC reactant target sequence. An expression vector, a genetically engineered
 CC host cell and a recombinant protease biosensor are also claimed. A
 CC claimed method for identifying compounds that modify protease activity in
 CC a cell involves contacting a host cell that possesses the recombinant
 CC protease biosensor with a test compound, and determining the recombinant
 CC biosensor distribution in the host cell, where changes in the
 CC distribution of the protease biosensor are correlated with the protease
 CC of protease activity by the test compound. Claimed kits for identifying
 CC compounds that modify protease activity in a host cell include the
 CC recombinant nucleic acid, or the recombinant protease biosensor, or the
 CC vector, or the host cell. The protease biosensor is useful in high
 CC content screens to detect in vivo activation of enzymatic activity, and
 CC to identify specific activity based on cleavage of a known recognition
 CC motif

XX Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
 SQ

Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 734 AGAACAACA 742
 DB 3 AGAACAACA 11

RESULT 397
 AAA27588
 ID AAA27588 standard; DNA; 12 BP.
 XX AAA27588;

XX 29-AUG-2000 (first entry)
 XX DNA encoding procaspase-8 substrate recognition sequence.
 XX Protease; biosensor; caspase-8; substrate recognition sequence;
 KW cell screening; assay; analysis; drug discovery; ss.
 XX Unidentified.

XX WO200026408-A2.
 XX 11-MAY-2000.
 XX 29-OCT-1999; 99WO-US025431.
 XX 30-OCT-1998; 98US-0106308P.
 PR 26-MAY-1999; 99US-0136078P.

PA (CELL-) CELLOMICS INC.
 XX Guiliano KA, Bright G, Olson K, Burroughs-Tencza S;
 PI WPI; 2000-365644/31.
 DR P-PSDB; AAY79599.
 XX Recombinant nucleic acid encoding a protease biosensor useful for
 PT fluorescence based cell and molecular biochemical assays for drug
 PT discovery comprising three operably linked nucleic acid sequences.
 PS Claim 6; Fig 29B; 218pp; English.

XX The present sequence is that of DNA encoding the substrate recognition
 CC sequence (see AAY79599) of procaspase-8. The DNA is used in a claimed
 CC recombinant nucleic acid encoding a protease biosensor. The nucleic acid
 CC (see AA227627-43) comprises: (1) a sequence (see AAA27568-76) encoding at
 CC least 1 detectable signal polypeptide; (2) a sequence (see AAA27577-611)
 CC that encodes at least 1 protease recognition site, such as the present
 CC sequence; and (3) a sequence (see AAA27611-26) that encodes at least 1
 CC reactant target sequence. An expression vector, a genetically engineered
 CC host cell and a recombinant protease biosensor are also claimed. A
 CC claimed method for identifying compounds that modify protease activity in
 CC a cell involves contacting a host cell that possesses the recombinant
 CC protease biosensor with a test compound, and determining the recombinant
 CC biosensor distribution in the host cell, where changes in the
 CC distribution of the protease biosensor are correlated with the protease
 CC of protease activity by the test compound. Claimed kits for identifying
 CC compounds that modify protease activity in a host cell include the
 CC recombinant nucleic acid, or the recombinant protease biosensor, or the
 CC vector, or the host cell. The protease biosensor is useful in high
 CC content screens to detect in vivo activation of enzymatic activity, and
 CC to identify specific activity based on cleavage of a known recognition
 CC motif

SQ Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 734 AGAACAACA 742
 DB 3 AGAACAACA 11

RESULT 398
 ABS71506
 ID ABS71506 standard; DNA; 12 BP.
 XX ABS71506;

XX 27-NOV-2002 (first entry)
 XX DNA encoding protease biosensor recognition site #12.
 XX Detection; classification; identification; toxin detection; protease;
 KW ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
 XX toxic threat agent; ds.
 XX Synthetic.

XX US6416959-B1.
 XX 09-JUL-2002.
 XX 25-FEB-2000; 2000US-00513783.
 XX 27-FEB-1997; 97US-00810983.
 PR 27-FEB-1998; 98US-00031271.
 PR 26-FEB-1999; 99US-0122152P.
 PR 08-MAR-1999; 99US-0123399P.
 PR 12-JUL-1999; 99US-00352171.

CC region of the cell. Once acted on by the protease of interest, the
 CC fluorescent protein is cleaved from the localisation sequence, and is
 CC free to migrate to other locations within the cell. The presence of a
 CC second localisation signal attached to the fluorescent protein enables
 CC the fluorescent protein to be directed to a different cellular
 CC compartment after cleavage of the protease recognition sequence. The
 CC change in distribution of the fluorescent protein can be detected using
 CC imaging methods with a high degree of spatial resolution. The methods and
 CC biosensors of the invention can be used to investigate a wide range of
 CC cellular activities and to screen compounds which modulate these
 CC activities. Biosensors containing a recognition site for caspase, for
 CC example, may be used for the screening of compounds which modulate
 CC apoptosis, while biosensors containing other protease recognition sites
 CC may be used for the detection of proteolytic toxins (such as anthrax
 CC lethal factor). The method provides improved target validation and
 CC candidate compound optimisation by combining many cell screening formats
 CC with fluorescence-based molecular reagents and computer-based feature
 CC extraction, data analysis and automation, resulting in increased quantity
 CC and speed of data collection and faster evaluation of drug candidates.
 CC Sequences AAA93377-A93411 and AAA93440 represent protease recognition
 CC sites (AAB22886-B22920, AAB22935) which may be used as components of
 CC biosensor fusion proteins of the invention

XX
 SQ Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAACACAGA 742
 Db 3 AGAACACAGA 11
 |||||

RESULT 395
 AAA93381
 ID AAA93381 standard; DNA; 12 BP.
 AC AAA93381;
 XX
 DT 10-JAN-2001 (first entry)
 DE DNA encoding procaspase-3 substrate recognition sequence, SEQ ID NO:61.
 KW Biotector protein; fusion protein; recognition site;
 KW cellular targeting sequence; cellular localisation; fluorescent protein;
 KW protease activity detection; toxin detection; cellular stress detection;
 KW drug discovery; cell based screening; protease recognition site;
 KW cleavage site; ds.
 XX Unidentified.
 OS
 XX WO200050872-A2.
 PN
 XX 31-AUG-2000.
 PD
 XX 25-FEB-2000; 2000WO-US004794.
 PF
 XX 26-FEB-1999; 9SUS-0122152P.
 PR 08-MAR-1999; 9SUS-0123399P.
 PR 12-JUL-1999; 9SUS-00352171.
 XX
 XX (CELL-) CELLOWICS INC.
 PA Giuliano KA, Kapur R;
 XX WPI; 2000-594086/56.
 XX P-FSDB; AAB22890.
 DR
 XX Automated cell-based characterization of toxin by contacting cells
 PT containing luminescent reporter molecules with test substance and
 PT analyzing optically.
 PT
 XX

PS
 XX Example 11; Fig 29B; 336pp; English.
 CC The invention relates to systems, methods and reagents for cell-based
 CC screening or detection of compounds which affect particular biological
 CC functions. The methods of the invention utilise fluorescent bioreactor
 CC molecules which, when acted on by a compound of interest, cause an
 CC alteration in the cellular distribution of at least the fluorescent
 CC moiety. In one embodiment, the biosensors comprise heat shock proteins
 CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
 CC protein (GFP), or derivatives thereof). Such biosensors are located in
 CC the cytoplasm, but on stress activation translocate to the nucleus. In
 CC another embodiment bioreactor proteins can be used to detect protease
 CC activity. Such protease bioreactor fusion proteins comprise one or more
 CC fluorescent proteins; a recognition signal which is cleaved by the
 CC protease; and at least one cellular localisation signal. The latter two
 CC components may be components of a single protein which is acted upon by
 CC the protease, or may be from heterologous sources. Due to the
 CC localisation signal, the bioreactor protein is localised to a particular
 CC region of the cell. Once acted on by the protease of interest, the
 CC fluorescent protein is cleaved from the localisation sequence, and is
 CC free to migrate to other locations within the cell. The presence of a
 CC second localisation signal attached to the fluorescent protein enables
 CC the fluorescent protein to be directed to a different cellular
 CC compartment after cleavage of the protease recognition sequence. The
 CC change in distribution of the fluorescent protein can be detected using
 CC imaging methods with a high degree of spatial resolution. The methods and
 CC biosensors of the invention can be used to investigate a wide range of
 CC cellular activities and to screen compounds which modulate these
 CC activities. Biosensors containing a recognition site for caspase, for
 CC example, may be used for the screening of compounds which modulate
 CC apoptosis, while biosensors containing other protease recognition sites
 CC may be used for the detection of proteolytic toxins (such as anthrax
 CC lethal factor). The method provides improved target validation and
 CC candidate compound optimisation by combining many cell screening formats
 CC with fluorescence-based molecular reagents and computer-based feature
 CC extraction, data analysis and automation, resulting in increased quantity
 CC and speed of data collection and faster evaluation of drug candidates.
 CC Sequences AAA93377-A93411 and AAA93440 represent protease recognition
 CC sites (AAB22886-B22920, AAB22935) which may be used as components of
 CC biosensor fusion proteins of the invention

XX
 SQ Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAACACAGA 742
 Db 3 AGAACACAGA 11
 |||||

RESULT 396
 AAA27581
 ID AAA27581 standard; DNA; 12 BP.
 XX
 AC AAA27581;
 XX
 DT 29-AUG-2000 (first entry)
 DE DNA encoding procaspase-3 substrate recognition sequence.
 XX
 KW Protease; biosensor; caspase-3; substrate recognition sequence;
 KW cell screening; assay; analysis; drug discovery; ss.
 XX Unidentified.
 OS
 XX WO200026408-A2.
 PN
 XX 11-MAY-2000.
 PD
 XX 29-OCT-1999; 99WO-US025431.
 PF
 XX

CC diseases. The human ESR-alpha gene is located on chromosome 6. ABA98969
 CC to ABA9972 represent ESR-alpha gene single nucleotide polymorphism (SNP)
 CC containing oligonucleotides, which are used in an example from the
 CC present invention
 XX
 SQ Sequence 11 BP; 7 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 736 AACAGAAC 744
 |||||
 Db 2 AACAGAAC 10

RESULT 393
 ABZ95855/C
 ID ABZ95855 standard; DNA; 11 BP.

XX AC ABZ95855;

XX DT 17-OCT-2003 (first entry)

XX DE Human prostaglandin D synthase antisense fragment no.1715.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;
 KW antasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX FN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIC-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 11097; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 729 CCAGGAGAA 737
 |||||
 Db 11 CCAGGAGAA 3

RESULT 394
 AAA93388
 ID AAA93388 standard; DNA; 12 BP.

XX AC AAA93388;

XX DT 10-JAN-2001 (first entry)

XX DE DNA encoding procaspase-8 substrate recognition sequence, SEQ ID NO:75.

XX KW Bioreactor protein; fusion protein; recognition site;
 KW cellular targeting sequence; cellular localisation; fluorescent protein;
 KW protease activity detection; toxin detection; cellular stress detection;
 KW drug discovery; cell based screening; protease recognition site;
 KW cleavage site; ds.

XX OS Unidentified.

XX FN WO2000050872-A2.

XX PD 31-AUG-2000.

XX PF 25-FEB-2000; 2000WO-US004794.

XX PR 26-FEB-1999; 99US-0122152P.

XX PR 08-MAR-1999; 99US-0123399P.

XX PR 12-JUL-1999; 99US-00352171.

XX PA (CELL-) CELLOMICS INC.

XX PI Giuliano KA, Kapur R;

XX DR WPI; 2000-594086/56.

XX DR P-PSDB; AAB22897.

XX PT Automated cell-based characterization of toxin by contacting cells

XX PT containing luminescent reporter molecules with test substance and

XX PT analyzing optically.

XX PS Example 11; Fig 29B; 336pp; English.

XX CC The invention relates to systems, methods and reagents for cell-based
 CC screening or detection of compounds which affect particular biological
 CC functions. The methods of the invention utilise fluorescent bioreactor
 CC molecules which, when acted on by a compound of interest, cause an
 CC alteration in the cellular distribution of at least the fluorescent
 CC moiety. In one embodiment, the biosensors comprise heat shock proteins
 CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
 CC protein (GFP), or derivatives thereof). Such biosensors are located in
 CC the cytoplasm, but on stress activation translocate to the nucleus. In
 CC another embodiment, bioreactor proteins can be used to detect protease
 CC activity. Such protease bioreactor fusion proteins comprise one or more
 CC fluorescent proteins; a recognition signal which is cleaved by the
 CC protease; and at least one cellular localisation signal. The latter two
 CC components may be components of a single protein which is acted upon by
 CC the protease, or may be from heterologous sources. Due to the
 CC localisation signal, the bioreactor protein is localised to a particular

XX SQ Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 739 CAGAACACC 747
Db 3 CAGAACACC 11
RESULT 391
ABA89897
ID ABA89897 standard; DNA; 11 BP.
XX AC ABA89897;
XX DT 11-FEB-2002 (first entry)
XX DE ESR-alpha gene Liverpool clinical tissue sample SNP oligo #29.
XX KW Human; oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Syne-2;
KW synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic;
KW cardiant; vasotropic; gene therapy; vaccine; cancer; osteoporosis;
KW cardiovascular disease; oestrogen receptor; SNP;
KW single nucleotide polymorphism; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT variation replace(6,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX WO200162969-A2.
XX PD 30-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005358.
XX PR 22-FEB-2000; 2000US-0183756P.
XX PR 20-OCT-2000; 2000US-00692414.
XX PR 24-JAN-2001; 2001US-00768184.
XX PA (PEXE) PE CORP NY.
XX PI Kalush F, Cassel MJ, Hwang SS, Winn-Deen ES;
XX WPI; 2002-041152/05.
XX PT Novel variant of estrogen receptor alpha polypeptide useful for
PT determining the biological activity of a protein for high throughput
PT screening and for raising antibodies that elicit an immune response in
PT host.
XX PS Claim 17; Fig 2a sheet 2; 333pp; English.
XX CC The present invention describes an isolated peptide (I) consisting of an
CC amino acid sequence selected from: (a) the amino acid sequence of a
CC variant of the estrogen receptor alpha (ESR-alpha) protein in AAG68251;
CC or (b) a fragment comprising at least 10 contiguous amino acids of the
CC protein in AAG68251. (I) has cytostatic, osteopathic, cardiant and
CC vasotropic activities, and can be used in gene therapy and vaccine
CC production. (I) is useful for identifying an agent that binds to (I), by
CC contacting (I) with an agent and assaying the contacted mixture to
CC determine whether a complex is formed with the agent bound to the
CC peptide. A polynucleotide (II), encoding (I), is useful in the
CC development of diagnostics and therapies for diseases and disorders
CC mediated/modulated by an oestrogen receptor (ER). (II) is also useful in
CC gene therapy for treating cancer, osteoporosis and cardiovascular
CC diseases. The human ESR-alpha gene is located on chromosome 6. ABA89897
CC to ABA89972 represent ESR-alpha gene single nucleotide polymorphism (SNP)

CC containing oligonucleotides, which are used in an example from the
CC present invention
XX SQ Sequence 11 BP; 7 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 736 AAACAGAAC 744
Db 2 AAACAGAAC 10
RESULT 392
ABA89949
ID ABA89949 standard; DNA; 11 BP.
XX AC ABA89949;
XX DT 11-FEB-2002 (first entry)
XX DE ESR-alpha gene Coriell Diversity panel oligo #29.
XX KW Human; oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Syne-2;
KW synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic;
KW cardiant; vasotropic; gene therapy; vaccine; cancer; osteoporosis;
KW cardiovascular disease; oestrogen receptor; SNP;
KW single nucleotide polymorphism; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT variation replace(6,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX WO200162969-A2.
XX PD 30-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005358.
XX PR 22-FEB-2000; 2000US-0183756P.
XX PR 20-OCT-2000; 2000US-00692414.
XX PR 24-JAN-2001; 2001US-00768184.
XX PA (PEXE) PE CORP NY.
XX PI Kalush F, Cassel MJ, Hwang SS, Winn-Deen ES;
XX WPI; 2002-041152/05.
XX PT Novel variant of estrogen receptor alpha polypeptide useful for
PT determining the biological activity of a protein for high throughput
PT screening and for raising antibodies that elicit an immune response in
PT host.
XX PS Claim 17; Fig 2b sheet 2; 333pp; English.
XX CC The present invention describes an isolated peptide (I) consisting of an
CC amino acid sequence selected from: (a) the amino acid sequence of a
CC variant of the estrogen receptor alpha (ESR-alpha) protein in AAG68251;
CC or (b) a fragment comprising at least 10 contiguous amino acids of the
CC protein in AAG68251. (I) has cytostatic, osteopathic, cardiant and
CC vasotropic activities, and can be used in gene therapy and vaccine
CC production. (I) is useful for identifying an agent that binds to (I), by
CC contacting (I) with an agent and assaying the contacted mixture to
CC determine whether a complex is formed with the agent bound to the
CC peptide. A polynucleotide (II), encoding (I), is useful in the
CC development of diagnostics and therapies for diseases and disorders
CC mediated/modulated by an oestrogen receptor (ER). (II) is also useful in
CC gene therapy for treating cancer, osteoporosis and cardiovascular

XX	CC	The invention relates to in vitro identification (M1) of genes expressed
XX	CC	in the skin of humans or animals by subjecting a mixture of genetically
XX	CC	encoded factors from skin, to serial analysis of gene expression (SAGE)
XX	CC	so as to identify skin-expressed genes and quantify their expression.
XX	CC	(M1) is useful for identifying genes involved in skin homeostasis; to
XX	CC	determine skin homeostasis and to test agent (A) that maintains or
XX	CC	promotes skin homeostasis or that can be used for treating skin
XX	CC	disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX	CC	ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX	CC	rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX	CC	skin. The present sequence is that of a human expressed sequence tag
XX	CC	(EST) of the invention
XX	SQ	Sequence 11 BP; 0 A; 2 C; 4 G; 5 T; 0 U; 0 Other;
		Query Match 40.9%; Score 9; DB 1; Length 11;
		Best Local Similarity 100.0%; Pred.No. 4.4e-02;
	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY		738 ACAGACAC 746
DB		
		9 ACAGACAC 1
	RESULT 390	
ABV67302		ID ID ABV67302 standard; cDNA; 11 BP.
XX	AC	ABV67302;
XX	DT	21-OCT-2002 (first entry)
XX	DE	Human skin EST 5098.
XX	KW	Human; skin; dermatological; vulnery; antipsoriatic; antisborrhoeic;
XX	KW	immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX	KW	psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX	OS	Homo sapiens.
XX	PN	WO200253774-A2.
XX	PD	11-JUL-2002.
XX	PF	20-DEC-2001; 2001WO-EP015179.
XX	PR	03-JAN-2001; 2001DE-01000127.
XX	PA	(HENK) HENKEL KGAA.
XX	PI	Petersohn D, Conzadt M, Hofmann K;
XX	PP	WPI; 2002-590638/53.
XX	PT	In vitro identification of skin-expressed genes, useful for determining
XX	PT	homeostasis and identifying cosmetic or pharmaceutical agents against
XX	PT	e.g. skin cancer.
XX	PS	Disclosure; Page 165; 1345pp; German.
XX	CC	The invention relates to in vitro identification (M1) of genes expressed
XX	CC	in the skin of humans or animals by subjecting a mixture of genetically
XX	CC	encoded factors from skin, to serial analysis of gene expression (SAGE)
XX	CC	so as to identify skin-expressed genes and quantify their expression.
XX	CC	(M1) is useful for identifying genes involved in skin homeostasis; to
XX	CC	determine skin homeostasis and to test agent (A) that maintains or
XX	CC	promotes skin homeostasis or that can be used for treating skin
XX	CC	disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX	CC	ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX	CC	rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX	CC	skin. The present sequence is that of a human expressed sequence tag
XX	CC	(EST) of the invention

DB 9 AAACAGAAC 1
 RESULT 386
 ABV65662/c
 ID ABV65662 standard; cDNA; 11 BP.
 AC ABV65662;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 3448.
 XX
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 PP (HENK) HENKEL KGAA.
 PR Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR In vitro identification of skin-expressed genes, useful for determining
 XX homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 PT
 XX Disclosure; Page 120; 1345pp; German.
 PS The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 0 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 734 AGAAACAGA 742
 DB 11 AGAAACAGA 3
 RESULT 387
 ABV64386
 ID ABV64386 standard; cDNA; 11 BP.
 AC ABV64386;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 2172.
 DE

XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 PP (HENK) HENKEL KGAA.
 PR Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR In vitro identification of skin-expressed genes, useful for determining
 XX homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 PT
 XX Disclosure; Page 85; 1345pp; German.
 PS The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 4 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 729 CCAGGAGAA 737
 DB 3 CCAGGAGAA 11
 RESULT 388
 ABV64098/c
 ID ABV64098 standard; cDNA; 11 BP.
 AC ABV64098;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 1884.
 DE
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF
 XX

PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.

PS Claim 24; Page 310; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention

XX SQ Sequence 11 BP; 4 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 CCAGGAGAA 737

DB 3 CCAGGAGAA 11

RESULT 384

ABV62393/c
ID ABV62393 standard; cDNA; 11 BP.

XX AC ABV62393;

XX 21-OCT-2002 (first entry)

XX Human skin EST 179.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.

XX Disclosure; Page 31; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention

XX SQ Sequence 11 BP; 0 A; 1 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGAAC 744

DB 9 AAACAGAAC 1

RESULT 385

ABV69814/c
ID ABV69814 standard; cDNA; 11 BP.

XX AC ABV69814;

XX 21-OCT-2002 (first entry)

XX Human skin EST 7600.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.

XX Claim 24; Page 240; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention

XX SQ Sequence 11 BP; 0 A; 1 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGAAC 744

XX PF 24-MAR-2000; 2000WO-US008020.
XX XX
XX PF 06-APR-1999; 99US-0127958P.
XX XX
XX (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX XX
XX NYCE JW;
XX XX
XX WPI; 2000-679539/66.
XX XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
XX PT adenosine receptors during metabolism, useful e.g. for treating cancers
XX PT and respiratory obstructions.
XX XX
XX Claim 14; Page 141; 1592pp; English.
XX XX
XX The present invention describes low adenosine (A) content antisense
XX CC oligonucleotides and compositions (I) comprising them. In the antisense
XX CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX CC The antisense oligonucleotides and (I) can be used to down-regulate the
XX CC expression and/or activity of target polypeptides associated with
XX CC lung/respiratory disorders and malignancies, such as stimulating and
XX CC activating peptide factors and transmitters, transcription factors,
XX CC immunoglobulins and antibodies, antibody receptors, cytokines and
XX CC chemokines, endogenously produced specific and non-specific enzymes,
XX CC binding proteins, adhesion molecules and their receptors, cytokine and
XX CC chemokine receptors, adenosine receptors, bradykinin receptors, central
XX CC nervous system (CNS) and peripheral nervous and non-nervous system
XX CC receptors, CNS and peripheral nervous and non-nervous system peptide
XX CC transmitters, defensins, growth factors, vasoactive peptides and
XX CC receptors, binding proteins and malignancy associated proteins. The
XX CC antisense oligonucleotides may be used in this way to treat disorders
XX CC including respiratory obstruction (especially pulmonary obstruction
XX CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
XX CC surfactant hypoproduction which are associated with a disease or
XX CC condition selected from pulmonary vasoconstriction, inflammation,
XX CC allergies, asthma, impaired respiration, respiratory distress syndrome
XX CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX CC fragments and antisense oligonucleotides used in the exemplification of
XX CC the present invention
XX XX
XX Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
XX
Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 CCAGGAGAA 737
Db 11 CCAGGAGAA 3
RESULT 382
ABQ86412
ID ABQ86412 standard; cDNA; 11 BP.
XX AC ABQ86412;
XX XX
XX 10-SEP-2002 (first entry)
XX DE Human skin stress/ageing related EST SEQ ID NO 167.
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX

PN WO200253773-A2.
XX 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-528865/56.
XX Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT expression.
XX PS Claim 8; Page 44; 325pp; German.
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX CC or animals, are important for skin ageing and/or skin stress by serial
XX CC analysis of gene expression between mixtures of transcribed and
XX CC optionally translated, genetically encoded factors (A) obtained from
XX CC young and aged skin, to identify that genes that show strong differential
XX CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX CC useful for: identifying markers of skin ageing and/or stress; determining
XX CC skin ageing and/or stress; and identifying or determining the effects of
XX CC pharmaceutical or cosmetic agents for control of skin ageing. The present
XX CC sequence is one of a group of human skin ageing/stress related expressed
XX CC sequence tags (ABQ86246-ABQ87680) of the invention
XX XX
XX Sequence 11 BP; 4 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
XX
Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 CCAGGAGAA 737
Db 3 CCAGGAGAA 11
RESULT 383
ABV71807
ID ABV71807 standard; cDNA; 11 BP.
XX AC ABV71807;
XX XX
XX 21-OCT-2002 (first entry)
XX DE Human skin EST 9593.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antisborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX
XX WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX XX

PI Nyce JW;
 DR WPI; 1999-229400/19.
 XX
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction.
 XX
 XX
 PS Disclosure; Page 45; 120pp; English.
 XX
 XX
 CC The specification describes antisense oligonucleotides (AA52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes. Gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 CC end and the juxta-section between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AA55272-74. These multiple target oligonucleotides
 CC (specifically AA55180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impaired respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer.
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 729 CCAGGAGAA 737
 DB 11 CCAGGAGAA 3
 RESULT 380
 ID AAA34039/c
 AC AAA34039 standard; DNA; 11 BP.
 XX
 XX
 XX
 XX 28-JUL-2000 (first entry)
 DT
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1728.
 XX
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 XX 24-FEB-2000.
 PD
 XX
 XX 03-AUG-1999; 99WO-US017712.
 PF
 XX
 XX 03-AUG-1998; 98US-0095212P.
 PR
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX
 PI Nyce JW;

XX WPI; 2000-205971/18.
 DR
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 XX
 PS Disclosure; Page 479; 1343pp; English.
 XX
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 729 CCAGGAGAA 737
 DB 11 CCAGGAGAA 3
 RESULT 381
 ID AAF20161/c
 AC AAF20161 standard; DNA; 11 BP.
 XX
 XX
 XX
 XX 14-MAR-2001 (first entry)
 DT
 DE Human prostaglandin D synthase polynucleotide fragment #1728.
 XX
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2000062736-A2.
 PN
 XX
 XX 26-OCT-2000.

XX 13-DEC-2001.
 XX
 XX
 PF 06-JUN-2001; 2001WO-US018321.
 XX
 XX
 PR 06-JUN-2000; 2000US-0209564P.
 XX
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 XX
 PI Kliehm SE, Koshy B, Tanguay DA;
 XX
 XX WPI; 2002-097928/13.
 DR
 XX
 XX New protocadherin 2 (PCDH2) polymorphic variants and encoding genes,
 PT useful in expressing PCDH2 protein for screening candidate drugs to treat
 PT diseases related to PCDH2 activity.
 XX
 XX Claim 18; Page 14; 127pp; English.
 PS
 XX The invention relates to haplotyping the protocadherin 2 (PCDH2) gene,
 CC comprising determining which of the haplotypes given in the specification
 CC defines one or both copies of the individual's PCDH2 gene. The
 CC polymorphisms are within a 30244 base pair sequence (ABA05413), fully
 CC defined in the specification. The polymorphic variants are useful in
 CC studying the expression and function of PCDH2, in expressing PCDH2
 CC protein for use in screening for candidate drugs to treat diseases such
 CC as cancer, related to PCDH2 activity, in studying the effect of the
 CC variation on the biological activity of PCDH2 and the binding affinity of
 CC candidate drugs targeting PCDH2. The haplotyping methods are useful in
 CC validating PCDH2 as a candidate target for treating a specific condition
 CC or disease predicted to be associated with PCDH2 activity or in the
 CC design of clinical trials of candidate drugs for treating a specific
 CC condition or disease associated with PCDH2 activity. The present sequence
 CC is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of
 CC the invention
 XX
 XX Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 735 GAAACAGAA 743
 Db 10 GAAACAGAA 2
 RESULT 378
 AAL39543
 ID AAL39543 standard; DNA; 10 BP.
 XX
 AC AAL39543;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 XX CCBP2 detecting ASO primer SEQ ID No 70.
 XX
 XX Chemokine binding protein 2; CCBP2; CCBP2 protein isoform; gene therapy;
 KW polymorphic gene variant; single nucleotide polymorphism; human; primer;
 KW PCR; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200232926-A2.
 XX
 XX 25-APR-2002.
 PD
 XX 12-OCT-2001; 2001WO-US042685.
 PF
 XX 12-OCT-2000; 2000US-0239638P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 XX

PI Armstrong B, Kazemi A, Koshy B;
 XX WPI; 2002-435524/46.
 DR
 XX
 XX New genetic variants having polymorphisms in the chemokine binding
 PT protein 2 (CCBP2) gene, useful for studying CCBP2 functions, and for
 PT treating disorders affected by expression or function of the CCBP2
 PT isogene.
 XX
 XX Claim 15; Page 14; 84pp; English.
 PS
 XX The invention relates to an isolated polynucleotide comprising genes and
 CC haplotypes of the chemokine binding protein 2 (CCBP2) gene. Polymorphic
 CC variants of the CCBP2 gene are useful in studying the expression and
 CC function of CCBP2, and in expressing CCBP2 proteins for use in screening
 CC candidate drugs for treating diseases associated with CCBP2 activity.
 CC Polynucleotides comprising a polymorphic gene variant or fragment may be
 CC used for therapeutic purposes, where a patient could benefit from
 CC expression or increased expression of a particular CCBP2 protein isoform,
 CC or an expression vector encoding the isoform may be administered to the
 CC patient. Haplotype information is useful in improving the efficiency and
 CC output of several steps in drug discovery and development process,
 CC including target validation, identifying lead compounds, and early phase
 CC clinical trials. The polynucleotides of the invention can be used to
 CC treat disorders related to the CCBP2 gene by gene therapy. This
 CC polynucleotide sequence represents a preferred ASO primer for detecting
 CC CCBP2 gene polymorphisms relating to the invention
 XX
 XX Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 731 AGGAGAAAC 739
 Db 2 AGGAGAAAC 10
 RESULT 379
 AAX54592/c
 ID AAX54592 standard; DNA; 11 BP.
 XX
 AC AAX54592;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 XX Prostaglandin D synthase antisense oligonucleotide fragment.
 DE
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9913886-A1.
 PN
 XX 25-MAR-1999.
 XX
 XX 17-SEP-1998; 98WO-US019419.
 PF
 XX 17-SEP-1997; 97US-0059160P.
 PR
 XX 09-JUN-1998; 98US-00093972.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX

ID ABK81376 standard; DNA; 10 BP.
 AC ABK81376;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human FOS gene allele-specific oligonucleotide PCR primer #19.
 XX
 KW Human: v-fos FBJ murine osteosarcoma viral oncogene homologue; FOS; PCR;
 KW cytostatic; gene therapy; single nucleotide polymorphism; haplotyping;
 KW haplotype pair; developmental bone disorder; cancer; tumour; ss; primer;
 KW chromosome 14q21-q31.
 XX
 OS Homo sapiens.
 XX
 PN WO200232931-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 19-OCT-2001; 2001WO-US046142.
 XX
 PR 19-OCT-2000; 2000US-0241620P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Anastasio AE, Klem SE, Koshy B, Lee HH;
 XX
 DR WPI; 2002-435529/46.
 XX
 PT Novel genetic variants of V-Fos FBJ Murine Osteosarcoma Viral Oncogene
 PT Homolog (FOS) isogenes, useful for improving efficiency and reliability
 PT in drug development for treating developmental bone disorders.
 XX
 PS Claim 17; Page 15; 73pp; English.
 XX
 CC The invention relates to single nucleotide polymorphisms in the gene
 CC encoding the human v-fos FBJ murine osteosarcoma viral oncogene homologue
 CC (FOS) polypeptide. A method for haplotyping the FOS gene in an individual
 CC comprises identifying the nucleotide at one or more polymorphic sites and
 CC determining whether one of the copies of the gene is defined by one of
 CC the FOS haplotypes given in the specification or whether both copies are
 CC defined by a haplotype pair. This method is useful in genotyping whereby
 CC all possible haplotype pairs can be assigned to specific genotypes. An
 CC association between a trait and a haplotype or haplotype pair of the FOS
 CC gene can be identified by comparing the frequency of the haplotype or
 CC haplotype pair in a population exhibiting the trait with the frequency of
 CC the haplotype or haplotype pair in a reference population, where a higher
 CC haplotype frequency in the trait population indicates the trait is
 CC associated with the haplotype or haplotype pair. FOS and its
 CC corresponding DNA are used for studying the expression and function of
 CC FOS, for use in screening for candidate drugs to treat diseases related
 CC to FOS activity, such as developmental bone disorders and tumours. The
 CC sequences are also useful for studying the effect of variation on the
 CC biological activity of FOS as well as on the binding affinity of
 CC candidate drugs targeting FOS. Sequences ABK81376-ABK81377 represent
 CC allele-specific oligonucleotide PCR primers used for detecting FOS gene
 CC polymorphisms
 XX
 SQ Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 732 GGAGAAACA 740
 |||||
 Db 1 GGAGAAACA 9
 RESULT 376
 ABV78423/C
 ID ABV78423 standard; cDNA; 10 BP.
 XX

AC ABV78423;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Human Th1 cell preferentially expressed gene SAGE tag, SEQ ID NO:134.
 XX
 KW SAGE tag; serial analysis of gene expression; human; Th1 cell;
 KW activated T cell; T lymphocyte; immune response; expression pattern;
 KW preferential expression; immune disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN JF2002186482-A.
 XX
 PD 02-JUL-2002.
 XX
 PF 19-DEC-2000; 2000JP-00385816.
 XX
 PR 19-DEC-2000; 2000JP-00385816.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2002-594261/54.
 XX
 PT Human activated Th1 and Th2 cell expression gene group, useful for the
 PT diagnosis and treatment of Th1 and Th2-related diseases.
 XX
 PS Claim 19; Page 10; 60pp; Japanese.
 XX
 CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are expressed in activated human Th1
 CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
 CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
 CC lying nearest to the polyA region of cDNAs derived from a variety of
 CC genes. These tags serve to uniquely identify each transcript and can thus
 CC be used to analyse the pattern of gene expression in particular cell
 CC types. The invention also relates to proteins encoded by the genes
 CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
 CC inhibitors of the expression of groups of genes that are expressed in
 CC either or both the two cell types. Groups of genes expressed in Th1
 CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
 CC and Th2-related disorders. Sequences ABV78350-ABV78560 are SAGE tags
 CC representing 171 genes which are more highly expressed in Th1 cells
 CC compared with Th2 cells
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 740 AGAACACCG 748
 |||||
 Db 10 AGAACACCG 2
 RESULT 377
 AB199152/C
 ID AB199152 standard; DNA; 10 BP.
 XX
 AC AB199152;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Human PCDH2 ASO PCR primer SEQ ID NO 109.
 XX
 KW Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;
 KW single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31;
 KW allele-specific oligonucleotide; ASO; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200194361-A2.

CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against CSF1R protein, and for testing the efficacy of
CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
CC are useful as probes and primers, and for assaying a polymorphism in the
CC target region. Without requiring any a priori knowledge of the phenotypic
CC effect of any particular CSF1R or haplotype the invention provides a
CC method for identifying lead compounds that are more likely to show
CC efficacy in clinical trials. This sequence is a primer used to detect
CC CSF1R gene polymorphisms by primer extension, described in the method of
CC the invention
XX
SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAAC 739
DB |||||
2 AGGAGAAAC 10

RESULT 373
ID ABL99040/C
AC ABL99040 standard; cDNA; 10 BP.
XX
XX ABL99040;
DT 25-JUN-2002 (first entry)
DE Mouse neuronal regeneration related SAGE EST 35.
XX
XX Mouse; neuronal; regeneration; nerve cell; synaptic efficiency; memory;
XX learning disorder; serial analysis of gene expression; SAGE;
XX Gene expression; hippocampus; expressed sequence tag; EST; ss.
XX Mus sp.
XX
XX DE10048893-A1.
XX
XX 11-APR-2002.
XX 02-OCT-2000; 2000DB-01048893.
XX 02-OCT-2000; 2000DB-01048893.
XX (LION-) LION BIOSCIENCE AG.
XX
XX WPI; 2002-341428/38.
XX
XX New nucleic acids involved in neuronal regeneration, useful in screening
XX for modulators of regeneration or synaptic efficiency, and potential
XX therapeutic agents.
XX
XX Example 6; Page 9; 38pp; German.
XX
XX The invention relates to nucleic acids (ABL98957-ABL99004) involved in
XX regenerative neuronal processes and encoded proteins (ABB79405-ABB79409)
XX used to screen for compounds and potential therapeutic agents that
XX modulate nerve cell regeneration and/or synaptic efficiency. They may
XX also be used for treatment or diagnosis of defective or pathological
XX memory and learning conditions. The present sequence is that of an EST
XX isolated from serial analysis of gene expression (SAGE) experiments
XX comparing gene expression in the hippocampus of GFAP/L1 transgenic mice
XX versus a wildtype control. The resultant EST were used to isolate the
XX nucleic acids of the invention
XX
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
DB |||||
9 CAGAACACC 1

RESULT 374
ID ABK96032 standard; DNA; 10 BP.
XX
XX AC ABK96032;
XX
XX 24-SEP-2002 (first entry)
DT
DE Human LIPE gene polymorphism detection oligonucleotide primer #7.
XX
XX Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;
XX polymorphism; primer; ss.
XX Homo sapiens.
XX
XX WO200240502-A2.
PN
XX
XX 23-MAY-2002.
PD
XX
XX 16-NOV-2001; 2001WO-US043518.
PF
XX
XX 16-NOV-2000; 2000US-0249302P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Anastasio AE, Bentivegna SC, Chew A, Koshy B, Rounds E;
PI WPI; 2002-519369/55.
XX
XX Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for
XX improving efficiency and reliability in drug development for treating
XX diseases associated with LIPE activity, e.g. obesity and male sterility.
XX
XX Claim 17; Page 16; 142pp; English.
XX
XX The present invention relates to a new polynucleotide comprising a
XX nucleotide sequence which comprises lipase, hormone sensitive (LIPE)
XX isogenes. The invention is useful in screening for drugs targeting LIPE
XX isogenes that are useful for treating obesity and male sterility. The
XX methods of the invention are useful for improving the efficiency and
XX reliability of several steps in the discovery and development of drugs
XX for treating diseases associated with LIPE activity. The polynucleotide
XX is useful in studying the expression and function of LIPE, and in
XX expressing LIPE protein for use in screening for candidate drugs to treat
XX diseases related to LIPE activity. It is also useful in studying the
XX effect of the variation on the biological activity of LIPE as well as on
XX the binding affinity of candidate drugs targeting LIPE for the treatment
XX of obesity and male sterility. The invention is useful for studying the
XX expression of LIPE isogenes in vivo, for in vivo screening and testing of
XX drugs targeted against LIPE protein, and for testing the efficacy of
XX therapeutic agents and compounds for treating obesity and male sterility
XX in a biological system. The present nucleic acid sequence represents one
XX of a collection (ABK96026-ABK96083) of oligonucleotide primers that were
XX used in the invention to detect polymorphisms in the human LIPE gene
XX
SQ Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
DB |||||
1 GCCAGGAGA 9

RESULT 375
ABK81376

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
 SQ Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 731 AGGAGAAAC 739
 Db |||||
 2 AGGAGAAAC 10

RESULT 371

AAS19577
 ID AAS19577 standard; DNA; 10 BP.
 XX
 AC AAS19577;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Primer-extension oligonucleotide #8 to detect human MPL polymorphisms.
 XX
 KW Human; single nucleotide polymorphism; SNP; MPL; chromosome 1p34;
 KW myeloproliferative leukaemia virus oncogene; haplotyping; genotyping;
 KW congenital amegakaryocytic thrombocytopaenia; CAMT; primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200179232-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US012301.
 XX
 PR 14-APR-2000; 2000US-0197839P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Choi JY, Koshy B, Stephens JC;
 XX
 DR WPI; 2002-055251/07.

XX Nucleotide polymorphisms in the human myeloproliferative leukemia virus
 CC oncogene (MPL) gene, useful for studying the function of and expressing
 PT MPL protein for use in screening drugs for treating diseases related to
 PT MPL activity.
 XX
 PS Claim 17; Page 16; 85pp; English.
 CC The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human myeloproliferative leukaemia virus oncogene (MPL)
 CC gene located on chromosome 1p34, and methods for haplotyping and/or
 CC genotyping the MPL gene. The methods of the invention make use of allele-

CC specific oligonucleotides (ASOs) as probes and primers and/or primer-
 CC extension oligonucleotides for detecting MPL gene polymorphisms. The
 CC polynucleotides and screened compounds are useful for the treatment of
 CC diseases associated with MPL activity, such as congenital amegakaryocytic
 CC thrombocytopaenia (CAMT). AAS19570-AAS19607 represent primer-extension
 CC oligonucleotides for detecting human MPL gene polymorphisms

SQ Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 732 GGAGAAACA 740
 Db |||||
 2 GGAGAAACA 10

RESULT 372

AAS98810
 ID AAS98810 standard; DNA; 10 BP.
 XX
 AC AAS98810;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #176.
 XX
 KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
 KW cytostatic; gene therapy; malignant histiocytosis; isogene;
 KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
 KW genotype; human; allele specific oligonucleotide; ASO; primer;
 KW primer extension; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200179225-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US012044.
 XX
 PR 12-APR-2000; 2000US-0196411P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Choi JY, Koshy B;
 XX
 DR WPI; 2002-075058/10.
 XX
 PT Novel polymorphic variants of colony stimulating factor 1 receptor useful
 PT in studying expression and function of the protein, useful for screening
 PT candidate drugs to treat diseases e.g. inflammatory disorders.
 XX
 PS Claim 17; Page 17; 164pp; English.

XX The invention describes a novel isolated polynucleotide (I) comprising a
 CC sequence which is a polymorphic variant (PV) of a reference sequence for
 CC colony stimulating factor 1 receptor (CSF1R) gene, found on The
 CC polypeptide are useful for improving the discovery and development of
 CC drugs for treating diseases associated with CSF1R activity, e.g.,
 CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
 CC and the haplotypes can be used to validate CSF1R as a candidate target
 CC for treating a specific condition or disease predicted to be associated
 CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
 CC be used in developing diagnostic tests and therapeutic treatments. (I) is
 CC useful in studying the expression and function of CSF1R, and in
 CC expressing CSF1R protein for use in screening for candidate drugs to
 CC treat diseases related to CSF1R activity and in studying the effect of
 CC the variation on the biological activity of CSF1R as well as on the
 CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
 CC useful in a variety of diagnostic and prognostic formats and therapeutic
 CC methods. A transgenic animal is useful in studying expression of the

CC (transient receptor potential) family protein; (ii) is connected with
CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC with tumors involving lip15.5 abnormalities. The products of the
CC invention have anticancer and developmental activity. MRL1 is involved in
CC regulation of intracellular calcium ion levels, which are essential for
CC cellular responses to hormones and/or growth factors; also in apoptosis
CC and cell growth, death and differentiation, and in urogenital diseases,
CC including polycystic kidney disease. (I) and related ribozymes, antisense
CC RNA, proteins and antibodies (Ab)) are used to treat or prevent diseases
CC associated with altered expression of the MRL1 gene or activity of its
CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
CC used for diagnosis of such diseases. (I) can also be used for recombinant
CC production of MRL1 proteins (II) (used for analysis, characterization and
CC therapy), as tissue or chromosomal markers, for identifying genetic
CC diseases and related sequences, as primers for genetic fingerprinting, as
CC source of oligonucleotides for biochips, and to raise anti-protein or
CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
CC competitive assays for (II), as tissue markers, for identifying
CC interacting proteins and in screening for (ant)agonists. This sequence
CC represents human MRL1 gene intron9/exon10 junction region described in
CC the method of the invention
XX
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 729 CCAGGAGAA 737
Db 2 CCAGGAGAA 10

RESULT 369
AAF70411/c
ID AAF70411 standard; DNA; 10 BP.
XX AAF70411;
AC AAF70411;
XX 20-APR-2001 (first entry)
XX Human DRD2 polymorphism detection oligonucleotide primer SEQ ID NO:154.
XX Human; dopamine receptor D2; DRD2; polymorphism; allele specific;
KW drug target isogene; detection; single nucleotide polymorphism; SNP;
KW genotype; schizophrenia; Parkinson's disease; myoclonus dystonia; MD;
KW probe; PCR primer; ss.
XX Homo sapiens.
XX WO200105832-A1.
XX 25-JAN-2001.
XX 19-JUL-2000; 2000WO-US019644.
XX 19-JUL-1999; 99US-0144493P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI WPI; 2001-091967/10.
XX
XX Polynucleotides comprising single nucleotide polymorphisms in the human
PT dopamine receptor D2, useful for detecting mutations associated with,
PT e.g. schizophrenia, Parkinson's and myoclonus dystonia.
XX
XX Disclosure; Page 24; 135pp; English.
XX
XX The present invention describes polynucleotides comprising single
CC nucleotide polymorphisms (SNPs) in the human dopamine receptor D2 (DRD2).

CC The polynucleotides may be used in assays to detect and characterise
CC polymorphisms in DRD2 that affect its expression and activity and are
CC involved in disorders such as schizophrenia, Parkinson's and myoclonus
CC dystonia (MD). This information would be useful for studying the
CC biological function of DRD2 as well as in identifying drugs targeting
CC this protein for the treatment of disorders related to its abnormal
CC expression or function. Polymorphisms in the DRD2 gene affect the
CC expression of active and functional polypeptides. Therefore it is
CC advantageous to detect polymorphisms in the DRD2 gene and how those
CC polymorphisms are combined in different copies of the gene. AAF70261 to
CC AAF70308 represent human DRD2 allele specific oligonucleotide probes, and
CC AAF70309 to AAF70404 represent human DRD2 allele specific oligonucleotide
CC primers which are used in the detection of DRD2 polymorphisms. AAF70405
CC to AAF70452 represent oligonucleotide primers for the detection of human
CC DRD2 polymorphisms which are given in the exemplification of the present
CC invention. AAF70453 to AAF70538 represent PCR primers for the human DRD2
CC gene which are used in examples from the present invention
XX
SQ Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAACACAGAA 743
Db 10 GAACACAGAA 2

RESULT 370
AAF42486
ID AAF42486 standard; DNA; 10 BP.
XX AAF42486;
AC AAF42486;
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10625.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
PN
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
PP
XX 16-JUN-1999; 99US-00335032.
PR
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 329; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log

CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACACA 742
 Db 2 AGAAACACA 10

RESULT 367
 AAZ86656
 ID AAZ86656 standard; DNA; 10 BP.

XX AC AAZ86656;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell downregulated transcript tag #5890.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; Gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX PN WO9965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX PA (GENZ) GENZYME CORP.

XX PA (ROBE/) ROBERTS B.L.

XX PA (SHAN/) SHANKARA S.

XX PI Roberts BL, Shankara S;

XX PF WPI; 2000-106079/09.

XX PT Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

XX PS Claim 1; Page 213; 219pp; English.

XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences), all-based
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX

SQ Sequence 10 BP; 5 A; 3 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
 Db 2 ACAGAACAC 10

RESULT 368

AAH20544

ID AAH20544 standard; DNA; 10 BP.

XX AC AAH20544;

XX DT 09-AUG-2001 (first entry)

XX DE Human MTR1 intron9/exon10 junction.

XX KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
 KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
 KW 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
 KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;
 KW cell growth; cell death; cell differentiation; urogenital disease;
 KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
 KW rhabdomyosarcoma; ds.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Intron

XX FT 1..5

XX FT /*tag= a

XX FT /number= 9

XX FT 6..10

XX FT /*tag= b

XX FT /number= 10

XX PN WO200132693-A2.

XX PD 10-MAY-2001.

XX PF 06-NOV-2000; 2000WO-DE003876.

XX PR 04-NOV-1999; 99DE-01053167.

XX PA (UYGU-) UNIV GUTENBERG JOHANNES.

XX PI Prawitt D, Pelletier J, Zabel B;

XX PF WPI; 2001-316417/33.

XX PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
 PT syndrome and tumors, also related proteins and antibodies.
 XX Example 2; Fig 2; 46pp; German.
 CC This invention describes a novel DNA sequence (I) encoding the MTR1
 CC protein that: (i) has at least one biological activity of a TRP

XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 119; 130pp; English.
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 0 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
DB 9 ACAGAACAC 1
|||||||
|||

RESULT 366
AAZ79359
ID AAZ79359 standard; DNA; 10 BP.
XX
XX AC AAZ79359;
XX
XX 10-APR-2000 (first entry)
DT
DE Human dendritic cell SAGE tag, SEQ ID NO:1787.
XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX

OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013800.
XX
XX 19-JUN-1998; 98US-0089823P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-008991P.
PR 19-JUN-1998; 98US-0089923P.
PR 19-JUN-1998; 98US-0089939P.
PR 19-JUN-1998; 98US-0089939P.
PR 19-JUN-1998; 98US-0089939P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-009000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
DR
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 116; 130pp; English.
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially

CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 745
 Db 14 GCAGAAAGAGGACA 1

RESULT 364
 ABZ96451/c
 ID ABZ96451 standard; DNA; 14 BP.

XX AC ABZ96451;

XX DT 17-OCT-2003 (first entry)

XX DE Human nucleic acid sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX XX 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPT; 2003-229219/22.

XX FT Pharmaceutical composition for treating ailments associated with impaired
 FT respiration, has oligo(s) antisense to specific gene(s) or its
 FT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 FT ubiquinone.

XX PS Disclosure; SEQ ID NO 11693; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 745
 Db 14 GCAGAAAGAGGACA 1

RESULT 365

AAZ79493/c
 ID AAZ79493 standard; DNA; 10 BP.

XX AC AAZ79493;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:1921.

XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN WO9965924-A2.

XX XX 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013800.

XX PR 19-JUN-1998; 98US-0089833P.

XX PR 19-JUN-1998; 98US-0089844P.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089878P.

XX PR 19-JUN-1998; 98US-0089911P.

XX PR 19-JUN-1998; 98US-0089922P.

XX PR 19-JUN-1998; 98US-0089933P.

XX PR 19-JUN-1998; 98US-0089944P.

XX PR 19-JUN-1998; 98US-0089977P.

XX PR 19-JUN-1998; 98US-0089999P.

XX PR 19-JUN-1998; 98US-0090000P.

XX PR 19-JUN-1998; 98US-0090035P.

XX PR 19-JUN-1998; 98US-0090036P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX PR 19-JUN-1998; 98US-0090042P.

XX PR 19-JUN-1998; 98US-0090043P.

XX PR 19-JUN-1998; 98US-0090044P.

XX PR 19-JUN-1998; 98US-0090045P.

XX PR 19-JUN-1998; 98US-0090047P.

XX PR 19-JUN-1998; 98US-0090048P.

XX PR 19-JUN-1998; 98US-0090072P.

XX PR 19-JUN-1998; 98US-0090076P.

XX PR 19-JUN-1998; 98US-0090077P.

XX PR 19-JUN-1998; 98US-0090078P.

XX PR 19-JUN-1998; 98US-0090079P.

XX PR 19-JUN-1998; 98US-0090080P.

XX PR 08-DEC-1998; 98US-0111715P.

Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 4.5e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 745
Db 14 GCAGAAAGAGGACA 1

RESULT 362
AAF21460/C
ID AAF21460 standard; DNA; 14 BP.
XX AC AAF21460;
XX DT 14-MAR-2001 (first entry)
XX DE Human multiple target antisense (MTA) oligonucleotide #3027.
XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX KW human; airway disorder; bronchoconstriction; lung inflammation;
XX KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
XX KW respiratory obstruction; pulmonary obstruction; impeded respiration;
XX KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX KW cancer; ss.
XX OS Homo sapiens.
XX XX
XX FN WO200062736-A2.
XX PD 26-OCT-2000.
XX PF 24-MAR-2000; 2000WO-US008020.
XX PR 06-APR-1999; 99US-0127958P.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX PI Nyce JW;
XX DR WPI; 2000-679539/66.
XX PT Low adenosine (A) content antisense oligonucleotides which do not trigger
XX PT adenosine receptors during metabolism, useful e.g. for treating cancers
XX PT and respiratory obstructions.
XX PS Disclosure; Page 296; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or

CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX XX
XX SQ Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 4.5e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 745
Db 14 GCAGAAAGAGGACA 1

RESULT 363
AB297154/C
ID AB297154 standard; DNA; 14 BP.
XX AC AB297154;
XX DT 17-OCT-2003 (first entry)
XX DE Human MTA oligonucleotide.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX XX
XX FN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 12396; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 XX
 XX 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-US017712.
 XX
 XX 03-AUG-1999; 98US-0095212P.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 XX
 XX Nyce JW;
 XX
 XX WPI; 2000-205971/18.
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 556; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;
 Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 732 GCAGAAACAGAACCA 745
 | | | | | | | | | | | | | |
 Db 14 GCAGAAAGAGGACCA 1
 RESULT 361
 AAF20757/c
 ID AAF20757 standard; DNA; 14 BP.

XX AAF20757;
 AC
 XX 14-MAR-2001 (first entry)
 DT
 XX Human multiple target antisense (MTA) oligonucleotide #2324.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO2000062736-A2.
 XX
 XX 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-US008020.
 XX
 XX 06-APR-1999; 99US-0127958P.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 PI
 XX WPI; 2000-679539/66.
 XX
 DR Low adenosine (A) content antisense oligonucleotides which do not trigger
 CC adenosine receptors during metabolism, useful e.g. for treating cancers
 CC and respiratory obstructions.
 PT
 XX Claim 14; Page 623; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and,
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 XX W09950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US006507.
 XX 27-MAR-1998; 98US-0079678P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX WPI; 1999-591315/50.
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 XX of an mRNA encoding an angiogenic factors.
 XX Claim 56; Page 136; 305pp; English.
 XX The present invention describes enzymatic nucleic acid molecules with RNA
 XX cleaving activity, which specifically cleave RNA encoded by an aryl
 XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAAl6775 to
 XX AAAl7167 and AAAl7561 to AAAl7622 represent ribozyme sequences for ARNT,
 XX and AAAl7168 to AAAl7560 and AAAl7623 to AAAl7684 represent their
 XX corresponding target sequences; AAAl7685 to AAAl8385 and AAAl9087 to
 XX AAAl9154 represent ribozyme sequences for Tie-2, and AAAl8386 to AAAl9086
 XX and AAAl9155 to AAAl9222 represent their corresponding target sequences;
 XX AAAl9223 to AAAl9361 and AAAl9501 to AAAl9595 represent ribozyme
 XX sequences for integrin alpha 6 subunit, and AAAl9362 to AAAl9500 and
 XX AAAl9596 to AAAl9688 represent their corresponding target sequences;
 XX AAAl9689 to AAAl9745 and AAAl9746 to AAAl9747 represent ribozyme sequences
 XX for integrin subunit beta 3, and AAAl9748 to AAAl9749, AAAl9750 to
 XX AAAl9751 to AAAl9752 represent their corresponding target sequences. The ribozymes of
 XX the invention are used for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding angiogenic factor, especially ARNT,
 XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 XX especially used to treat cancer, diabetic retinopathy, age related
 XX macular degeneration (ARMD), inflammation, and arthritis, as well as
 XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
 XX integrin subunit alpha-6, or integrin subunit beta-3
 XX Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
 SQ Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGAAC 744
 Db 14 AGAGGAAACAGCAC 1
 RESULT 359
 AAAX55188/C
 ID AAAX55188 standard; DNA; 14 BP.
 AC AAAX55188;
 XX 05-JUL-1999 (first entry)
 XX Multiple antisense oligonucleotide 9.
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 XX Synthetic.
 XX W09913886-A1.
 XX 25-MAR-1999.
 XX 17-SEP-1998; 98WO-US019419.
 XX 17-SEP-1997; 97US-0059160P.
 XX 09-JUN-1998; 98US-00093972.
 XX (UYEC-) UNIV EAST CAROLINA.
 XX Nyce JW;
 XX WPI; 1999-229400/19.
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 XX vasoconstriction.
 XX Disclosure; Page 73; 120pp; English.
 XX The specification describes antisense oligonucleotides (AAAX52869-XS5271)
 XX directed against at least 2 mRNAs selected from target genes, coding and
 XX non-coding regions of RNAs corresponding to target genes, gene initiation
 XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 XX end and the juxta-section between coding and non-coding regions and all
 XX segments of RNAs encoding proteins associated with one or more diseases,
 XX conditions or mixtures. The antisense oligonucleotides may be derived
 XX from sequences AAAX5272-74. These multiple target oligonucleotides
 XX (specifically AAAX5180-271) can be used for the antisense treatment of
 XX diseases and conditions. Typical diseases and conditions are those
 XX associated with impaired respiration and inflammation, including lung
 XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 XX acute asthma, allergies, asthma, impeded respiration, respiratory
 XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 XX colon cancer, breast cancer, lung cancer, pancreatic cancer,
 XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 XX well as all types of cancers which may metastasize or have metastasized
 XX to the lungs, including breast and prostate cancer
 XX Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;
 SQ Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 732 GGAGAAACAGAAC 745
 Db 14 GCAGAAAGAGGACA 1
 RESULT 360
 AAAX34635/C
 ID AAAX34635 standard; DNA; 14 BP.
 AC AAAX34635;
 XX 28-JUL-2000 (first entry)
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2324.

KW inflammation; heart burn; infection; colon cancer; malignant melanoma;
 KW skin disorder; antisense oligonucleotide; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX WO2003006478-A1.
 XX 23-JAN-2003.
 XX 10-JUL-2002; 2002WO-US021664.
 XX 10-JUL-2001; 2001US-0303820P.
 XX (OLIG-) OLIGOS ETC INC.
 XX Dale RMK, Arrow A, Thompson T;
 XX WPI; 2003-221709/21.
 XX Composition with a modified oligonucleotide useful for treating a patient
 PT with a pathological disorder such as abnormal appetite, hypertension,
 PT eczema, anxiety, stress, and cancer.
 XX Claim 17; Page 6; 173pp; English.
 XX The present invention describes a composition (I) suitable for
 CC administration in a mammal, which comprises a modified oligonucleotide
 CC (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups
 CC linked by achiral 5'-3' internucleoside phosphate linkages, where the
 CC modified oligonucleotide is complementary to a region of a gene
 CC associated with a pathological disorder. Also described: (1) a
 CC nutritional supplement comprising (II); and (2) a cosmetic composition
 CC comprising (II), where the modified oligonucleotide is complementary to a
 CC region of a gene associated with a skin disorder. (I) and (II) can have
 CC hypotensive, antilipemic, vasotropic, dermatological, antidepressant,
 CC tranquilizer, antiinflammatory, antitumor, laxative, antimigraine,
 CC neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,
 CC vulnary, antiarthritic, antipsoriatic antimicrobial, cytostatic and
 CC litholytic activities. (I) can be used for treating a patient with a
 CC pathological disorder selected from abnormal appetite, hypertension,
 CC hypercholesterolemia, hyperlipidaemia, erectile dysfunction, eczema,
 CC depression, anxiety, stress, inflammatory bowel syndrome, ulcerative
 CC colitis, Crohn's disease, renal stones, gall stones, constipation, colds,
 CC migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,
 CC fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
 CC chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,
 CC inflammation, rosacea, arthritis, psoriasis, prostatitis,
 CC inflammation, heart burn, infection, poison ivy, colon cancer, malignant
 CC melanoma, and malignant nasal polyps. The nutritional supplement is
 CC useful for supplementing the diet of an individual, and the cosmetic
 CC composition is useful for improving the appearance of the skin in an
 CC individual with a skin disorder. ACF63279 to ACF63410 represent
 CC nucleotide sequence given in the exemplification of the present invention
 XX
 XX Sequence 14 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCAGGAGGAA 737
 Db 3 TGTGAGGAGAA 13

RESULT 357

AAQ78386
 ID AAQ78386 standard; DNA; 14 BP.
 AC AAQ78386;
 XX

DT 25-MAR-2003 (revised)

DT 27-JUN-1995 (first entry)
 XX Antisense oligonucleotide hybridising to TGF-beta gene.
 DE
 XX
 XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.
 XX Synthetic.
 OS
 XX WO9425588-A2.
 XX 10-NOV-1994.
 XX 29-APR-1994; 94WO-EP001362.
 XX 30-APR-1993; 93EP-00107089.
 XX 13-MAY-1993; 93EP-00107849.
 XX (BT0G-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 XX Bogdahn U;
 XX WPI; 1994-358266/44.
 XX New transforming growth factor beta antisense oligonucleotide(s) - for
 PT treating immunosuppression, tumours, etc.
 XX Claim 6; Page 34; 74pp; English.
 XX The antisense oligonucleotides are useful in the treatment of tumours in
 CC which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 14 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 730 CAGGACAAACAGAA 743
 Db 1 CATGAGAGCAGGA 14
 RESULT 358
 AAAL19155/C
 ID AAAL19155 standard; RNA; 14 BP.
 XX
 XX AAAL19155;
 XX
 XX 19-JUN-2000 (first entry)
 XX Human TIE-2 target site SEQ ID NO:2381.
 DE
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW

XX 23-APR-2002; 2002WO-US013135.
 XX PF
 XX 24-APR-2001; 2001US-0286137P.
 XX PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI
 XX WPI; 2003-229219/22.
 DR
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 PT
 XX Disclosure; SEQ ID NO 10555; 872bp; English.
 PS
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAA 738
 Db |||||
 12 GCCAGGAGAA 2
 RESULT 356
 ACF63279
 ID ACF63279 standard; DNA; 14 BP.
 XX
 XX ACF63279;
 XX
 XX 09-OCT-2003 (first entry)
 DT
 XX Human phosphodiesterase 4 antisense oligonucleotide SEQ ID NO:1.
 DE
 XX Human; pharmacological; hypotensive; antilipemic; vasotropic; laxative;
 KW dermatological; antidepressant; tranquilizer; antiinflammatory; eczema;
 KW antiulcer; antimitigaine; neuroprotective; antiparkinsonian; analgesic;
 KW gynaecological; virucide; vulvar; antiarthritic; antipsoriatic; cold;
 KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;
 KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
 KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
 KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
 KW constipation; headache; seizure; multiple lateral sclerosis; trauma;
 KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis;
 KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
 KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;
 KW

XX 23-APR-2002; 2002WO-US013135.
 XX PF
 XX 24-APR-2001; 2001US-0286137P.
 XX PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI
 XX WPI; 2003-229219/22.
 DR
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 PT
 XX Disclosure; SEQ ID NO 11128; 872bp; English.
 PS
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 731 AGGAGAACAG 741
 Db |||||
 11 AGGAGAACAG 1
 RESULT 355
 ABZ95313/c
 ID ABZ95313 standard; DNA; 14 BP.
 XX
 XX ABZ95313;
 XX
 XX 17-OCT-2003 (first entry)
 DT
 XX Human IL-6 receptor fragment no.1177.
 DE
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 XX Homo sapiens.
 OS
 XX WO200285308-A2.
 XX
 XX 31-OCT-2002.
 PD

PN EP1174514-A1.
XX 23-JAN-2002.
XX
XX 20-JUL-2000; 2000EP-00115626.
XX
XX 20-JUL-2000; 2000EP-00115626.
PR (ARTE-) ARTEMIS PHARM GMBH.
XX
XX Hobom G, Menke A, Meyer-Rogge S;
PI WPI; 2002-156694/21.
XX
XX Recombinant influenza virus for transfer and expression of foreign genes
PT and RNA molecules into cells and for preventing, treating influenza, has
PT bisclstronic viral RNAs coding for two genes in tandem arrangement.
XX
XX Disclosure; Page 15; 39pp; English.
XX
XX The invention describes a recombinant influenza virus (I), stable in the
CC absence of any helper virus, that has a viral RNA segment being a
CC bisclstronic RNA molecule coding for two genes in tandem arrangement
CC (tandem RNA segment, TRS). (I) is useful for expression of incorporated
CC foreign gene(s) and RNA molecules in cells. (II), preferably a recombinant
CC influenza A virus is useful for: preventing and/or treating influenza,
CC and for preparing a medicament for vaccination purposes; somatic gene
CC therapy, and as immunogen for inducing antibodies; as an expression
CC vector for producing proteins or glycoproteins; preparing agents for
CC somatic gene therapy; immunotherapy, preferably autologous immunotherapy;
CC transfer and expression of foreign genes and RNA molecules into cells
CC infected by such viruses, where the RNA molecules to be expressed include
CC antisense or double-stranded sequences relative to the target cell
CC cellular mRNA molecules, and/or the agent is suitable for sequence-
CC specific gene silencing, preferably by antisense RNA or RNA interference
CC mechanisms. (I) gives high-yield expression for foreign genes. This
CC sequence represents a 3' conserved region mutant of influenza C virus
CC that is incorporated into the mutant influenza C construct, described in
CC the method of the invention
XX
SQ Sequence 14 BP; 1 A; 6 C; 1 G; 0 T; 6 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
DB 14 AGTAGAAACAG 4
RESULT 353
ABZ95299/C
ID ABZ95299 standard; DNA; 14 BP.
XX
XX ABZ95299;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human IL-6 receptor fragment no.1163.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antialsthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
PD

XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
XX Disclosure; SEQ ID NO 10541; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antialsthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAA 738
DB 14 GCCAGGAGACA 4
RESULT 354
ABZ95886/C
ID ABZ95886 standard; DNA; 14 BP.
XX
XX ABZ95886;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human monocyte activating factor antisense fragment no.1746.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antialsthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
PD


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XX AC AAA65226;
XX DT 19-DEC-2000 (first entry)
XX DE Modified end-blocked acid-resistant oligonucleotide #1.
XX KW End-blocked acid-resistant oligonucleotide; infection;
XX KW inflammatory disease; cancer; antibacterial application;
XX KW phosphorothioate linkage; primer; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..14
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Optional phosphorothioate backbone"
XX PN WO200040592-A1.
XX PD 13-JUL-2000.
XX PF 16-DEC-1999; 99WO-US030266.
XX PR 30-DEC-1998; 98US-00223498.
XX PR 19-JUL-1999; 99US-00356069.
XX PA (OLIG-) OLIGOS ETC INC.
XX PI Dale RMK, Gatton SL, Arrow A;
XX WPI; 2000-465945/40.
XX PT Modified nucleic acid polymer used for treating inflammation, cancer,
XX PT bacterial, viral and fungal infections and in disinfectants has a
XX PT blocking chemical modification at the end of the polymer.
XX PS Example 2; Page 32; 56pp; English.
XX CC The present sequence is an oligonucleotide which was used to demonstrate
XX CC the invention. The invention concerns end-blocked acid resistant
XX CC oligonucleotides which are also resistant to nuclease degradation and are
XX CC capable of binding specifically in an antisense manner. This means that
XX CC they are useful in the treatment and prevention of infections,
XX CC inflammatory diseases and cancer, as well as having non-therapeutic
XX CC applications in cosmetics, for example in skin tanning products. In
XX CC addition, they can be used in antibacterial applications such as
XX CC sterilisation of surgical instruments, and in antibacterial lotions and
XX CC soaps. A number of different versions of this sequence were produced,
XX CC including an unblocked 2'-O-methyl RNA, a 2'-O-methyl RNA with 3' and 5'
XX CC buranol blocked ends, a 3'-O-methyl phosphodiester, a 2'-O-propargyl and
XX CC a 2'-O-methyl phosphodiester. These were all used to show that the
XX CC modified sequence is less susceptible to degradation than the natural
XX CC sequence
XX SQ Sequence 14 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAA 737
Db 3 TGTCAGGAGAA 13

RESULT 349
AAA57799
ID AAA57799 standard; DNA; 14 BP.
XX AC AAA57799;
XX CC

20-OCT-2000 (first entry)
Antisense oligonucleotide for the human PDE4D gene.

Antisense oligonucleotide; phosphodiesterase 4; PDE4; cystic fibrosis;
acid resistant polymer; nuclease resistance; depression; thrombosis;
pulmonary hypertension; glaucoma; multiple sclerosis; gastric lesion;
atopic dermatitis; asthma; allergy; ss.

Homo sapiens.
WO200040714-A2.
13-JUL-2000.
15-DEC-1999; 99WO-US029976.
30-DEC-1998; 98US-00223586.
29-JUL-1999; 99US-00364626.
(OLIG-) OLIGOS ETC INC.
Dale RMK, Arrow A, Thompson T;
WPI; 2000-465980/40.

New acid resistant polymer complementary to phosphodiesterase 4 for
treating depression, thrombosis, cystic fibrosis, gastric lesions,
pulmonary hypertension, glaucoma, multiple sclerosis, atopic dermatitis
and asthma.

Claim 7; Page 17; 48pp; English.

The present sequence represents an antisense oligonucleotide, directed
against the phosphodiesterase 4D (PDE4D) gene. The oligonucleotide is
used to construct the polymer of the invention. The specification
describes an acid resistant polymer which is complementary to PDE4, and
comprises a nucleic acid with a backbone structure that is modified from
that of a naturally occurring nucleotide polymer and a blocking chemical
modification at or near one end of the nucleic acid. The acid resistant
polymer is characterized by a pH stability of an hour at pH 0.01 to 10
and a nuclease resistance of twice that of naturally occurring nucleic
acids which have the same number of nucleotides. The polymers are used to
inhibit the expression of genes encoding PDE4. They are useful as
analytical tools in the study of individual PDE isoforms and can treat
depression, thrombosis, cystic fibrosis, gastric lesions, pulmonary
hypertension, glaucoma, multiple sclerosis, atopic dermatitis, asthma,
and other allergic disorders. Other illnesses in which an increase of
cyclic AMP or decrease in phosphodiesterase levels is useful, can also be
treated

Sequence 14 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAA 737
Db 3 TGTCAGGAGAA 13

RESULT 350
AAL37793/C
ID AAL37793 standard; RNA; 14 BP.
XX AC AAL37793;
XX CC
XX 05-AUG-2002 (first entry)
XX DT RNA region of modified influenza C virus #2.
XX DE Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell;
XX WPI

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PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 XX Claim 14; Page 209; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, defensins, growth factors, vasoactive peptides and
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 728 GCCAGGAGAAA 738
 Db 12 GCCAGGAGAAA 2
 RESULT 347
 AAF19605/C
 ID AAF19605 standard; DNA; 14 BP.
 XX
 AC AAF19605;
 XX
 XX 14-MAR-2001 (first entry)
 DT
 XX Human IL6 receptor polynucleotide fragment #1172.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000062736-A2.
 XX
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US008020.
 PF
 XX 06-APR-1999; 99US-0127958P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 PA
 XX Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 XX Claim 14; Page 209; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, defensins, growth factors, vasoactive peptides and
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 728 GCCAGGAGAAA 738
 Db 14 GCCAGGAGACA 4
 RESULT 348
 AAF65226
 ID AAF65226 standard; DNA; 14 BP.

CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytosolic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AA33213 to AA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
 Db 12 GCCAGGAGAAA 2

RESULT 345

AAAF20192/C
 ID AAFA19619 standard; DNA; 14 BP.

AC AAFA19619;

XX 14-MAR-2001 (first entry)

XX Human endothelial monocyte activating factor DNA fragment #1759.

DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.

OS WO200062736-A2.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

PF 06-APR-1999; 99US-0127958P.

PR (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX Nyce JW;

XX WPI; 2000-6795539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger

PT adenosine receptors during metabolism, useful e.g. for treating cancers
 XX and respiratory obstructions.

PS Claim 14; Page 207; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS), and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AA18434 to AA21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

XX Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;

Best Local Similarity 90.9%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGCAGAACACAG 741

Db 11 AGCAGAACACAG 1

RESULT 346

AAFI9619/C
 ID AAFA19619 standard; DNA; 14 BP.

XX AAFA19619;

XX 14-MAR-2001 (first entry)

DE Human IL6 receptor polynucleotide fragment #1186.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONS from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAGAA 738
 Db 14 GCCAGGAGAGACA 4
 RESULT 343
 AAA34070/C
 ID AAA34070 standard; DNA; 14 BP.
 XX AC AAA34070;
 XX DT 28-JUL-2000 (first entry)
 XX DE Human adenosine receptor related polynucleotide SEQ ID NO:1759.
 XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX OS Homo sapiens.
 XX XX
 XX PN WO200009525-A2.
 XX PD 24-FEB-2000.
 XX XX
 XX PF 03-AUG-1999; 99WO-US017712.
 XX PR 03-AUG-1998; 98US-0095212P.
 XX PA (UYEC-) UNIV EAST CAROLINA.
 XX PI Nyce JW;
 XX DR WPI; 2000-205971/18.
 XX XX
 PS Disclosure; Page 483; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation.
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,

CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONS reduces side effects. The A-containing ONS break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing the
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONS from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAG 741
 Db 11 AGGAGAAACAG 1
 RESULT 344
 AAA33497/C
 ID AAA33497 standard; DNA; 14 BP.
 XX AC AAA33497;
 XX DT 28-JUL-2000 (first entry)
 XX DE Low adenosine antisense oligonucleotide SEQ ID NO:1186.
 XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX OS Homo sapiens.
 XX XX
 XX PN WO200009525-A2.
 XX PD 24-FEB-2000.
 XX XX
 XX PF 03-AUG-1999; 99WO-US017712.
 XX PR 03-AUG-1998; 98US-0095212P.
 XX PA (UYEC-) UNIV EAST CAROLINA.
 XX PI Nyce JW;
 XX DR WPI; 2000-205971/18.
 XX XX
 PS New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Claim 18; Page 413; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or

CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
 |||||
 Db 14 GCCAGGAGACA 4

RESULT 341
 AAX54623/C
 ID AAX54623 standard; DNA; 14 BP.

AC AAX54623;

DT 05-JUL-1999 (first entry)

DE Endothelial mocyte activating factor antisense oligonucleotide.

XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impaired respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.

OS Synthetic.

XX WO9913886-A1.

XX 25-MAR-1999.

XX 17-SEP-1998; 98WO-US019419.

XX 17-SEP-1997; 97US-0059160P.

XX 09-JUN-1998; 98US-00093972.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction.

PS Disclosure; Page 47; 120pp; English.

XX The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 CC end and the juxta-section between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AAX5272-74. These multiple target oligonucleotides
 CC (specifically AAX5180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impaired respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.

CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer

XX Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;

Best Local Similarity 90.9%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
 |||||
 Db 11 AGGAGGACAG 1

RESULT 342

AAX33483/C

ID AAX33483 standard; DNA; 14 BP.

XX AC AAX33483;

XX 28-JUL-2000 (first entry)

XX Low adenosine antisense oligonucleotide SEQ ID NO:1172.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.

PS Claim 18; Page 411; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the

XX	Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;	
SQL	Query Match 42.7%; Score 9.4; DB 1; Length 14;	
	Best Local Similarity 90.9%; Pred. No. 4.2e+02;	
	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	728 GCCAGGAGAAA 738	
Db	12 GCCAGGGGAAA 2	
RESULT 340		
AXX54039/C		
ID	AXX54039 standard; DNA; 14 BP.	
XX	AC	
XX	AAX54039;	
XX	XX	
DT	05-JUL-1999 (first entry)	
DE	Human IL-6 receptor antisense oligonucleotide fragment.	
XX	Antisense oligonucleotide; multiple target; antisense treatment;	
KW	impaired respiration; inflammation; lung disease;	
KW	pulmonary vasoconstriction; inflammation; allergic rhinitis;	
KW	acute asthma; allergy; asthma; impeded respiration;	
KW	respiratory distress syndrome; pain; cystic fibrosis;	
KW	pulmonary hypertension; pulmonary vasoconstriction; emphysema;	
KW	chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;	
KW	colon cancer; breast cancer; lung cancer; pancreatic cancer;	
KW	hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;	
KW	prostate cancer; ss.	
OS	Synthetic.	
XX	WO9913886-A1.	
XX	25-MAR-1999.	
XX	17-SEP-1998; 98WO-US019419.	
XX	17-SEP-1997; 97US-0059160P.	
PR	09-JUN-1998; 98US-00093972.	
XX	(UYEC-) UNIV EAST CAROLINA.	
XX	Nyce JW;	
PI	WPI; 1999-229400/19.	
DR	New antisense oligonucleotides used in treatment of, e.g. pulmonary	
PT	vasoconstriction.	
PT	vasoconstriction.	
XX	Disclosure; Page 50; 120pp; English.	
PS	The specification describes antisense oligonucleotides (AA52969-X55271)	
XX	directed against at least 2 mRNAs selected from target genes, coding and	
CC	non-coding regions of RNAs corresponding to target genes, gene initiation	
CC	codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'	
CC	-end and the juxta-section between coding and non-coding regions and all	
CC	segments of RNAs encoding proteins associated with one or more diseases,	
CC	conditions or mixtures. The antisense oligonucleotides may be derived	
CC	from sequences AA5272-74. These multiple target oligonucleotides	
CC	(specifically AA55180-271) can be used for the antisense treatment of	
CC	diseases and conditions. Typical diseases and conditions are those	
CC	associated with impaired respiration and inflammation, including lung	
CC	diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,	
CC	acute asthma, allergies, asthma, impeded respiration, respiratory	
CC	distress syndrome, pain, cystic fibrosis, pulmonary hypertension,	
CC	pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary	
CC	disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.	
CC	colon cancer, breast cancer, lung cancer, pancreatic cancer, e.g.	
CC	hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as	

CC The present invention describes a recombinant adeno-associated virus
 CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
 CC first ribozyme that specifically cleaves an mRNA encoding a protein,
 CC polypeptide, or peptide selected from the group of rod opsin, INOS,
 CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
 CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
 CC vector comprising a polynucleotide encoding the ribozyme, where the
 CC polynucleotide operably positioned downstream of at least a first
 CC promoter that directs expression of the polynucleotide in a selected
 CC mammalian cell transformed with the vector; (c) a viral particle
 CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
 CC comprising the ribozyme or the polynucleotide; or (e) a host cell
 CC comprising the ribozyme or the polynucleotide. Also described is a method
 CC for decreasing the amount of mRNA encoding a selected polypeptide in a
 CC retinal cell of a mammalian eye, comprising providing to the eye the
 CC composition described above, and for a time effective to specifically
 CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
 CC be used in gene therapy. (I) can be used for treating a disease or
 CC dysfunction of the mammalian eye, such as a retinal disease or retinal
 CC dysfunction, (diabetic) retinopathy, or (age-related) macular
 CC degeneration. (I) is also useful for manufacturing a medicament for
 CC treating the diseases mentioned above, including autosomal dominant
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
 CC for treating, decreasing the severity, or ameliorating the symptoms of a
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
 CC blindness, a reduction in central or peripheral vision, or a reduction in
 CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
 CC exemplification of the present invention

XX
 SQ Sequence 13 BP; 1 A; 3 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741

DB 11 AGCAGAAACAG 1

RESULT 337
 AAT76263/C
 ID AAT76263 standard; DNA; 14 BP.

XX AAT76263;

DT 15-SEP-1997 (first entry)

XX Human IL6 receptor antisense oligonucleotide.

XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
 KW chronic obstructive pulmonary disease; bronchitis; interleukin; ss.

XX Synthetic.

XX WO9640162-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US009306.

XX 07-JUN-1995; 95US-00474497.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW, Metzger WJ;

XX WPI; 1997-051871/05.

XX Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligo:nucleotide to airway epithelium of
 PT subject.

PS Example 5; Page 32; 71pp; English.

XX A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide specific
 CC for the human IL6 receptor. The method can be used to treat airway
 CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
 CC disease, bronchitis and other airway diseases characterised by an
 CC inflammatory response. By eliminating adenosine from the antisense ON,
 CC its liberation upon antisense degradation is prevented, thereby
 CC preventing adenosine-induced bronchoconstriction in patients with hyper-
 CC reactive airways

SQ Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738

DB 12 GCCAGGAGAAA 2

RESULT 338

AAT76249/C
 ID AAT76249 standard; DNA; 14 BP.

XX AAT76249;

DT 15-SEP-1997 (first entry)

XX Human IL6 receptor antisense oligonucleotide.

XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
 KW chronic obstructive pulmonary disease; bronchitis; interleukin; ss.

XX Synthetic.

XX WO9640162-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US009306.

XX 07-JUN-1995; 95US-00474497.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW, Metzger WJ;

XX WPI; 1997-051871/05.

XX Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligo:nucleotide to airway epithelium of
 PT subject.

PS Example 5; Page 32; 71pp; English.

XX A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide specific
 CC for the human IL6 receptor. The method can be used to treat airway
 CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
 CC disease, bronchitis and other airway diseases characterised by an
 CC inflammatory response. By eliminating adenosine from the antisense ON,
 CC its liberation upon antisense degradation is prevented, thereby
 CC preventing adenosine-induced bronchoconstriction in patients with hyper-
 CC reactive airways

SQ Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-1B000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 175624; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIC00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 1 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 735 GAACAGAACACC 747
Db 1 RAACAGAACACC 13
RESULT 335
ABF56510/c
ID ABF56510 standard; DNA; 13 BP.
XX
XX AC ABF56510;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 156507 for detecting SNP TSC0039462.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-1B000713.
XX
XX PG 07-APR-2000; 2000DE-01019173.
XX
XX PH (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX PJ WPI; 2001-657177/75.
XX
XX PK Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 175624; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIC00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 1 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 735 GAACAGAACACC 747
Db 1 RAACAGAACACC 13
RESULT 335
ABF56510/c
ID ABF56510 standard; DNA; 13 BP.
XX
XX AC ABF56510;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 156507 for detecting SNP TSC0039462.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-1B000713.
XX
XX PG 07-APR-2000; 2000DE-01019173.
XX
XX PH (EPIG-) EPIGENOMICS AG.
XX

XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 156507; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIC00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 0 A; 1 C; 6 G; 5 T; 0 U; 1 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 735 GAACAGAACACC 747
Db 13 RAACAGAACACC 1
RESULT 336
ABZ72819/c
ID ABZ72819 standard; RNA; 13 BP.
XX
XX AC ABZ72819;
XX
XX DT 09-APR-2003 (first entry)
XX
XX DE Rod opsin hammerhead ribozyme target oligonucleotide SEQ ID NO:59.
XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
XX ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
XX diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
XX blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
XX OS Homo sapiens.
XX
XX PN WC200288320-A2.
XX
XX PD 07-NOV-2002.
XX
XX PF 01-MAY-2002; 2002WO-US013679.
XX
XX PR 01-MAY-2001; 2001US-00847601.
XX
XX PA (UYFL) UNIV FLORIDA.
XX
XX PI Lewin AS, Shaw LC, Grant MB;
XX
XX DR WPI; 2003-111880/10.
XX
XX PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX Claim 1; Page 72; 115pp; English.
XX
XX PS

CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACACAGAACAC 746
 ||||| |||||
 Db 3 AACACATACAC 13

RESULT 332

ABF50801
 ID ABF50801 standard; DNA; 13 BP.

AC ABF50801;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 150798 for detecting SNP TSC0038055.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 150798; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 7 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACACAGAACAC 747
 ||||| |||||
 Db 1 AACACATACAC 11

RESULT 333

ABH48837

ID ABH48837 standard; DNA; 13 BP.

XX ABH48837;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 248814 for detecting SNP TSC0060796.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 248814; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACACAGAACAC 746
 ||||| |||||
 Db 3 AACACATACAC 13

RESULT 334

ABF75627

ID ABF75627 standard; DNA; 13 BP.

XX ABF75627;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 175624 for detecting SNP TSC0043631.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX Claim 1; SEQ ID NO 82745; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 736 AACACGACAC 746
DB 12 AACATAACAC 2
XXXXXX
RESULT 330
ABF30259
ID ABF30259 standard; DNA; 13 BP.
XX
AC ABF30259;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 130256 for detecting SNP TSC0032538.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT

XX Claim 1; SEQ ID NO 130256; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 736 AACACGACAC 746
DB 2 AACATAACAC 12
XXXXXX
RESULT 331
ABH19619
ID ABH19619 standard; DNA; 13 BP.
XX
AC ABH19619;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 219596 for detecting SNP TSC0053410.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX Claim 1; SEQ ID NO 219596; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 736 AACACGACAC 746
DB 2 AACATAACAC 12
XXXXXX
RESULT 331
ABH19619
ID ABH19619 standard; DNA; 13 BP.
XX
AC ABH19619;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 219596 for detecting SNP TSC0053410.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT

DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 250884; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
SQ Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACGAGAACAC 746
Db |||||
2 AAACGAGAACAC 12

RESULT 325
ABC71283
ID ABC71283 standard; DNA; 13 BP.
XX
XX ABC71283;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 71300 for detecting SNP TSC0018470.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 71300; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 1 Other;
SQ Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACGAGAACAC 748
Db |||||
1 AAAACGAGAACAC 13

RESULT 326
ABC72903
ID ABC72903 standard; DNA; 13 BP.
XX
XX ABC72903;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 72920 for detecting SNP TSC0018823.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 72920; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 1 Other;
SQ Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 1 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 733 GACAAACAGAACAC 745
Db 13 RACAAACACACAC 1
RESULT 320
ABC82726/c
ID ABC82726 standard; DNA; 13 BP.
XX AC ABC82726;
XX DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 82743 for detecting SNP TSC0020863.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 82743; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 0 A; 0 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 736 AACACAGAACAC 746
Db 12 AACACAGAACAC 2
RESULT 321
ABC83626/c
ID ABC83626 standard; DNA; 13 BP.
XX AC ABC83626;
XX DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 83643 for detecting SNP TSC0021064.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 83643; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 2 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 736 AACACAGAACAC 746
Db 12 AACACAGAACAC 2
RESULT 322
ABF56386

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 XX
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PF (EPIG-) EPIGENOMICS AG.
 PR Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 214794; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AACACGAAACAC 746
 Db ||||| |||||
 3 AACACGAAACAC 13
 RESULT 318
 ABC72271
 ID ABC72271 standard; DNA; 13 BP.
 AC ABC72271;
 XX 21-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 72288 for detecting SNP TSC0018670.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PF (EPIG-) EPIGENOMICS AG.
 PR Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 72919; 29pp + Sequence Listing; German.

XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT Claim 1; SEQ ID NO 72288; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 1 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AACACGAAACAC 746
 Db ||||| |||||
 3 AACACGAAACAC 13
 RESULT 319
 ABC72902/c
 ID ABC72902 standard; DNA; 13 BP.
 AC ABC72902;
 XX 21-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 72919 for detecting SNP TSC0018823.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 72919; 29pp + Sequence Listing; German.

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. NO. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAACAC 746
||||| |||||
Db 3 AACATAACAC 13

RESULT 315
ABCI1965/c
ID ABCI1965 standard; DNA; 13 BP.
XX AC ABCI1965;
XX
DT 20-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 11972 for detecting SNP TSC0002869.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 11972; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 6 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. NO. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAC 741
||||| |||||

Db 11 AGGAGAAAGAG 1

RESULT 316
ABHI4816/c
ID ABHI4816 standard; DNA; 13 BP.
XX
AC ABHI4816;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 214793 for detecting SNP TSC0052269.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 214793; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 1 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. NO. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAACAC 746
||||| |||||
Db 11 AACAGAACAC 1

RESULT 317
ABHI4817
ID ABHI4817 standard; DNA; 13 BP.
XX
AC ABHI4817;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 214794 for detecting SNP TSC0052269.
XX


```
RESULT 305
ABC66043/c
ID ABC66043 standard; DNA; 13 BP.
XX
XX
AC ABC66043;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 66060 for detecting SNP TSC0017378.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 66060; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 5 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 733 GAGAAACAGAA 743
XX 11 GAGAAAGAGAA 1
XX
XX RESULT 306
ABF30261
ID ABF30261 standard; DNA; 13 BP.
XX
XX
AC ABF30261;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 130258 for detecting SNP TSC0032538.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
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XX OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 130258; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 736 AAACAGAACAC 746
XX 2 AAACATAACAC 12
XX
XX RESULT 307
ABF80901
ID ABF80901 standard; DNA; 13 BP.
XX
XX
AC ABF80901;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 180898 for detecting SNP TSC0044758.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX
```

PS Claim 1; SEQ ID NO 57798; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 8 A; 4 C; 1 G; 0 T; 0 U; 0 Other;

XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACGACAC 746
DB |||||
2 AAACGACAC 12

RESULT 303

ABF66156/c
ID ABF66156 standard; DNA; 13 BP.

XX AC ABF66156;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 166153 for detecting SNP TSC0041649.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX Claim 1; SEQ ID NO 166153; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 1 Other;

XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAACAGACAC 747
DB |||||
13 GAACAGACAC 1

RESULT 304

ABC73158
ID ABC73158 standard; DNA; 13 BP.

XX AC ABC73158;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 73175 for detecting SNP TSC0018861.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX Claim 1; SEQ ID NO 73175; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 6 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
DB |||||
1 GAGAAACGAA 11


```
DE Oligonucleotide SEQ ID NO 16265 for detecting SNP TSC0041660.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 16265; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 1 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 735 GAACAGAACACC 747
Db 13 RAACCGAAACCC 1
:|||||
:|||||

RESULT 301
ABH50906/C
ID ABH50906 standard; DNA; 13 BP.
XX
XX AC ABH50906;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 250883 for detecting SNP TSC0061240.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
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XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 250883; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 736 AAACGAGACAC 746
Db 12 AAACCGAACAC 2
:|||||
:|||||

RESULT 302
ABC57781
ID ABC57781 standard; DNA; 13 BP.
XX
XX AC ABC57781;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 57798 for detecting SNP TSC0015564.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
```

CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 GAAACAGAACACC 746

DB 11 AAACAAACACC 1

RESULT 298

ABF74448/c

ID ABF74448 standard; DNA; 13 BP.

XX AC ABF74448;

XX DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 174445 for detecting SNP TSC0043390.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX FN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 174445; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 1 A; 1 C; 4 G; 6 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACC 747
 DB 13 RAAATCGAACACC 1

RESULT 299

ABF66159

ID ABF66159 standard; DNA; 13 BP.

XX AC ABF66159;

XX DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 166156 for detecting SNP TSC0041649.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX XX WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 166156; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACC 747

DB 1 RAAACAAACACC 13

RESULT 300

ABF66268/c

ID ABF66268 standard; DNA; 13 BP.

XX AC ABF66268;

XX DT 22-FEB-2002 (first entry)

PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX PF
XX 07-APR-2000; 2000DE-01019173.
XX PR
XX (EPIG-) EPIGENOMICS AG.
XX PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 6059; 29pp + Sequence Listing; German.
XX PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
Db 3 GAGAAACAGAA 13
|||||
3 GAGAAACAGAA 13
RESULT 296
ABF25407/C
ID ABF25407 standard; DNA; 13 BP.
XX
AC ABF25407;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 125404 for detecting SNP TSC0031343.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PP 07-APR-2000; 2000DE-01019173.
XX
PR (EPIG-) EPIGENOMICS AG.
XX
PA Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
DR

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 125404; 29pp + Sequence Listing; German.
XX PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 5 C; 0 G; 7 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
Db 11 AGGAGAAACAG 1
|||||
11 AGGAGAAACAG 1
RESULT 297
ABF74292/C
ID ABF74292 standard; DNA; 13 BP.
XX
AC ABF74292;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 174289 for detecting SNP TSC0043357.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PP 07-APR-2000; 2000DE-01019173.
XX
PR (EPIG-) EPIGENOMICS AG.
XX
PA Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 174289; 29pp + Sequence Listing; German.
XX PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 5 C; 0 G; 7 T; 0 U; 0 Other;
SQ

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACG 748
Db 13 RAAACACACACG 1

RESULT 293
ABC51769
ID ABC51769 standard; DNA; 13 BP.

AC ABC51769;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 51786 for detecting SNP TSC0014434.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 51786; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAC 745
Db 1 RAAACACACACG 13

RESULT 294

ID ABC83627 standard; DNA; 13 BP.

XX ABC83627;
AC 21-FEB-2002 (first entry)
DT Oligonucleotide SEQ ID NO 83644 for detecting SNP TSC0021064.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 83644; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 6 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
Db 2 AAACCGAACAC 12

RESULT 295
ABC66042
ID ABC66042 standard; DNA; 13 BP.

XX ABC66042;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 66059 for detecting SNP TSC0017378.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 223068; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 SQ This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 SQ

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 736 AAACAGAACAC 746
 DB 1 AAACAGAACAC 11
 |||||
 |||||

RESULT 291
 ABF75626/C
 ID ABF75626 standard; DNA; 13 BP.
 AC ABF75626;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 175623 for detecting SNP TSC0043631.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WC200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 175623; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 1 Other;
 SQ

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 735 GAACAGAACAC 747
 DB 13 GAACAGAACAC 1
 |||||
 |||||

RESULT 292
 ABC71282/C
 ID ABC71282 standard; DNA; 13 BP.
 AC ABC71282;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 71299 for detecting SNP TSC0018470.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 71299; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 1 Other;
 SQ

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RESULT 288
ABC10581/c
ID ABC10581 standard; DNA; 13 BP.
XX
AC ABC10581;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 10572 for detecting SNP TSC0002662.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 10572; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 4 C; 0 G; 9 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 733 GAGAAACAGAA 743
DB 11 GAGAAAAAGAA 1
XX
RESULT 289
ABF96836/c
ID ABF96836 standard; DNA; 13 BP.
XX
AC ABF96836;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 196833 for detecting SNP TSC0048453.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

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KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 196833; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 1 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 735 GAACAGACACC 747
DB 13 RAACACAAACC 1
XX
RESULT 290
ABH23091
ID ABH23091 standard; DNA; 13 BP.
XX
AC ABH23091;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 223068 for detecting SNP TSC0054311.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX

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PT methylation status.
XX Claim 1; SEQ ID NO 124392; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 733 GAGAACAGAACCA 745
XX Db 1 RAACACATAACA 13
XX
XX RESULT 286
XX ABF80900/C
XX ID ABF80900 standard; DNA; 13 BP.
XX AC ABF80900;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 180897 for detecting SNP TSC0044758.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 180897; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 733 GAGAACAGAACCA 745
XX Db 1 RAACACATAACA 13
XX
XX RESULT 287
XX ABC57783
XX ID ABC57783 standard; DNA; 13 BP.
XX AC ABC57783;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 57800 for detecting SNP TSC0015564.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 57800; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 736 AAACAGAACAC 746
XX Db 2 AAACCGAACAC 12
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DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 77843 for detecting SNP TSC0019825.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 77843; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 1 A; 1 C; 5 G; 6 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGACACCG 748
DB 12 ACAAAACACG 2
RESULT 284
ABF24376/C
ID ABF24376 standard; DNA; 13 BP.
XX AC ABF24376;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 124373 for detecting SNP TSC0031092.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.

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XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 124373; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 0 A; 1 C; 4 G; 8 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 735 GAAACAGAAC 745
DB 11 GAAACAAACA 1
RESULT 285
ABF24395
ID ABF24395 standard; DNA; 13 BP.
XX AC ABF24395;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 124392 for detecting SNP TSC0031094.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

```


CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACAC 747

Db 1 RAACCGAAACAC 13

RESULT 281

ABC67296/C
ID ABC67296 standard; DNA; 13 BP.

XX
AC ABC67296;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 67313 for detecting SNP TSC0017613.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

OS Homo sapiens.

XX WO200177384-A2.

PN 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 67313; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 1 A; 1 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 735 GAAACAGAACAC 745
Db 12 GAAACAGAACAC 2

RESULT 282

ABC50423
ID ABC50423 standard; DNA; 13 BP.

XX
AC ABC50423;

XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 50440 for detecting SNP TSC0014176.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 50440; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 9 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746.

Db 3 AAACAGAACAC 13

RESULT 283

ABC77826/C
ID ABC77826 standard; DNA; 13 BP.

XX
AC ABC77826;

XX

XX	ID	ABF56387	standard; DNA; 13 BP.	
XX	AC	ABF56387;		
XX	DT	21-FEB-2002	(first entry)	
XX	DE	OLIGONUCLEOTIDE SEQ ID NO 156384	for detecting SNP TSC0039445.	
XX	SNP;	single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;		
XX	KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;		
XX	KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.		
XX	OS	Homo sapiens.		
XX	WO	20010177384-A2.		
XX	PD	18-OCT-2001.		
XX	PP	06-APR-2001; 2001WO-IB000713.		
XX	PR	07-APR-2000; 2000DE-01019173.		
XX	PA	(EPIC-) EPIGENOMICS AG.		
XX	PI	Olek A, Piepenbrock C, Berlin K;		
XX	DR	WPI; 2001-657177/75.		
XX	PT	Set of oligonucleotides, useful for diagnosis and cell typing, is		
XX	PT	designed to detect single-nucleotide polymorphisms and cytosine		
XX	PT	methylation status.		
XX	PS	Claim 1; SEQ ID NO 156384; 29pp + Sequence Listing; German.		
XX	PP	This invention describes novel oligonucleotide primers or peptide nucleic		
XX	CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)		
XX	CC	and cytosine methylation status in chemically pretreated genomic DNA. The		
XX	CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a		
XX	CC	range of diseases including immune system, gastrointestinal, respiratory,		
XX	CC	central nervous system, cardiovascular and metabolic disorders. The		
XX	CC	oligomers are also used for detecting cell type differentiation. ABC00010		
XX	CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073		
XX	CC	represent the oligomers described in the invention. NOTE: The sequence		
XX	CC	data for this patent did not form part of the printed specification, but		
XX	CC	was obtained in electronic format from WIPO at		
XX	CC	ftp.wipo.int/pub/published_pct_sequences		
XX	SQ	Sequence 13 BP; 0 A; 3 C; 0 G; 10 T; 0 U; 0 Other;		
	Query Match	42.7%; Score 9.4; DB 1; Length 13;		
	Best Local Similarity	90.9%; Pred. No. 4.1e+02;		
	Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0		
QY	733	GAGAAACAGAA 743		
DB	12	GAGAAAAGAA 2		
RESULT 278				
ABH15112/C				
ID	ABH15112	standard; DNA; 13 BP.		
XX	AC	ABH15112;		
XX	DT	22-FEB-2002	(first entry)	
XX	DE	OLIGONUCLEOTIDE SEQ ID NO 215089	for detecting SNP TSC0052336.	
XX	SNP;	single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;		
XX	KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;		
XX	KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.		

```

PR 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 11971; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 731 AGGAGAAACAG 741
Db 3 AGGAGAAAGG 13
|||||
|

RESULT 274
ABF24377
ID ABF24377 standard; DNA; 13 BP.
XX
XX AC ABF24377;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 124374 for detecting SNP TSC0031092.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 124374; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 731 AGGAGAAACAG 741
Db 3 AGGAGAAAGG 13
|||||
|

RESULT 275
ABF74449
ID ABF74449 standard; DNA; 13 BP.
XX
XX AC ABF74449;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 174446 for detecting SNP TSC0043390.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 174446; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

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PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 130257; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746

Db 12 AAACATAACAC 2

RESULT 269

ABC72270/c
 ID ABC72270 standard; DNA; 13 BP.

XX AC ABC72270;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 72287 for detecting SNP TSC0018670.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 72287; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746

Db 11 AAACAAAACAC 1

RESULT 270

ABC51768/c
 ID ABC51768 standard; DNA; 13 BP.

XX AC ABC51768;

XX DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 51785 for detecting SNP TSC0014434.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 51785; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 0 A; 0 C; 2 G; 10 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAACAC 745

AC ABC37748;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 37765 for detecting SNP TSC0011740.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
PN
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
CC Set of oligonucleotides, useful for diagnosis and cell typing, is
CC designed to detect single-nucleotide polymorphisms and cytosine
CC methylation status.
XX
PS Claim 1; SEQ ID NO 37765; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 1 Other;
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 1 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
OY 735 GAACAGAACACC 747
Db :|||||
13 RAAACCGAACAC 1
XX
RESULT 267
ABF24394/C
ID ABF24394 standard; DNA; 13 BP.
XX
AC ABF24394;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 124391 for detecting SNP TSC0031094.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
PN

XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
PT
XX Claim 1; SEQ ID NO 124391; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 1 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
OY 733 GAGAACAGAAC 745
Db :|||||
13 RAAACACATAC 1
XX
RESULT 268
ABF30260/C
ID ABF30260 standard; DNA; 13 BP.
XX
AC ABF30260;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 130257 for detecting SNP TSC0032538.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
PN
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACAC 747
 Db 13 RAACATAAACCC 1

RESULT 264

ABC82727
 ID ABC82727 standard; DNA; 13 BP.

XX AC ABC82727;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 82744 for detecting SNP TSC0020863.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 82744; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 8 A; 5 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
 Db 2 AAACAGAACAC 12

RESULT 265

ABC58200/c
 ID ABC58200 standard; DNA; 13 BP.

XX AC ABC58200;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 58217 for detecting SNP TSC0015626.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 58217; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAACAGAACAC 745
 Db 13 RACAAACAAACA 1

RESULT 266

ABC37748/c
 ID ABC37748 standard; DNA; 13 BP.

XX

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 0 A; 1 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
||| |||||
Db 12 AAACCGAACAC 2

RESULT 259

ABF30258/c
ID ABF30258 standard; DNA; 13 BP.

XX AC ABF30258;

DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 130255 for detecting SNP TSC0032538.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

OS WO200177384-A2.

PN 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PA Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 130255; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
||| |||||
Db 12 AAACAAACAC 2

RESULT 260

ABF96837
ID ABF96837 standard; DNA; 13 BP.

XX AC ABF96837;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 196834 for detecting SNP TSC0048453.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

OS WO200177384-A2.

PN 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 196834; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACC 747
:||||| |||||
Db 1 RAAACACAAACACC 13

RESULT 261

ABC83625
ID ABC83625 standard; DNA; 13 BP.

XX AC ABC83625;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 83642 for detecting SNP TSC0021064.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

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PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 73176; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
SQ
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
DB 13 GAGAAACGAA 3
RESULT 257
ABC77827
ID ABC77827 standard; DNA; 13 BP.
XX
AC ABC77827;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 77844 for detecting SNP TSC0019825.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
```

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XX Claim 1; SEQ ID NO 77844; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
SQ
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGAACACCG 748
DB 2 ACMAAACACCG 12
RESULT 258
ABC57780/C
ID ABC57780 standard; DNA; 13 BP.
XX
AC ABC57780;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 57797 for detecting SNP TSC0015564.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 57797; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
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QY 735 GAACAGACACC 747
Db 1 RAACCGAACCC 13

RESULT 254
ABH15113
ID ABH15113 standard; DNA; 13 BP.
XX
AC ABH15113;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 215090 for detecting SNP TSC0052336.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 215090; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGACAC 746
Db 1 AAACAGACAC 11

RESULT 255
ABH48836/C
ID ABH48836 standard; DNA; 13 BP.
XX
AC ABH48836;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 73176 for detecting SNP TSC0018861.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 248813; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 1 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGACAC 746
Db 1 AAACAGACAC 11

RESULT 256
ABC73159/C
ID ABC73159 standard; DNA; 13 BP.
XX
AC ABC73159;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 73176 for detecting SNP TSC0018861.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 215090; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 174290; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACAGAACAC 746
DB 3 AACAAACAC 13
RESULT 252
ABF50800/C
ID ABF50800 standard; DNA; 13 BP.
XX AC ABF50800;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 150797 for detecting SNP TSC0038055.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 150797; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACAGAACAC 746
DB 3 AACAAACAC 13
RESULT 252
ABF50800/C
ID ABF50800 standard; DNA; 13 BP.
XX AC ABF50800;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 150797 for detecting SNP TSC0038055.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 150797; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 1 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 737 AACAGAACAC 747
DB 13 AACAAACAC 3
RESULT 253
ABF56511
ID ABF56511 standard; DNA; 13 BP.
XX AC ABF56511;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 156508 for detecting SNP TSC0039462.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 156508; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 5 A; 6 C; 1 G; 0 T; 0 U; 1 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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ID ABC83624 standard; DNA; 13 BP.
XX AC ABC83624;
XX AC
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 83641 for detecting SNP TSC0021064.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 83641; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 0 A; 1 C; 5 G; 7 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 736 AACACGACAC 746
XX Db 12 AACCGACAC 2
XX RESULT 250
XX ABC10580
XX ID ABC10580 standard; DNA; 13 BP.
XX AC ABC10580;
XX AC
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 10571 for detecting SNP TSC0002662.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.

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XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 10571; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 9 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 733 GAGAAACAGAA 743
XX Db 3 GAGAAACAGAA 13
XX RESULT 251
XX ABF74293
XX ID ABF74293 standard; DNA; 13 BP.
XX AC ABF74293;
XX AC
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 174290 for detecting SNP TSC0043357.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;

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CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 3 AGGAGAAACAG 13
|||||

RESULT 247
ABH23090/C
ID ABH23090 standard; DNA; 13 BP.
XX AC ABH23090;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 223067 for detecting SNP TSC0054311.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX Claim 1; SEQ ID NO 223067; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 3 AGGAGAAACAG 13
|||||

RESULT 248
ABH54889
ID ABH54889 standard; DNA; 13 BP.
XX AC ABH54889;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 254866 for detecting SNP TSC0062123.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX Claim 1; SEQ ID NO 254866; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 8 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACACCG 748
Db 1 ACAGAACACCG 11
|||||

RESULT 249
ABC83624/c

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 27537; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AACAGAACAC 746
 DB 11 AACATAACAC 1
 RESULT 245
 ABC82729
 ID ABC82729 standard; DNA; 13 BP.
 AC
 XX ABC82729;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 82746 for detecting SNP TSC0020863.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX

XX (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 82746; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AACAGAACAC 746
 DB 2 AACATAACAC 12
 RESULT 246
 ABP25406
 ID ABP25406 standard; DNA; 13 BP.
 XX
 AC ABP25406;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 125403 for detecting SNP TSC0031343.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 125403; 29pp + Sequence Listing; German.
 XX


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OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 5
FT /*tag= a
FT /note= "Thiol-substituted nucleoside derivative, 5-(3-
FT thiopropyn-1-yl)-2'-deoxyurine, optionally disulphide
FT bonded to the nucleoside derivative at position 5 of
FT another strand of the same sequence"
FT modified_base 6
FT /*tag= b
FT /note= "Thiol-substituted nucleoside derivative, 5-(3-
FT thiopropyn-1-yl)-2'-deoxyurine, optionally disulphide
FT bonded to the nucleoside derivative at position 6 of
FT another strand of the same sequence"
FT modified_base 7
FT /*tag= c
FT /note= "Thiol-substituted nucleoside derivative, 5-(3-
FT thiopropyn-1-yl)-2'-deoxyurine, optionally disulphide
FT bonded to the nucleoside derivative at position 7 of
FT another strand of the same sequence"
XX WO9714708-A1.
PN 24-APR-1997.
XX 29-MAR-1996; 96WO-US004525.
XX 04-OCT-1995; 95US-0004778P.
XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX Kool ET;
XX WPI; 1997-245044/22.
XX New C-5 thiol-substituted nucleoside derivatives - whose presence in
XX PT oligonucleotide(s) allows formation of covalent cross-links between non-
XX PT complementary DNA domains.
XX Example 11; Page 101; 122pp; English.
XX The present sequence represents a bridged oligonucleotide derivative. The
XX invention relates to C-5 thiol-substituted nucleoside derivatives which
XX can be incorporated into an RNA or DNA strand during synthesis of
XX oligonucleotides. These compounds can be in the form of cross-linked
XX linear, cross-linked hairpin or bridged circular oligonucleotides. The
XX oligonucleotides may be used for detection and isolation of target
XX nucleic acids, or for targeting drugs to specific cell types (e.g. for
XX treatment of Alzheimer's disease, beta-thalassemia, osteogenesis
XX imperfecta, arthritis, sickle cell anaemia or viral infections). The
XX presence of the nucleoside derivatives in a linear oligonucleotide allows
XX the formation of covalent crosslinks between non-complementary DNA
XX domains
XX SQ Sequence 13 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 1 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAA 743
DB |||||||
13 GAAGAAANAGAA 2
RESULT 243
AAF61477/C
ID AAF61477 standard; RNA; 13 BP.
XX AC AAF61477;
XX 18-JUN-2001 (first entry)
DT
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XX Wildtype influenza virus C promoter-UP variant 1104 RNA fragment 2.
XX Major histocompatibility complex restricted antigen; antitumor vaccine;
XX MHC-restricted antigen; T cell-restricted antigen;
XX antigen identification; promoter; ss.
XX Influenza virus.
XX DE19962508-A1.
XX 29-MAR-2001.
XX 23-DEC-1999; 99DE-01062508.
XX 21-SEP-1999; 99DE-01045171.
XX 26-OCT-1999; 99DE-01051543.
XX (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
XX (ARTE-) ARTEMIS PHARM GMBH.
XX Mautner J, Bornkamm GW, Nimmerjahn F, Hobom G;
XX WPI; 2001-246290/26.
XX Identifying major histocompatibility complex-restricted antigens, useful
XX potentially in antitumor vaccines, by forming DNA bank in virus and
XX testing for T cell stimulation.
XX Disclosure; Col 5; 10pp; German.
XX This invention describes a novel method for identifying major
XX histocompatibility complex (MHC)-restricted antigens. A gene or cDNA bank
XX is constructed from the cells or organism under test, then incorporated
XX into a retroviral genome or, as additional RNA, into a modified influenza
XX virus that has increased transcription, replication and/or expression
XX rate, relative to the wild type, so as to produce viral particles (VP).
XX VP are used to infect immortalized autologous cells that express MHC
XX Class I and/or II molecules on the surface, so that proteins encoded by
XX the gene bank inserts are expressed and their cleavage products exposed
XX on the cell surface. These cells are co-cultured with T cells which are
XX stimulated if the autologous cells express a T cell-restricted antigen.
XX Clones that express antigens are isolated and the antigens sequenced. The
XX products of the invention can be used for identifying antigens for
XX possible use in antitumor vaccines, but may also identify autoantigens or
XX microbial antigens. The method does not require knowledge of the
XX restricted MHC molecule, allows unlimited proliferation of target cells
XX and can identify, simultaneously, both Class I and II antigens. The
XX lymphoblastic cells lines used as target cells ensure efficient gene
XX transfer, with high level expression of the inserted gene, providing high
XX sensitivity and simple detection
XX SQ Sequence 13 BP; 1 A; 5 C; 1 G; 0 T; 6 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
DB |||||||
13 AGTAGAAACAG 3
RESULT 244
ABC27520/C
ID ABC27520 standard; DNA; 13 BP.
XX AC ABC27520;
XX DT 20-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 27537 for detecting SNP TSC0007662.
XX
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PD 22-MAY-2003.
 XX
 XX 19-MAR-2002; 2002US-00100957.
 XX
 XX 27-FEB-1997; 97US-00810983.
 PR 27-FEB-1998; 98US-00031271.
 PR 26-FEB-1999; 98US-0122152P.
 PR 08-MAR-1999; 99US-0123399P.
 PR 12-JUL-1999; 99US-00352171.
 PR 31-AUG-1999; 99US-0151797P.
 PR 17-SEP-1999; 99US-00398965.
 PR 29-OCT-1999; 99US-00430656.
 PR 01-DEC-1999; 99US-0168408P.
 PR 25-FEB-2000; 2000US-00513783.
 XX
 PA (CELL-) CELLOMICS INC.
 XX
 PI Giuliano K, Kapur R;
 XX
 XX WPI: 2003-786988/74.
 DR P-PSDB; ADC18386.
 XX
 XX Cell based toxin characterization method for e.g. in drug discovery
 PT paradigm, involves treating cells possessing luminescent reporter
 PT molecules with fluorescence based molecules reagents to detect presence
 PT of toxins.
 XX
 XX Example 10; SEQ ID NO 73; 98pp; English.
 PS
 XX The invention relates to characterising cell based toxins, where the cell
 CC possessing luminescent reporter molecules (biosensors) are provided on a
 CC microchip, and are treated with fluorescence based molecular reagents.
 CC The cells are photographed with fluorescence optics, and the optical
 CC information is converted into digital data. The presence of the toxin in
 CC a reagent, is detected using the digital data, based on changes in the
 CC localisation, distribution structure of identifier, detector and
 CC classifier in each cell. Also included are a computer readable storage
 CC medium storing a cell based toxin characterisation program, and a kit for
 CC cell based toxin detection. The method is used for characterising or
 CC detecting a biological cell based toxin that affect particular biological
 CC functions and for preparing molecular biochemical arrays for new drug
 CC discovery paradigm. It is also used in automated DNA sequencing, PCR
 CC application, positional cloning, hybridisation arrays and bioinformatics
 CC using cell based scanning and screening system. The method improves the
 CC target validation and candidate optimisation by combining many cell
 CC screening formats with fluorescence based molecular reagents, thereby
 CC resulting in increased quantity and speed of data collection, shortened
 CC cycle times and faster evaluation of promising drug candidates. The
 CC method also provides increased throughput while decreasing the volumes of
 CC reagent and test compounds required in each assay. The biosensor
 CC comprises a signal component (fluorescent protein (fused e.g. MAP4,
 CC tethering it to microtubules) or detectable signal (epitope or affinity
 CC tag), a protease recognition site (e.g. for a caspase protein) and a
 CC target domain (localising the biosensor to a particular cellular
 CC compartment). The present sequence encodes a protease recognition site
 CC for a biosensor of the invention.
 XX
 XX Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02; Mismatches 0; Gaps 0;
 Matches 10; Conservative 0; Indels 1; Indels 0; Gaps 0;
 QY 732 GGAGAAACAGCA 742
 DB 1 GTAGAAACAGCA 11
 RESULT 241
 AAV06771/c
 ID AAV06771 standard; DNA; 13 BP.
 XX
 XX AAV06771;
 AC

XX
 DT 02-JUN-1998 (first entry)
 XX
 DE Oligonucleotide containing a thiol-substituted nucleoside derivative.
 XX
 KW Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
 KW circular; bridged; hairpin; detection; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_difference 6 /tag= a
 FT /note= "thiopropynyldeoxyuridine or unmodified thymidine"
 XX
 FN WO9714708-A1.
 XX
 XX 24-APR-1997.
 XX
 XX 29-MAR-1996; 96WO-US004525.
 XX
 XX 04-OCT-1995; 95US-0004778P.
 XX
 PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
 XX
 XX Kool ET;
 XX
 XX WPI: 1997-245044/22.
 DR
 XX New C-5 thiol-substituted nucleoside derivatives - whose presence in
 PT oligo:nucleotide(s) allows formation of covalent cross-links between non-
 PT complementary DNA domains.
 XX
 XX Example 5; Page 82; 122pp; English.
 PS
 XX This sequence represents an oligonucleotide containing a thiol-
 CC substituted nucleoside derivative or an unmodified oligonucleotide. The
 CC invention relates to a C-5 thiol-substituted nucleoside derivatives which
 CC can be incorporated into an RNA or DNA strand during synthesis of
 CC oligonucleotides. These compounds can be in the form of cross-linked
 CC linear, cross-linked hairpin or bridged circular oligonucleotides. The
 CC oligonucleotides may be used for detection and isolation of target
 CC nucleic acids, or for targeting drugs to specific cell types (e.g. for
 CC treatment of Alzheimer's disease, beta-thalassemia, osteogenesis
 CC imperfecta, arthritis, sickle cell anaemia or viral infections). The
 CC presence of the nucleoside derivatives in a linear oligonucleotide allows
 CC the formation of covalent crosslinks between non-complementary DNA
 CC domains
 XX
 XX Sequence 13 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 1 Other;
 SQ
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 4.1e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 732 GGAGAAACAGCA 743
 DB 13 GAAGAAANAGAA 2
 RESULT 242
 AAV06762/c
 ID AAV06762 standard; DNA; 13 BP.
 XX
 XX AAV06762;
 XX
 XX 02-JUN-1998 (first entry)
 DT
 XX Bridged oligonucleotide derivative.
 DE
 XX Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
 KW circular; bridged; hairpin; detection; ss.
 XX
 XX

XX WPI; 2002-657594/70.
XX
XX
XX New human influenza virus comprising an RNA-sequence encoding a modified
PT RNA-polymerase, useful for preparing agents for therapeutic and
PT prophylactic vaccination, or treating a growing tumor or a chronic
PT infectious disease.
XX
XX Claim 10; Page 50; 172pp; English.
XX
XX The present invention describes a human influenza virus (I) comprising an
CC RNA-sequence encoding a modified RNA-polymerase that differs from the
CC wild-type RNA-polymerase of the human influenza virus in that at least 1
CC of the amino acid residues distinguishing the wild-type RNA-polymerase of
CC the human influenza virus from FV Bratistava RNA-polymerase has been
CC replaced with the corresponding amino acid residue(s) as present in FV
CC Bratislava RNA-polymerase. (I) has virucide, cytostatic, anti-HIV,
CC hepatotropic, antiinflammatory and immunomodulator activities and can be
CC used in gene therapy and vaccines. The influenza virus is useful for
CC preparing agents for: (a) gene transfer into cells, preferably into
CC mammalian cells, particularly into human cells, by viral infection; (b)
CC gene transfer into antigen-presenting cells, and the use of the obtained
CC product for ex vivo immunotherapy; in vivo somatic gene therapy; in vivo
CC vaccination, including therapeutic and prophylactic vaccination; (c)
CC eliciting an immune response, including the induction of a T-cell
CC response; (d) treating a growing tumor or a chronic infectious disease;
CC (e) immunotherapy, preferably for autologous immunotherapy; (f) transfer
CC and expression of foreign genes into cells infected by such viruses; or
CC (g) transfer and expression of RNA molecules into cells infected by such
CC viruses, preferably the RNA molecules to be expressed are antisense
CC sequences or double-strand sequences relative to the target cellular
CC molecules, and/or the agent is suitable for sequence-specific gene
CC silencing, preferably by antisense RNA or RNA interference mechanisms
CC such as ribozyme cleavages of target RNAs. The recombinant viruses can be
CC made for use in vaccines against HIV, hepatitis B or C virus, herpes
CC viruses or papilloma viruses. The present sequence represents a modified
CC 3' conserved region of an influenza virus, given in the exemplification
XX of the present invention
SQ Sequence 12 BP; 1 A; 4 C; 1 G; 0 T; 6 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAACAG 741
Db 12 AGTAAACAG 2
RESULT 239
ABQ75464/C
ID ABQ75464 standard; RNA; 12 BP.
XX AC ABQ75464;
XX
XX 07-NOV-2002 (first entry)
XX
XX Modified influenza virus A 3' conserved region SEQ ID NO:6.
DE
XX Influenza virus; transcription; replication; RNA polymerase; vaccine;
KW gene therapy; cytostatic; anti-HIV; hepatotropic; antiinflammatory;
KW immunomodulator; virucide; infectious disease; ss.
XX
XX Influenza virus.
OS Synthetic.
XX
XX WO200264757-A2.
FN
XX 22-AUG-2002.
PD
XX 07-FEB-2002; 2002WO-EP001257.
PP
XX

PR 09-FEB-2001; 2001EP-00103060.
XX
XX (ARTE-) ARTEMIS PHARM GMBH.
XX
XX Hobom G, Menke A;
XX
XX WPI; 2002-657594/70.
DR
XX
XX New human influenza virus comprising an RNA-sequence encoding a modified
PT RNA-polymerase, useful for preparing agents for therapeutic and
PT prophylactic vaccination, or treating a growing tumor or a chronic
PT infectious disease.
XX
XX Disclosure; Page 16; 172pp; English.
PS
XX The present invention describes a human influenza virus (I) comprising an
CC RNA-sequence encoding a modified RNA-polymerase that differs from the
CC wild-type RNA-polymerase of the human influenza virus in that at least 1
CC of the amino acid residues distinguishing the wild-type RNA-polymerase of
CC the human influenza virus from FV Bratislava RNA-polymerase has been
CC replaced with the corresponding amino acid residue(s) as present in FV
CC Bratislava RNA-polymerase. (I) has virucide, cytostatic, anti-HIV,
CC hepatotropic, antiinflammatory and immunomodulator activities and can be
CC used in gene therapy and vaccines. The influenza virus is useful for
CC preparing agents for: (a) gene transfer into cells, preferably into
CC mammalian cells, particularly into human cells, by viral infection; (b)
CC gene transfer into antigen-presenting cells, and the use of the obtained
CC product for ex vivo immunotherapy; in vivo somatic gene therapy; in vivo
CC vaccination, including therapeutic and prophylactic vaccination; (c)
CC eliciting an immune response, including the induction of a T-cell
CC response; (d) treating a growing tumor or a chronic infectious disease;
CC (e) immunotherapy, preferably for autologous immunotherapy; (f) transfer
CC and expression of foreign genes into cells infected by such viruses; or
CC (g) transfer and expression of RNA molecules into cells infected by such
CC viruses, preferably the RNA molecules to be expressed are antisense
CC sequences or double-strand sequences relative to the target cellular
CC molecules, and/or the agent is suitable for sequence-specific gene
CC silencing, preferably by antisense RNA or RNA interference mechanisms
CC such as ribozyme cleavages of target RNAs. The recombinant viruses can be
CC made for use in vaccines against HIV, hepatitis B or C virus, herpes
CC viruses or papilloma viruses. The present sequence represents a modified
CC 3' conserved region of an influenza virus, given in the exemplification
XX of the present invention
SQ Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAACAG 741
Db 12 AGGAGAACAG 2
RESULT 240
ADC18385
ID ADC18385 standard; DNA; 12 BP.
XX AC ADC18385;
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Protease recognition site for caspase-8 DNA.
DE
XX ds; cell based toxin; luminescent reporter molecule; biosensor;
KW microchip; drug discovery; MAP4; epitope; affinity tag;
KW protease recognition site; caspase; target domain.
XX
XX Unidentified.
OS
XX US2003096322-A1.
PP
XX

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XX PN EP1201760-A1.
XX XX
XX PD 02-MAY-2002.
XX XX
XX PF 30-OCT-2000; 2000EP-00123687.
XX XX
XX PR 30-OCT-2000; 2000EP-00123687.
XX XX
XX PA (ARTE-) ARTEMIS PHARM GMBH.
XX XX
XX PI Schuler G, Hobom G, Steinkasserer A, Strobel I, Grassmann R;
XX XX
XX DR WPI; 2002-418777/45.
XX XX
XX PT Expressing tumor or viral associated antigens by dendritic cells, used
XX PT for treating tumors or viral infections, comprises using recombinant
XX PT influenza virus containing nucleic acid encoding the antigens.
XX XX
XX PS Claim 7; Page 19; 33pp; English.
XX XX
XX CC The invention relates to a method for the expression of tumour associated
XX CC antigens (TAA) or virus-associated antigens (VAA) by dendritic cells
XX CC comprising: preparing a recombinant influenza virus containing a
XX CC nucleotide sequence coding for the TAA or VAA; and infecting dendritic
XX CC cells with the recombinant virus. The method is used for expressing TAA
XX CC or VAA in dendritic cells. The cells are used for preparing a medicament
XX CC for treating tumours or viral infections. A vaccine can be created by
XX CC using dendritic cells presenting tumour antigens to induce an immune
XX CC response. This polynucleotide sequence represents a preferred 3'
XX CC conserved RNA influenza virus region of the invention
XX XX
XX SQ Sequence 12 BP; 1 A; 4 C; 1 G; 0 T; 6 U; 0 Other;
XX XX
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 12 AGTAGAACAG 2

RESULT 237
ABS71505
ID ABS71505 standard; DNA; 12 BP.
XX XX
XX AC ABS71505;
XX XX
XX DT 27-NOV-2002 (first entry)
XX XX
XX DE DNA encoding protease biosensor recognition site #11.
XX XX
XX KW Detection; classification; identification; toxin detection; protease;
XX KW ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
XX KW toxic threat agent; ds.
XX XX
XX OS Synthetic.
XX XX
XX PN US6416959-B1.
XX XX
XX PD 09-JUL-2002.
XX XX
XX PF 25-FEB-2000; 2000US-00513783.
XX XX
XX PR 27-FEB-1997; 97US-00810983.
XX PR 27-FEB-1998; 98US-00031271.
XX PR 26-FEB-1999; 99US-0122152P.
XX PR 08-MAR-1999; 99US-0123395P.
XX PR 12-JUL-1999; 99US-0035217P.
XX PR 31-AUG-1999; 99US-0151757P.
XX PR 17-SEP-1999; 99US-00398965.
XX PR 29-OCT-1999; 99US-00430656.
XX PR
XX PI Hobom G, Menke A;

PR 01-DEC-1999; 99US-0168408P.
XX XX
XX PA (GIUL/) GIULIANO K.
XX PA (KAPU/) KAPUR R.
XX XX
XX PI Giuliano K, Kapur R;
XX XX
XX DR WPI; 2002-634730/68.
XX DR P-PSDB; ABG94458.
XX XX
XX PT Automated cell-based toxin detection, classification, and/or
XX PT identification by treating cells involves use of three classes of
XX PT luminescent reporter molecules such as detectors, classifiers or
XX PT identifiers.
XX XX
XX PS Example 10; Fig 29B; 214pp; English.
XX XX
XX CC The invention describes methods of automated detection, classification
XX CC and identification comprising treating cells containing luminescent
XX CC reporter molecules (I) in array of locations with a test substance, where
XX CC (I) are detectors, classifiers or identifiers, imaging cells in each
XX CC location to obtain luminescent signals and converting optical information
XX CC into digital data to interpret presence of toxins in the test substance.
XX CC The method are useful for detection of toxins chosen from proteases, ADP-
XX CC ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
XX CC Three classes of cell-based luminescent reporter molecules such as
XX CC detectors, classifiers and identifiers are described and serve as
XX CC reporters of toxic threat agents. The first two levels of
XX CC characterization ensure a rapid readout of toxin class without
XX CC sacrificing the ability to detect many new mutant toxins or dissect
XX CC several complex mixtures of known toxins. This sequence encodes a
XX CC protease biosensor recognition site used in the cell-based screening
XX CC system
XX XX
XX SQ Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
XX XX
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 742
DB 1 GTAGAACAG 11

RESULT 238
ABQ75463/C
ID ABQ75463 standard; RNA; 12 BP.
XX XX
XX AC ABQ75463;
XX XX
XX DT 07-NOV-2002 (first entry)
XX XX
XX DE Modified influenza virus A 3' conserved region SEQ ID NO:5.
XX XX
XX KW Influenza virus; transcription; replication; RNA polymerase; vaccine;
XX KW gene therapy; cytostatic; anti-HIV; hepatotropic; antiinflammatory;
XX KW immunomodulator; virucide; infectious disease; ss.
XX XX
XX OS Influenza virus.
XX OS Synthetic.
XX XX
XX PN WO200264757-A2.
XX XX
XX PD 22-AUG-2002.
XX XX
XX PF 07-FEB-2002; 2002WO-EP001257.
XX XX
XX PR 09-FEB-2001; 2001EP-00103060.
XX XX
XX PA (ARTE-) ARTEMIS PHARM GMBH.
XX XX
XX PI Hobom G, Menke A;

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ABIS1887
XX ID ABIS1887 standard; DNA; 12 BP.
XX AC ABIS1887;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 351860 for detecting SNP TSC0047526.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN W0200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 351860; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI92073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
SQ Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACAGACAC 746
Db ||||| |||||
2 AACACACAC 12
RESULT 235
AAL37781/C
XX ID AAL37781 standard; RNA; 12 BP.
XX AC AAL37781;
XX DT 05-AUG-2002 (first entry)
XX DE 3'-terminal RNA influenza virus mutant G3C, USC, C8G.
XX KW Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell;
XX virus-associated antigen; VAA; recombinant influenza virus; vaccine;
XX viral infection; immune; mutant; ss.
XX OS Influenza virus.
OS Influenza virus.
XX Key Location/Qualifiers
FT mutation 3
FT /*tag= a
FT /*note= "The wild-type nucleotide G has been replaced with
C"
FT mutation 5
FT /*tag= b
FT /*note= "The wild-type nucleotide U has been replaced with
C"
FT mutation 8
FT /*tag= c
FT /*note= "The wild-type nucleotide C has been replaced with
G"
XX EP1201760-A1.
XX 02-MAY-2002.
XX 30-OCT-2000; 2000EP-00123687.
XX 30-OCT-2000; 2000EP-00123687.
XX (ARTE-) ARTEMIS PHARM GMBH.
XX Schuler G, Hobom G, Steinkasserer A, Strobel I, Grassmann R;
XX WPI; 2002-418777/45.
XX Expressing tumor or viral associated antigens by dendritic cells, used
XX for treating tumors or viral infections, comprises using recombinant
XX influenza virus containing nucleic acid encoding the antigens.
XX Disclosure; Page 6; 33pp; English.
XX The invention relates to a method for the expression of tumour associated
XX antigens (TAA) or virus-associated antigens (VAA) by dendritic cells
XX comprising: preparing a recombinant influenza virus containing a
XX nucleotide sequence coding for the TAA or VAA; and infecting dendritic
XX cells with the recombinant virus. The method is used for preparing TAA
XX or VAA in dendritic cells. The cells are used for preparing a medicament
XX for treating tumours or viral infections. A vaccine can be created by
XX using dendritic cells presenting tumour antigens to induce an immune
XX response. This polynucleotide sequence represents a preferred 3'-terminal
XX RNA region of an influenza virus mutant G3C, USC, C8G of the invention
XX Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
SQ Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
Db ||||| |||||
12 AGGAGAACCCAG 2
RESULT 236
AAL37780/C
XX ID AAL37780 standard; RNA; 12 BP.
XX AC AAL37780;
XX DT 05-AUG-2002 (first entry)
XX DE Preferred 3' conserved RNA influenza virus region.
XX KW Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell;
XX virus-associated antigen; VAA; recombinant influenza virus; vaccine;
XX viral infection; immune; ss.
XX OS Influenza virus.
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XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
      Query Match      42.7%; Score 9.4; DB 1; Length 12;
      Best Local Similarity 90.9%; Pred No. 4e+02;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
Db 1 AACATAACACC 11

RESULT 232
ABI23313/C
ID ABI23313 standard; DNA; 12 BP.
XX AC ABI23313;
XX AC ABI23313;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 323286 for detecting SNP TSC0031304.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 323286; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
      Query Match      42.7%; Score 9.4; DB 1; Length 12;
      Best Local Similarity 90.9%; Pred No. 4e+02;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
Db 1 AACATAACACC 11

RESULT 232
ABI23313/C
ID ABI23313 standard; DNA; 12 BP.
XX AC ABI23313;
XX AC ABI23313;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 323286 for detecting SNP TSC0031304.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 323286; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

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XX SQ Sequence 12 BP; 0 A; 6 C; 0 G; 6 T; 0 U; 0 Other;
      Query Match      42.7%; Score 9.4; DB 1; Length 12;
      Best Local Similarity 90.9%; Pred No. 4e+02;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
Db 12 GGAGAAACAGA 2

RESULT 233
ABI48554/C
ID ABI48554 standard; DNA; 12 BP.
XX AC ABI48554;
XX AC ABI48554;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 348527 for detecting SNP TSC0045634.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 348527; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
      Query Match      42.7%; Score 9.4; DB 1; Length 12;
      Best Local Similarity 90.9%; Pred No. 4e+02;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGGAGAAACAG 2

RESULT 234

```

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 275098; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACGACAC 746
Db ||||| |||||
11 AACCCGACAC 1
RESULT 230
AB113566/C
ID AB113566 standard; DNA; 12 BP.
XX
XX AB113566;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 313539 for detecting SNP TSC0025831.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
FN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX

PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 313539; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACGACAC 746
Db ||||| |||||
12 AACCAACAC 2
RESULT 231
ABH96894
ID ABH96894 standard; DNA; 12 BP.
XX
XX ABH96894;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 296887 for detecting SNP TSC0017334.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
FN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIC-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 296887; 29pp + Sequence Listing; German.
PS

```

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
Db 1 AACAAACAC 11

RESULT 227
ABH69260/C
ID ABH69260 standard; DNA; 12 BP.
XX
AC ABH69260;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 269237 for detecting SNP TSC0001673.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 269237; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAACACC 746
Db 1 AACAAACAC 11

RESULT 229
ABH75111/C
ID ABH75111 standard; DNA; 12 BP.
XX
AC ABH75111;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 275098 for detecting SNP TSC0003783.

```

```

Db 11 AACAAACAC 1
RESULT 228
ABH99600
ID ABH99600 standard; DNA; 12 BP.
XX
AC ABH99600;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 299593 for detecting SNP TSC0018645.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 299593; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 0 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACG 741
Db 1 AGGAGAACACG 11

RESULT 229
ABH75111/C
ID ABH75111 standard; DNA; 12 BP.
XX
AC ABH75111;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 275098 for detecting SNP TSC0003783.

```


XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 277756; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
Db 1 GAGAAACAGAA 11
|||||
RESULT 225
ABI28538
ID ABI28538 standard; DNA; 12 BP.
XX
AC ABI28538;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 328511 for detecting SNP TSC0034363.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 368871; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAA 742
Db 1 GGAGAAACAGAA 11
|||||
RESULT 226
ABI68898
ID ABI68898 standard; DNA; 12 BP.
XX
AC ABI68898;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 368871 for detecting SNP TSC0057287.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 368871; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAA 742
Db 1 GGAGAAACAGAA 11
|||||
RESULT 226
ABI68898
ID ABI68898 standard; DNA; 12 BP.
XX
AC ABI68898;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 368871 for detecting SNP TSC0057287.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 368871; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
Db 1 GAGAAACAGAA 11
|||||
RESULT 225
ABI28538
ID ABI28538 standard; DNA; 12 BP.
XX
AC ABI28538;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 328511 for detecting SNP TSC0034363.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX

```

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
Db 2 AAACAAACAC 12

RESULT 222
ABI24222
ID ABI24222 standard; DNA; 12 BP.
XX
AC ABI24222;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 324195 for detecting SNP TSC0031857.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 324195; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
Db 2 GAGAAACAGAA 12

RESULT 223
ABI03119
ID ABI03119 standard; DNA; 12 BP.
XX

```

```

AC ABI03119;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 303092 for detecting SNP TSC0020318.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 303092; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
Db 1 AAACATACAC 11

RESULT 224
ABH77763
ID ABH77763 standard; DNA; 12 BP.
XX
AC ABH77763;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 277756 for detecting SNP TSC0004835.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
WO200177384-A2.

```

XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 309289; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligonucleotides are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 0 A; 1 C; 5 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AACACGAGAACAC 746
 DB 11 AACACGAGAACAC 1
 |||||
 |||||
 RESULT 220
 AB166282
 ID AB166282 standard; DNA; 12 BP.
 XX AC AB166282;
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 366255 for detecting SNP TSC0055626.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 366255; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AACACGAGAACAC 746
 DB 2 AACACGAGAACAC 12
 |||||
 |||||
 RESULT 221
 ABH95965
 ID ABH95965 standard; DNA; 12 BP.
 XX AC ABH95965;
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 295958 for detecting SNP TSC0016826.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 295958; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 SQ

RESULT 217
 ABI59474
 ID ABI59474 standard; DNA; 12 BP.
 XX
 AC ABI59474;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 359447 for detecting SNP TSC0051611.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS
 XX Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 359447; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0;
 QY 736 AACACAGACAC 746
 DB 1 AACACAAACAC 11
 RESULT 218
 ABH71042/c
 ID ABH71042 standard; DNA; 12 BP.
 XX
 AC ABH71042;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 271019 for detecting SNP TSC0002368.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 271019; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0;
 QY 736 AACACAGACAC 746
 DB 1 AACACAAACAC 1
 RESULT 219
 ABI09316/c
 ID ABI09316 standard; DNA; 12 BP.
 XX
 AC ABI09316;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 309289 for detecting SNP TSC0023461.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS
 XX Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.

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XX Claim 1; SEQ ID NO 36398; 29pp + Sequence Listing; German.
PS
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
Db 12 GAGAAAAGAA 2
|||||
RESULT 215
ABI22641
ID ABI22641 standard; DNA; 12 BP.
XX
AC ABI22641;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 322614 for detecting SNP TSC0030968.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
Claim 1; SEQ ID NO 322614; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
Db 12 GAGAAAAGAA 2
|||||
RESULT 215
ABI22641
ID ABI22641 standard; DNA; 12 BP.
XX
AC ABI22641;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 322614 for detecting SNP TSC0030968.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
Claim 1; SEQ ID NO 322614; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACAAACAC 746
Db 12 AACAAAAACAC 2
|||||
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CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
Db 2 GAGAAAAGAA 12
|||||
RESULT 216
ABI03293/C
ID ABI03293 standard; DNA; 12 BP.
XX
AC ABI03293;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 303266 for detecting SNP TSC0020413.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
Claim 1; SEQ ID NO 303266; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACAAACAC 746
Db 12 AACAAAAACAC 2
|||||
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XX DE Oligonucleotide primer SEQ ID NO 309520 for detecting SNP TSC0023558.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 309520; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02; Mismatches 0; Gaps 0;
XX Matches 10; Conservative 0; Indels 1; Indels 0; Gaps 0;

Oy 736 AAACAGAACAC 746
Db 1 AAACATACAC 11
|||||
|||||

RESULT 213
ABI45019
ID ABI45019 standard; DNA; 12 BP.
XX AC ABI45019;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 344992 for detecting SNP TSC0010376.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 344992; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02; Mismatches 0; Gaps 0;
XX Matches 10; Conservative 0; Indels 1; Indels 0; Gaps 0;

Oy 736 AAACAGAACAC 746
Db 1 AAACATACAC 11
|||||
|||||

RESULT 213
ABI45019
ID ABI45019 standard; DNA; 12 BP.
XX AC ABI45019;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 344992 for detecting SNP TSC0053822.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

```


SQ Sequence 12 BP; 5 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 731 AGGAGAAACAG 741
Db 2 AGGAGAAACGG 12
RESULT 205
AAH21574
ID AAH21574 standard; DNA; 12 BP.
XX AC AAH21574;
XX XX
XX 10-AUG-2001 (first entry)
XX DE Human hypocretin receptor 2 (HCRTR2) splice acceptor site SEQ ID NO:36.
XX KW Human; narcolepsy; hypocretin receptor 2; orexin receptor 2; HCRTR2;
XX KW diagnosis; PCR primer; ss.
XX OS Homo sapiens.
XX XX
XX WO200130991-A2.
XX PD
XX 03-MAY-2001.
XX PF
XX 22-AUG-2000; 2000WO-US023021.
XX XX
XX 25-OCT-1999; 99US-00426290.
XX PA (DECO-) DECODE GENETICS EHF.
XX XX
XX Olafsdottir BR, Gulcher J;
XX XX
XX WPI; 2001-300504/31.
XX XX
XX Gene for hypocretin (orexin) receptor 2 (HCRTR2) which is associated with
XX PT narcolepsy, useful in methods of diagnosis of narcolepsy and
XX PT pharmaceutical compositions for therapy.
XX XX
XX Example 1; Page 26; 85pp; English.
XX XX
XX The present invention describes the human hypocretin (orexin) receptor 2
XX CC (HCRTR2) gene (given in AAH21613), which is associated with narcolepsy.
XX CC Identification of the HCRTR2 nucleic acid molecule permits the diagnosis
XX CC of narcolepsy. A method from the present invention is provided for
XX CC treating narcolepsy by administering to the individual an isolated HCRTR2
XX CC nucleic acid in a therapeutically effective amount so that the cells
XX CC produce native HCRTR2 receptor. The diagnosis of narcolepsy has been
XX CC difficult to differentiate from other conditions such as chronic fatigue
XX CC syndrome or other sleep disorders but detection of HCRTR2 nucleic acid
XX CC makes it possible to accurately diagnose narcolepsy. AAH21541 to AAH21612
XX CC represent primers used in the identification of the narcolepsy gene in an
XX CC example from the present invention. AAH21613 represents the HCRTR2 gene
XX CC which encodes the HCRTR2 protein given in AAH98007
XX XX
XX SQ Sequence 12 BP; 5 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 727 TGCACGAGAA 737
Db 1 TGCACGAGAAA 11
RESULT 206
ABH75383
SQ Sequence 12 BP; 8 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 733 GAGAAACAGAA 743
Db 1 GAGAAACAGAA 11
RESULT 207
ABH8475
ID ABH8475 standard; DNA; 12 BP.
XX AC ABH8475;
XX XX
XX 22-FEB-2002 (first entry)
XX XX
XX Oligonucleotide primer SEQ ID NO 288468 for detecting SNP TSC0013526.
XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.

CC second localisation signal attached to the fluorescent protein enables
 CC the fluorescent protein to be directed to a different cellular
 CC compartment after cleavage of the protease recognition sequence. The
 CC change in distribution of the fluorescent protein can be detected using
 CC imaging methods with a high degree of spatial resolution. The methods and
 CC biosensors of the invention can be used to investigate a wide range of
 CC cellular activities and to screen compounds which modulate these
 CC activities. Biosensors containing a recognition site for caspase, for
 CC example, may be used for the screening of compounds which modulate
 CC apoptosis, while biosensors containing other protease recognition sites
 CC may be used for the detection of proteolytic toxins (such as anthrax
 CC lethal factor). The method provides improved target validation and
 CC candidate compound optimisation by combining many cell screening formats
 CC with fluorescence-based molecular reagents and computer-based feature
 CC extraction, data analysis and automation, resulting in increased quantity
 CC and speed of data collection and faster evaluation of drug candidates.
 CC Sequences AAA93377-A93411 and AAA93440 represent protease recognition
 CC sites (AAB22886-B22920, AAB22935) which may be used as components of
 CC biosensor fusion proteins of the invention
 CC
 XX Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
 SQ

Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
 Db 1 GTAGAAACAGA 11

RESULT 203
 AAA27587
 ID AAA27587 standard; DNA; 12 BP.

AC AAA27587;
 XX 29-AUG-2000 (first entry)
 DT
 DE DNA encoding caspase-8 substrate recognition sequence.
 XX
 XX Protease; biosensor; caspase-8; substrate recognition sequence;
 XX cell screening; assay; analysis; drug discovery; ss.

Unidentified.

WO200026408-A2.

11-MAY-2000.

XX 29-OCT-1999; 99WO-US025431.

XX 30-OCT-1998; 98US-0106308P.

PR 26-MAY-1999; 99US-0136078P.

XX (CELL-) CELLOMICS INC.

XX Guiliano KA, Bright G, Olson K, Burroughs-Tencza S;

XX WPI; 2000-365644/31.

DR P-PSDB; AAY79598.

XX Recombinant nucleic acid encoding a protease biosensor useful for
 PT fluorescence based cell and molecular biochemical assays for drug
 PT discovery comprising three operably linked nucleic acid sequences.

XX Claim 6; Fig 29B; 218pp; English.

XX The present sequence is that of DNA encoding the substrate recognition
 CC sequence (see AAY79598) of caspase-8. The DNA is used in a claimed
 CC recombinant nucleic acid encoding a protease biosensor. The nucleic acid
 CC (see AAZ27627-43) comprises: (1) a sequence (see AAA27568-76) encoding at
 CC least 1 detectable signal polypeptide; (2) a sequence (see AAA27577-611)

CC that encodes at least 1 protease recognition site, such as the present
 CC sequence; and (3) a sequence (see AAA27611-26) that encodes at least 1
 CC reactant target sequence. An expression vector, a genetically engineered
 CC host cell and a recombinant protease biosensor are also claimed. A
 CC claimed method for identifying compounds that modify protease activity in
 CC a cell involves contacting a host cell that possesses the recombinant
 CC protease biosensor with a test compound, and determining the recombinant
 CC biosensor distribution in the host cell, where changes in the
 CC distribution of the protease biosensor are correlated with modification
 CC of protease activity by the test compound. Claimed kits for identifying
 CC compounds that modify protease activity in a host cell include the
 CC recombinant nucleic acid, or the recombinant protease biosensor, or the
 CC vector, or the host cell. The protease biosensor is useful in high
 CC content screens to detect in vivo activation of enzymatic activity, and
 CC to identify specific activity based on cleavage of a known recognition
 CC motif

XX Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
 Db 1 GTAGAAACAGA 11

RESULT 204
 AAC97936

ID AAC97936 standard; DNA; 12 BP.

XX AAC97936;

XX 28-FEB-2001 (first entry)

DE Primer used to illustrate DNA amplification method SEQ ID 162.

XX Primer; amplification; selective; ss.

XX Synthetic.

PN JP2000270867-A.

PD 03-OCT-2000.

PF 19-MAR-1999; 99JP-00076844.

PR 19-MAR-1999; 99JP-00076844.

XX (SAOL) SANYO ELECTRIC CO LTD.

PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.

XX WPI; 2001-011047/02.

PT Amplification of a DNA fragment and its apparatus.

XX Example 1; Page 11; 32pp; Japanese.

XX This invention relates to a method for amplifying a DNA fragment. The
 CC method comprises successive repetitions of heat-denaturing, annealing of
 CC a primer and an extending step using a DNA polymerase. The method makes
 CC use of a cDNA pool in which the primer is one primer or a pair of primer
 CC sets and has an amplification probability which allows it to amplify a
 CC DNA fragment from a limited number of the cDNAs among the DNA pool (where
 CC the limited number is in the range of 1 to 25). Also included in the
 CC invention are apparatus used for carrying out the method, a primer and a
 CC DNA polymerase and a kit used for amplifying a DNA fragment. The method
 CC can be used to amplify a limited number of cDNAs from a pool in which a
 CC wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
 CC represent primers used in an example illustrating the method of the
 CC invention

XX PS Disclosure; Page 26; 32pp; Japanese.

XX CC The specification describes a method for the determination of the

CC CC nucleotide sequence of a polynucleotide. The method comprises providing a

CC CC set of primers in which each primer has an extension region containing a

CC CC terminal nucleotide, a template arranging segment and at least one

CC CC complexity-decreasing nucleotide, forming a template containing primer-

CC CC combining sites and the polynucleotide in which the primer-combining

CC CC sites are complementary to at least one primer of the set, forming an

CC CC amplicon from the template by amplifying a double-stranded DNA formed

CC CC selectively by extending the primer from the set in which the extending

CC CC region forms a double-strand completely matched to primer-combining sites

CC CC of the template, identifying the terminal nucleotide of the extending

CC CC region of the primer by an identification of the amplicon, shifting the

CC CC primer-combining sites by one nucleotide to the direction of extension by

CC CC varying the primer-combining sites of the template, and repeating this

CC CC until the nucleotide sequence of the polynucleotide is determined. The

CC CC method can be used for DNA sequencing. The present sequence represents a

CC CC primer used to demonstrate the invention

XX SQ Sequence 12 BP; 1 A; 5 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;

Best Local Similarity 90.9%; Pred. NO. 4e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738

DB 12 GCCAGGAGAGA 2

RESULT 201

AAZ41585

ID AAZ41585 standard; DNA; 12 BP.

AC AAZ41585;

XX 19-JAN-2000 (first entry)

DE Microbe detection in organic waste arbitrarily primed PCR primer #162.

XX Microbe; detection; organic waste; arbitrarily primer PCR;

KW random amplified polymorphic DNA; amplification; PCR primer; ss.

OS Synthetic.

XX JP11276176-A.

XX 12-OCT-1999.

XX 31-MAR-1998; 98JP-00087652.

XX 31-MAR-1998; 98JP-00087652.

XX (SAOL) SANYO ELECTRIC CO LTD.

PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.

XX WPI; 1999-626940/54.

XX Amplification of a DNA fragment - in order to establish the state of

PT existence of a microbe.

XX Example; Page 9; 40pp; Japanese.

XX A method has been developed for the amplification of a DNA fragment in

CC which amplification is carried out on the DNA fragments of a number of

CC different DNAs. The method comprises a PCR reaction repeatedly carrying

CC out a heat-denaturing step, a primer annealing step and a polymerase

CC extending step, to amplify the DNA fragments of a plural of different

CC DNAs. The method can detect the existence of a microbe in organic waste.

CC AAZ41424 to AAZ41639 represent PCR primers used in random amplified

CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in

CC organic waste

XX Sequence 12 BP; 5 A; 1 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;

Best Local Similarity 90.9%; Pred. NO. 4e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741

DB 2 AGGAGAAACGG 12

RESULT 202

AAA93387

ID AAA93387 standard; DNA; 12 BP.

XX AAA93387;

AC AAA93387;

XX 10-JAN-2001 (first entry)

DE DNA encoding caspase-8 substrate recognition sequence, SEQ ID NO:73.

XX Bioreactor protein; fusion protein; recognition site;

KW cellular targeting sequence; cellular localisation; fluorescent protein;

KW protease activity detection; toxin detection; cellular stress detection;

KW drug discovery; cell based screening; protease recognition site;

XX cleavage site; ds.

OS Synthetic.

XX WO2000050872-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US004794.

XX 26-FEB-1999; 99US-0122152P.

PR 08-MAR-1999; 99US-0123399P.

PR 12-JUL-1999; 99US-00352171.

XX (CELL-) CELLOMICS INC.

PA Giuliano KA, Kapur R;

XX WPI; 2000-594086/56.

DR P-PSDE; AAB22896.

XX Automated cell-based characterization of toxin by contacting cells

PT containing luminescent reporter molecules with test substance and

PT analyzing optically.

XX Example 11; Fig 29B; 336pp; English.

XX The invention relates to systems, methods and reagents for cell-based

CC screening or detection of compounds which affect particular biological

CC functions. The methods of the invention utilise fluorescent bioreactor

CC molecules which, when acted on by a compound of interest, cause an

CC alteration in the cellular distribution of at least the fluorescent

CC moiety. In one embodiment, the biosensors comprise heat shock proteins

CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent

CC protein (GFP), or derivatives thereof). Such biosensors are located in

CC the cytoplasm, but on stress activation translocate to the nucleus. In

CC another embodiment bioreactor proteins can be used to detect protease

CC activity. Such protease bioreactor fusion proteins comprise one or more

CC fluorescent proteins; a recognition signal which is cleaved by the

CC protease; and at least one cellular localisation signal. The latter two

CC components may be components of a single protein which is acted upon by

CC the protease, or may be from heterologous sources. Due to the

CC localisation signal, the bioreactor protein is localised to a particular

CC region of the cell. Once acted on by the protease of interest, the

CC fluorescent protein is cleaved from the localisation sequence, and is

CC free to migrate to other locations within the cell. The presence of a

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RESULT 198
AAQ37032
ID AAQ37032 standard; DNA; 12 BP.
XX
AC AAQ37032;
XX
DT 25-MAR-2003 (revised)
DT 01-JUL-1993 (first entry)
XX
DE NF-AT complex binding oligonucleotide.
XX
XX NF-AT transcription factor; immunomodulatory agent; screening;
KW immunosuppressive; interleukin 2 enhancer; promoter; ss.
XX
OS Synthetic.
XX
XX WO9304203-A1.
XX
XX 04-MAR-1993.
XX
XX 24-AUG-1992; 92WO-US007104.
XX
XX 22-AUG-1991; 91US-00749385.
XX
XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
XX Flanagan WM, Crabtree GR;
PI
XX
XX WPI; 1993-094028/11.
XX
XX Immunomodulatory agents screening compsn. for immunosuppressant tests -
PT comprises isolated transcription factor binding nucleic acid sequence of
PT 20 base pairs and polypeptide activating NF AT dependent transcription.
XX
XX Claim 17; Page 50; 72pp; English.
XX
XX The sequence is homologous to that upstream of the interleukin-2 gene, in
CC the enhancer region. DNA sequence analysis of the promoter/ enhancer
CC regions of several genes that respond to T-cell activation signals has
CC identified putative NF-AT protein binding sites. The oligonucleotide, and
CC ones homologous to it, may be used in methods for screening
CC immunomodulant and immunosuppressive agents. See also AAQ37029-35.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 12 BP; 8 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 730 CAGGAGAAACA 740
Db 1 CAGGAGAAAAA 11
XX
RESULT 199
AAZ41801
ID AAZ41801 standard; DNA; 12 BP.
XX
AC AAZ41801;
XX
XX 20-MAR-2003 (revised)
DT 21-JAN-2000 (first entry)
XX
XX Organic material detecting primer 162.
XX
XX Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW detection; pollutant; soil; food; agricultural chemical; polymer;
KW organochlorine; primer; ss.
XX
XX Synthetic.
OS
XX DE19914461-A1.
FN

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XX
PD 21-OCT-1999.
XX
XX 30-MAR-1999; 99DE-01014461.
XX
XX 31-MAR-1998; 98JP-00087651.
PR 16-MAR-1999; 99JP-00069694.
XX
XX (SAOL ) SANYO ELECTRIC CO LTD.
PA (NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
XX Inoue T;
PI
XX WPI; 1999-592157/51.
XX
XX Novel polymerase chain reaction method, for differentiating between
DR microorganisms and for detecting contaminants.
XX
XX Example 1; Page 21; 78pp; German.
XX
XX This invention describes a novel method for the amplification of DNA
CC comprising (i) preparing many primers (P) with different probabilities of
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC many different DNA using these primers. The method is used (i) to
CC differentiate between different microorganisms in a mixed population and
CC (ii) to determine presence/absence of an impurity (pollutant), or its
CC concentration, in e.g. soil, foods, compost etc., typically metals,
CC agricultural chemicals, polymers, organochlorine compounds etc. A
CC particular use is monitoring composting of organic material.
CC Amplification with many primers produces a lot of information, so
CC reliability of the test is improved, and many samples may be tested
CC quickly. AAZ41640-24185s represent the primers described in the method of
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
XX Sequence 12 BP; 5 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 731 AGGAGAAACAG 741
Db 2 AGGAGAAACGG 12
XX
RESULT 200
AAZ41696/c
ID AAZ41696 standard; RNA; 12 BP.
XX
XX AAZ41696;
AC
XX
XX 03-SEP-1999 (first entry)
DT
XX
XX Released tag used in a novel method of DNA sequencing.
XX
XX Extension region; terminal nucleotide; template arranging segment;
KW complexity decreasing nucleotide; DNA sequencing; primer; ss.
XX
XX Synthetic.
OS
XX
XX JP11151092-A.
FN
XX
XX 08-JUN-1999.
PD
XX
XX 24-AUG-1998; 98JP-00237840.
XX
XX 22-AUG-1997; 97US-00916120.
PR
XX (LYNX-) LYNX THERAPEUTICS INC.
PA
XX
XX WPI; 1999-388481/33.
XX
XX Extension of DNA using rolling primer - useful as DNA sequencing method.
PT

```

XX The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 1 A; 2 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 734 AGAACAGAAC 744
DB 11 AGAACAGATC 1
RESULT 196
ABV66898/c
ID ABV66898 standard; cDNA; 11 BP.
XX
AC ABV66898;
XX
DT 21-OCT-2002 (first entry)
DE Human skin EST 4684.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrheic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 154; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX

SQ Sequence 11 BP; 1 A; 2 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 734 AGAACAGAAC 744
DB 11 AGAACAGATC 1
RESULT 197
AAQ24029/c
ID AAQ24029 standard; DNA; 12 BP.
XX
AC AAQ24029;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1992 (first entry)
XX
DE Herpesvirus inhibiting antisense oligonucleotide.
XX
KW HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;
KW Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.
XX
OS Synthetic.
XX
PN WO9205284-A.
XX
PD 02-APR-1992.
XX
PF 18-SEP-1991; 91WO-US006646.
XX
PR 21-SEP-1990; 90US-00586185.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Aurelian L, Tso P;
XX
DR WPI; 1992-132145/16.
XX
PT New anti-sense oligonucleotide(s) for inhibiting HSV - also used for
PT diagnosis and for inhibiting HIV activation by herpes virus.
XX
PS Claim 1; Page 38; 77pp; English.
XX
CC The sequence is that of an antisense oligonucleotide which can be used
CC for inhibiting growth or replication of herpesviruses. It corresponds to
CC an antisense sequence of a herpesvirus site, pref. in a gene that is
CC essential for synthesising nucleic acids e.g. the immediate early genes
CC or VMW65. It can be prepd. by solid phase triester or phosphor- amide
CC chemistry or by recombinant DNA techniques. It can be used for treating
CC infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2
CC (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus
CC (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the
CC inhibition of herpesvirus growth or replication may indirectly forestall
CC the progression of events from HIV exposure to the clinical manifestation
CC of AIDS. It may also be useful in the detection, diagnosis and
CC manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-
CC Q24044. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 12 BP; 0 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAA 738
DB 12 GCCAAGAGAAA 2

CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic bacteria or viruses for
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGACACA 745

Db 14 GAGAAACAGACAAA 2

RESULT 194

ABX76569/C
 ID ABX76569 standard; DNA; 15 BP.

XX ABX76569;

DT 01-APR-2003 (first entry)

XX M. avium 23S rRNA mutated probe #6.

XX Probe; 23S rRNA; 16SrRNA; tuberculosis; MTC; MOTT; peptide nucleic acid;
 KW mycobacterium tuberculosis complex; precursor rRNA; rDNA; ss rRNA; ss;
 KW mycobacterium other than tuberculosis; 23S-mediated macrolide resistance;
 KW mutant.

OS Mycobacterium avium.
 OS Synthetic.

XX Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "G is covalently linked to Lys (Rho) where Rho=
 FT Rhodamine, optional"
 FT modified_base 15
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "C is amidated"

PN US2002137035-A1.

XX 26-SEP-2002.

XX 07-APR-2000; 2000US-00544934.

XX 07-APR-2000; 2000US-00544934.

XX (STEN/) STENDER H.
 PA (LUND/) LUND K.
 PA (MOLL/) MOLLERUP T A.

XX Stender H, Lund K, Mollerup TA;

XX WPI; 2003-174116/17.

XX Peptide nucleic acid probes for detecting target sequences of

PT Mycobacteria in samples, e.g., sputum, which are capable of hybridizing
 PT to a target sequence of mycobacterial rDNA, precursor rRNA or rRNA
 PT forming detectable hybrids.

XX Claim 22; Page 40; 74pp; English.

XX The invention relates to a peptide nucleic acid capable of hybridising to
 CC a target sequence of mycobacterial rDNA, precursor rRNA or rRNA (5S, 16S
 CC or 23S) forming detectable hybrids. Also included are detecting a target
 CC sequence of mycobacteria in a sample comprising contacting rRNA or rDNA
 CC in the sample with peptide nucleic acid probes (hybridisation takes place
 CC between the probe and the rRNA or rDNA), observing or measuring any
 CC formed detectable hybrids and relating the observation or measurement to
 CC the presence of a target sequence of mycobacteria in the sample, and a
 CC kit for detecting a target sequence of mycobacteria in particular a
 CC target sequence of mycobacteria of M. tuberculosis complex (MTC). The
 CC probes are used for detecting a target sequence of MTC (and
 CC distinguishing them from mycobacterium other than tuberculosis, MOTT)
 CC present in a sample, e.g. sputum, laryngeal swabs, gastric lavage,
 CC bronchial washings, biopsies, aspirates, expectorates, body fluids,
 CC urine, tissue sections as well as food samples, soil, air and water
 CC samples and their cultures. The probe is able to penetrate the cell wall
 CC of the mycobacteria. It is able to hybridise to mycobacterial precursor
 CC rRNA and rRNA without harsh treatment of the mycobacterial cells,
 CC therefore avoiding a risk of interfering with the morphology of the
 CC cells. The present sequence is an M. avium mutated probe for 23S rRNA
 CC around positions 2568-2569, associated with 23S-mediated macrolide
 CC resistance

XX Sequence 15 BP; 0 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGA 742

Db 14 CAGGACGACACAGA 2

RESULT 195

ABQ87464/C
 ID ABQ87464 standard; CDNA; 11 BP.

XX ABQ87464;

XX 10-SEP-2002 (first entry)

XX Human skin stress/ageing related EST SEQ ID NO 1219.

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

XX Homo sapiens.

XX WO200253773-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015178.

XX 03-JAN-2001; 2001DE-01000121.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-528865/56.

XX Identifying genes involved in skin stress and aging, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.

XX Claim 8; Page 87; 325pp; German.

PS Claim 14; Page 14; 84pp; English.

CC The invention relates to an isolated polynucleotide comprising genes and

CC haplotypes of the chemokine binding protein 2 (CCBP2) gene. Polymorphic

CC variants of the CCBP2 gene are useful in studying the expression and

CC function of CCBP2, and in expressing CCBP2 proteins for use in screening

CC candidate drugs for treating diseases associated with CCBP2 activity.

CC Polynucleotides comprising a polymorphic gene variant or fragment may be

CC used for therapeutic purposes, where a patient could benefit from

CC expression or increased expression of a particular CCBP2 protein isoform,

CC or an expression vector encoding the isoform may be administered to the

CC patient. Haplotype information is useful in improving the efficiency and

CC output of several steps in drug discovery and development process,

CC including target validation, identifying lead compounds, and early phase

CC clinical trials. The polynucleotides of the invention can be used to

CC treat disorders related to the CCBP2 gene by gene therapy. This

CC polynucleotide sequence represents a preferred ASO primer for detecting

CC CCBP2 gene polymorphisms relating to the invention

XX SQ Sequence 15 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 1 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCAGGAGAAAC 739

Db 1 TGCAGGAGAAAC 13

RESULT 192

ABV99157/C

ID ABV99157 standard; DNA; 15 BP.

XX AC ABV99157;

XX DT 17-JAN-2003 (first entry)

XX DE Human CYP7A1 allele-specific oligonucleotide probe #7.

XX KW Human; CYP7A1; hepatotropic; antilipaemic; cholesterol disorder;

XX KW cirrhosis; bile disorder; hypertriglyceridaemia; hypercholesterolaemia;

XX KW cytochrome P450, subfamily VIIA, polypeptide 1; probe; ss.

XX OS Homo sapiens.

XX PN WO200260915-A1.

XX PD 08-AUG-2002.

XX PF 31-JAN-2001; 2001WO-US003164.

XX PR 31-JAN-2001; 2001WO-US003164.

XX PA (GENA-) GENAISANCE PHARM INC.

XX PI Chew A, Denton RR, Nandabalan K, Stephens JC;

XX DR WPI; 2002-713314/77.

XX PT New cytochrome P450 subfamily VIIA (cholesterol 7 alphanomoxigenase)

XX PT polypeptide 1 gene variants, useful for studying the expression and

XX PT activity of CYP7A1 and screening drugs for treating disorders of

XX PT cholesterol and bile metabolism.

XX PS Claim 16; Page 21; 84pp; English.

XX CC The invention relates to a novel polymorphic variant of a sequence of

CC CYP7A1 protein or its fragment. The polypeptide has hepatotropic and

CC antilipemic activity. The polymorphic variants are useful in studying

CC the expression and function of CYP7A1, in expressing CYP7A1 protein for

CC use in screening candidate drugs to treat diseases related to CYP7A1

CC activity, in studying the effect of the variation on the biological

CC activity of CYP7A1, and the binding affinity of candidate drugs targeting

CC CYP7A1 for the treatment of disorders such as cholesterol and bile

CC disorders. Haplotyping methods are useful in validating CYP7A1 as a

CC candidate target for treating a specific condition or disease predicted

CC to be associated with CYP7A1 activity, or in the design of clinical

CC trials of candidate drugs for treating a specific condition or disease

CC associated with CYP7A1 activity, such as cirrhosis, familial

CC hypertriglyceridaemia and hypercholesterolaemia. Transgenic animals are

CC also useful for studying expression of the CYP7A1 isogenes in vivo, for

CC in vivo screening and testing of drugs targeted against CYP7A1 protein,

CC and for testing the efficacy of therapeutic agents and compounds related

CC to cholesterol and bile acid metabolism. The present sequence represents

CC an allele-specific oligonucleotide (ASO) probe, used in the invention to

XX detect CYP7A1 gene polymorphisms

SQ Sequence 15 BP; 1 A; 3 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743

Db 14 AAGACAAACAGAA 2

RESULT 193

ABX98147/C

ID ABX98147 standard; DNA; 15 BP.

XX AC ABX98147;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #30.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;

XX KW gene expression; regulatory sequence; pathogenic double-stranded DNA;

XX KW pathogenic bacteria; virus; replication; virulence; cancer;

XX KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX PN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-00168920.

XX PR 17-SEP-1992; 92US-00946976.

XX PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX PT A triple-helix comprising a double helical nucleic acid (DHNA) and an

XX PT oligonucleotide which binds in parallel and antiparallel orientation,

XX PT respectively, for targeting sequences on alternate strands of DHNA to

XX PT control gene expression.

XX PS Example 2; Fig 4B; 108pp; English.

XX CC The present invention relates to methods and oligonucleotides for forming

CC a triple-helix comprising a double helical nucleic acid comprising first

CC and second substantially complementary strands, and an oligonucleotide

CC bound to a purine-rich target sequence within the double helical nucleic

CC acid, where the oligonucleotide binds in a parallel and antiparallel

CC orientation, respectively, to target sequences on alternate strands of

CC the double helical nucleic acid. The method has therapeutic applications,

CC where gene expression is controlled by selective triple-helix formation

CC within expression regulatory sequences of a target gene. The

```

OS Homo sapiens.
XX
PN US6333152-B1.
XX
PD 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 53; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
XX that has the same sequence as a mRNA found in humans and is a SAGE
XX (serial analysis of gene expression) tag comprising a single stranded
XX probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX diagnostic and prognostic markers of cancer, especially of the colon and
XX pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
XX SAGE tags of the invention
XX
XX
XX
SQ Sequence 15 BP; 1 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACA 740
Db 15 GCGACGAGAAACA 3
RESULT 190
ABX00872/c
ID ASX00872 standard; RNA; 15 BP.
AC ABX00872;
XX
XX 23-DEC-2002 (first entry)
XX
XX Hepatitis C virus substrate #654 for HCV hammerhead ribozyme #654.
XX
XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
XX liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX type I interferon; interferon alpha; interferon beta; cytostatic;
XX interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
XX Hepatitis C virus.
XX
XX US2002082225-A1.
XX
XX 27-JUN-2002.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (ROBE/) ROBERTS B.
XX (PAVC/) PAVCO P A.
XX (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX
XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX replication and are useful to treat hepatitis C virus infections and
XX cirrhosis, liver failure or hepatocellular carcinoma.
XX
XX Claim 1; Page 40; 80pp; English.
XX
XX The present invention relates to enzymatic nucleic acids which
XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX (HP) motif where the binding arms comprise sequences complementary to one
XX of the substrate sequences defined in the specification. The HCV
XX ribozymes are useful for modulating the expression and/or replication of
XX HCV. They can be used to treat cirrhosis, liver failure and/or
XX hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX a condition associated with HCV infection in conjunction with one or more
XX other drug therapies, particularly type I interferon, especially
XX interferon alpha, beta or gamma or consensus interferon. The present
XX sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
XX Some of the sequence data for this patent did not form part of the
XX printed specification. The complete sequence data for this patent was
XX obtained in electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/psaipdipentry.html
XX
XX Sequence 15 BP; 2 A; 6 C; 2 G; 0 T; 5 U; 0 Other;
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAAC 744
Db 13 GGTGAACAGTAC 1
RESULT 191
AAL39513
ID AAL39513 standard; DNA; 15 BP.
XX
XX AAL39513;
XX
XX 05-SEP-2002 (first entry)
XX
XX CCBP2 detecting ASO primer SEQ ID No 40.
XX
XX Chemokine binding protein 2; CCBP2; CCBP2 protein isoform; gene therapy;
XX polymorphic gene variant; single nucleotide polymorphism; human; primer;
XX PCR; ss.
XX
XX Homo sapiens.
XX
XX WO200232926-A2.
XX
XX 25-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US042685.
XX
XX 12-OCT-2000; 2000US-0239638P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Armstrong B, Kazemi A, Koshy B;
XX WPI; 2002-435524/46.
XX
XX New genetic variants having polymorphisms in the chemokine binding
XX protein 2 (CCBP2) gene, useful for studying CCBP2 functions, and for
XX treating disorders affected by expression or function of the CCBP2
XX isogene.

```



```

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 3.8e+02;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAACAG 741
Db 15 TGCCAGGAGGTTCAG 1

RESULT 187
ABN80567/C
ID ABN80567 standard; DNA; 15 BP.
XX
AC ABN80567;
XX
DT 19-JUL-2002 (first entry)
DE Human P450(cytochrome) oxidoreductase allele specific PCR primer #7.
XX
KW Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;
KW single nucleotide polymorphism; flavoprotein; enzyme; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200226768-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-US030877.
XX
PR 29-SEP-2000; 2000US-0236449P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kazemi A, Kliem SE, Lanz EM, Messer C, Tanguay DA;
XX
DR WPI; 2002-394236/42.
XX
XX New genetic variants comprising haplotypes of the P450 (cytochrome)
PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug
PT screening protocols for compounds targeting POR.
XX
PS Claim 14; Page 14; 141pp; English.
XX
XX The present invention provides the protein, gene and cDNA sequences of
CC human P450(cytochrome) oxidoreductase POR, and single nucleotide
CC polymorphisms (SNPs) identified therein. The sequences can be used to
CC haplotype the POR gene of an individual, and to establish whether POR is
CC a suitable target for drugs to treat cancer and disorders associated with
CC impaired protein synthesis in cells. The present sequence is an allele
CC specific primer for the coding sequences of the invention
XX
SQ Sequence 15 BP; 1 A; 3 C; 5 G; 5 T; 0 U; 1 Other;

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACA 740
Db 13 GCCTGCAGAAACA 1

RESULT 188
AAD24257/C
ID AAD24257 standard; DNA; 15 BP.
XX
AC AAD24257;
XX
DT 07-MAR-2002 (first entry)
DE Duplex forming PNA #1 targetted to Escherichia coli ribosomal RNA.
XX
XX Bacterial growth inhibitor; bacterial infection; disinfectant; PNA;
KW antibacterial; peptide nucleic acid; ribosomal RNA; ss.
XX
OS Escherichia coli.
XX
SY Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This sequence is a peptide nucleic acid i.e it
FT contains a N-acetyl (2-aminoethyl) glycine backbone
FT instead of a deoxyribose-phosphate backbone"
FT 15
FT modified_base
FT /*tag= b
FT /mod_base= OTHER
FT /note= "N-acetyl (2-aminoethyl) -C-lysine- glycine
FT backbone"
XX
US6300318-B1.
XX
PD 09-OCT-2001.
XX
PF 16-SEP-1997; 97US-00932140.
XX
PR 16-SEP-1997; 97US-00932140.
XX
PA (NIEL/) NIELSEN P E.
XX
PI Nielsen PE, Good L;
XX
DR WPI; 2002-033179/04.
XX
XX Killing or inhibiting growth of bacteria using peptide nucleic acids
PT complementary to a region of the bacterial ribosomal RNA is useful to
PT treat a bacterial infection in a mammal and as a disinfectant.
XX
PS Example 5; Col 12; 32pp; English.
XX
XX The patent discloses methods and compositions for killing or inhibiting
CC growth of bacteria comprising contacting the bacteria with a peptide
CC nucleic acid (PNA) complementary to a region of the bacterial ribosomal
CC RNA. The method is used to treat a bacterial infection in a mammal and as
CC a disinfectant. The present sequence is a duplex forming peptide nucleic
CC acid (PNA) which is targetted to Escherichia coli ribosomal RNA. This
CC sequence is used in the exemplification of the invention
XX
SQ Sequence 15 BP; 2 A; 6 C; 0 G; 7 T; 0 U; 0 Other;

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db 15 AGGAGAAAGAGTA 3

RESULT 189
ABX32359/C
ID ABX32359 standard; DNA; 15 BP.
XX
AC ABX32359;
XX
DT 23-APR-2002 (first entry)
DE Human colon cancer SAGE tag #460.
XX
KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW serial analysis of gene expression; diagnostic; prognostic; probe;
KW cancer marker; ss.
XX
```

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGACAC 746
 DB 2 AGCAACACAGACAC 14

RESULT 185
 AAF79911/c
 ID AAF79911 standard; DNA; 15 BP.

XX AAF79911;

XX 11-JUN-2001 (first entry)

XX Nucleotide sequence of a control peptide nucleic acid.

XX Peptide nucleic acid; PNA; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..14

FT /tag= a

FT /note= "N-acetyl(2-aminoethyl)glycine backbone"

FT modified_base 15

FT /tag= b

FT /note= "N-[acetyl(2-aminoethyl)]-C-lysine-glycine backbone"

XX US6190866-B1.

XX 20-FEB-2001.

XX 27-MAR-1998; 98US-00049190.

XX 16-SEP-1997; 97US-00932140.

XX (NIEL/) NIELSEN P E.

XX Nielsen PE, Good L;

XX WPI; 2001-256212/26.

XX Determining bacterial target gene function, involves preparing peptide
 PT nucleic acid (PNA) compounds complementary to bacterial nucleotide
 PT sequence, determining activity of PNA, contacting active PNA compounds
 PT and determining the effect.

XX Example 5; Col 13; 34pp; English.

XX The present sequence represents a control peptide nucleic acid (PNA),
 CC which used in the method of the invention. The specification describes a
 CC method for determining target gene function in bacteria. The method
 CC comprises providing a nucleotide sequence of the target gene from the
 CC bacteria, selecting and preparing PNAs with regions complementary to a
 CC part of the nucleotide sequence, in anti-parallel orientation,
 CC determining activity of PNA by selected assay to identify active PNA
 CC compounds, contacting the bacteria with the active PNA compounds, and
 CC determining effect of these on the bacteria. The method is useful for
 CC determining the function of target gene in a bacteria. The method is also
 CC useful in the design of antisense antibacterial drugs and gene function
 CC analysis in bacteria. The method is used for killing or inhibiting of

CC bacteria

XX Sequence 15 BP; 2 A; 6 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743

DB 15 AGGAGAAAGCTA 3

RESULT 186

ABA99292/c
 ID ABA99292 standard; DNA; 15 BP.

XX ABA99292;

XX 13-MAY-2002 (first entry)

XX Human ALDH5 allele-specific oligonucleotide SEQ ID No 12.

XX ALDH5; human; gene; polymorphism; haplotype; aldehyde dehydrogenase 5;
 KW binding affinity; drug targeting; alcoholism; alcohol-induced disorder;
 KW antialcoholic; ss.

XX Homo sapiens.

XX WO200192279-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US017253.

XX 26-MAY-2000; 2000US-0207508P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Duda A, Finkel K, Kazemi A, Messer C, Sanchis A;

XX WPI; 2002-122054/16.

XX New genetic variants with polymorphisms in the aldehyde dehydrogenase 5
 PT (ALDH5) gene, useful for studying the function of ALDH5, and for
 PT expressing ALDH5 protein which is useful in screening drugs for treating
 PT ALDH5-related diseases.

XX Claim 17; Page 76; 96pp; English.

XX This invention describes a novel isolated genes and haplotypes of the
 CC human aldehyde dehydrogenase 5 (ALDH5) gene containing polymorphic sites.
 CC The polymorphic ALDH5 variant is useful in studying the effect of the
 CC variation on the biological activity of ALDH5 and on the binding affinity
 CC of candidate drugs targeting ALDH5 for the treatment of alcoholism and
 CC alcohol-induced disorders. Polynucleotides comprising a polymorphic gene
 CC variant or fragment may be used for therapeutic purposes. ALDH5 protein
 CC isoforms may be used in assays to measure the binding affinities of one
 CC or more candidate drugs targeting the ALDH5 protein. ALDH5 proteins may
 CC be used to generate antibodies. Haplotyping method can be used by
 CC scientists to validate ALDH5 as a candidate target for treating a
 CC specific condition or disease predicted to be associated with ALDH5
 CC activity, and in the design of clinical trials of candidate drugs for
 CC treating a specific condition or disease predicted to be associated with
 CC ALDH5 activity. Information on polymorphisms on the ALDH5 gene can be
 CC applied for studying the biological function of ALDH5 as well as in
 CC identifying drugs targeting this protein for the treatment of disorders
 CC related to its abnormal expression or function. The products of the
 CC invention have antialcoholic activity. This sequence represents a human
 CC ALDH5 allele-specific oligonucleotide described in the disclosure of the
 CC invention

XX Sequence 15 BP; 3 A; 6 C; 3 G; 2 T; 0 U; 1 Other;

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAACAGAAC 744
 Db 3 GGAGAGCTGAAC 15
 ||||| |||||
 ||||| |||||

RESULT 183
 AAF50112/c
 ID AAF50112 standard; DNA; 15 BP.
 XX
 AC AAF50112;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGF-I oligonucleotide #1072.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 67; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 1 A; 4 C; 2 G; 8 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGAGAACAGAGA 742
 Db 13 CAGAGAGTAACAGA 1
 ||||| |||||
 ||||| |||||

RESULT 184
 AAF53454
 ID AAF53454 standard; DNA; 15 BP.
 XX
 AC AAF53454;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGF-I oligonucleotide #4414.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 89; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

PS Example 8; Page 93; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 744

Db 1 GGAGAGCTGAC 13

RESULT 181

AAF50109/c
 ID AAF50109 standard; DNA; 15 BP.

XX AAF50109;

XX 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #1069.

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

Example 8; Page 67; 201pp; English.

PS The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 2 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743

Db 15 AGAAGTAACAGAA 3

RESULT 182

AAF54011
 ID AAF54011 standard; DNA; 15 BP.

XX AAF54011;

XX 30-MAR-2001 (first entry)

XX IGF-I oligonucleotide #4971.

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

Example 8; Page 93; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an

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XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX PT WPI; 2001-041421/05.
XX DR
XX XX
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX PS Example 8; Page 89; 20pp; English.
XX XX
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX SQ Sequence 15 BP; 7 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 734 AGAACAACAGACAC 746
DB ||||| |||||
3 AGCAACAGACAC 15
RESULT 179
AAF54012
ID AAF54012 standard; DNA; 15 BP.
XX AC AAF54012;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #4972.
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX PN WO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000WO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX PT WPI; 2001-041421/05.
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX PS Example 8; Page 93; 20pp; English.
XX XX
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX SQ Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 732 GGAGAAACAGAAC 744
DB ||||| |||||
2 GGAGAACTCAAC 14
RESULT 180
AAF54013
ID AAF54013 standard; DNA; 15 BP.
XX AC AAF54013;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #4973.
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX PN WO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000WO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX PT WPI; 2001-041421/05.
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering

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FT XX C-5"

PN XX US2001002314-A1.

XX XX 31-MAY-2001.

XX XX 04-AUG-1998; 98US-00128732.

XX XX 30-OCT-1987; 87US-00115922.

PR XX 16-NOV-1990; 90US-00614205.

PR XX 12-NOV-1993; 93US-00152250.

XX XX (FLEH-) FLEHR HOEBACH TEST ALBRITTON & HERBERT.

PA XX Dervan PB, Moser HE;

PI XX WPI; 2001-342909/36.

DR XX

XX XX New hybridization probe for specific triplex formation with large double helices, useful e.g. for site-specific diagnostic cleavage, contains attached functional residue.

PT XX

PT XX

XX XX

PS Example 2; Fig 4B; 20pp; English.

XX XX

CC This invention relates to hybridisation probes which target a specific sequence within a large double-helical nucleic acid. The probe is complementary to the target sequence and contains at least one nucleotide with an attached molecule that is able to cleave double-helical DNA e.g. EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes where the attached molecule is a label or compound that alters gene expression, are used for specific detection and/or cleavage of double-helical DNA, e.g. for diagnosis, for treatment of disease (particularly caused by viruses, genetic defects or oncogenes), for chromosomal analysis, and for the isolation and mapping of genes. The present sequence represents probe of the invention which is used in an example illustrating how it binds to and cleaves a double stranded fragment of CC plasmid pDMG10 given in AHH20315

XX XX

SQ Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAACAC 745

Db 14 GAGAAAGAGAAAA 2

RESULT 177

AAF53455

ID AAF53455 standard; DNA; 15 BP.

XX XX

AC AAF53455;

XX XX

DT 30-MAR-2001 (first entry)

XX XX

DE IGF-I oligonucleotide #4415.

XX XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

OS Homo sapiens.

XX XX

PN WO200078341-A1.

XX XX

PD 28-DEC-2000.

XX XX 21-JUN-2000; 2000WO-AU000693.

XX XX 21-JUN-1999; 99US-0140345P.

PR XX (MURD-) MURDOCH CHILDRENS RES INST.

PA XX

PI XX Wright CU, Werther GA, Edmondson SR;

XX XX WPI; 2001-041421/05.

XX XX

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

PT XX

XX XX

PS Example 8; Page 89; 201pp; English.

XX XX

CC The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153- F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

XX XX

SQ Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAACAC 746

Db 1 AGCAACAGACAC 13

RESULT 178

AAF53453

ID AAF53453 standard; DNA; 15 BP.

XX XX

AC AAF53453;

XX XX

DT 30-MAR-2001 (first entry)

XX XX

DE IGF-I oligonucleotide #4413.

XX XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

OS Homo sapiens.

XX XX

PN WO200078341-A1.

XX XX

PD 28-DEC-2000.

XX XX

PF 21-JUN-2000; 2000WO-AU000693.

XX XX

PR 21-JUN-1999; 99US-0140345P.

```

DT 15-MAR-2000 (first entry)
XX Control polynucleotide sequence SEQ ID NO:2.
DE
XX Dendrimer; polynucleotide multimer; hybridisation assay; ss.
XX
XX OS Synthetic.
XX
XX WO9961662-A1.
XX
XX PD 02-DEC-1999.
XX
XX PF 27-MAY-1999; 99WO-GB001697.
XX
XX PR 27-MAY-1998; 98GB-00011403.
XX
XX PA (ISIS-) ISIS INNOVATION LTD.
XX
XX PI Shchepinov MS, Southern EM;
XX
XX DR WPI; 2000-072636/06.
XX
XX PT New dendrimer compositions, used in hybridization assays for the
XX detection of target nucleic acids.
XX
XX PS Example 1; Page 7; 25pp; English.
XX
CC The present invention describes a dendrimer having branches that
CC terminate with the same polynucleotide (PN) sequence. Also described are:
CC (1) use of a multimeric PN for hybridisation interaction; and (2) an
CC assay for a target PN by hybridisation with an immobilised PN, which
CC comprises the preliminary step of conjugating the target to a dendrimer
CC having reactive terminal groups. The dendrimers comprising PN multimers
CC can be used in hybridisation assays for the detection of target nucleic
CC acids. The use of multimeric PNs allows multiple hybridisation reactions
CC to occur with a resulting increase in the stability of the hybridised
CC components compared to a duplex formed between PN monomers. This increase
CC in stability is characterised by higher melting temperatures and higher
CC temperatures of reassociation exhibited by the multimeric PNs in
CC comparative tests with PN monomers. The present sequence represents a
CC control polynucleotide sequence, which is used in an example from the
XX present invention
XX
SQ Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db | | | | | | | | | |
14 AAGAGAAAGAGAA 2

RESULT 176
AAH20313/c
ID AAH20313 standard; DNA; 15 BP.
XX
XX AC AAH20313;
XX
XX DT 31-JUL-2001 (first entry)
XX
XX DE DNA-EDTA-FE(II) probe 7.
XX
XX KW Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 5
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Thymidine has EDTA-FE(II) covalently attached at

```

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RESULT 174
AAZ63819/c
ID AAZ63819 standard; RNA; 15 BP.
XX
XX AC AAZ63819;
XX
XX DT 28-MAR-2000 (first entry)
XX
XX DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 1866.
XX
XX KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
XX cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX autoimmune disease; ss.
XX
XX OS Hepatitis C virus.
XX
XX PN WO9955847-A2.
XX
XX PD 04-NOV-1999.
XX
XX PF 26-APR-1999; 99WO-US009027.
XX
XX PR 27-APR-1998; 98US-0083217P.
XX
XX PR 18-SEP-1998; 98US-0100842P.
XX
XX PR 25-FEB-1999; 99US-00257608.
XX
XX PR 23-MAR-1999; 99US-00274553.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX
XX DR WPI; 2000-062023/05.
XX
XX PT Novel ribozymes for the treatment of diseases and conditions related to
XX hepatitis C infection.
XX
XX PS Claim 1; Page 71; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
XX SQ Sequence 15 BP; 2 A; 6 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 744
Db | | | | | | | | | |
13 GGTGAACAGTAC 1

RESULT 175
AAZ48115/c
ID AAZ48115 standard; DNA; 15 BP.
XX
XX AC AAZ48115;
XX

```

CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer

XX SQ Sequence 15 BP; 1 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACA 740
 DB 15 GCGAGGAGAAACA 3

RESULT 172
 AAX61194
 ID AAX61194 standard; DNA; 15 BP.

AC AAX61194;

XX 28-JUL-1999 (first entry)

XX Human chromosome alpha-satellite region.

XX Probe; human; chromosome 17 triple-helix forming oligonucleotide;
 KW genetic disorder; missing chromosome; aneuploidy; chromosome 21;
 KW infectious disease; diagnosis; alpha-satellite region; ss.

XX Homo sapiens.

XX WO9924622-A1.

XX 20-MAY-1999.

XX 10-NOV-1998; 98WO-US023765.

XX 10-NOV-1997; 97US-0064997P.

XX (UYPR-) UNIV PRINCETON.

XX Johnson MD, Fresco JR;

XX WPI; 1999-327425/27.

XX Novel use of triple helix forming oligonucleotides, useful for in situ
 PT detection of double stranded target sequence.

XX Claim 19; Page 13; 45pp; English.

XX This sequence represents a human chromosome alpha-satellite region. The
 CC invention relates to the use of a triple-helix forming oligonucleotide
 CC for in situ detection of a double-stranded target nucleic acid sequence.
 CC The method can be used to detect a genetic disorder e.g. to detect an
 CC extra or missing chromosome or fragment or aneuploidy, especially for
 CC detecting an extra or missing chromosome 17 or 21. The method can be also
 CC be used to screen for individuals at risk of developing a disease or for
 CC diagnosing an infectious disease. The use of triple helix forming
 CC oligonucleotides allows in situ detection of double stranded target
 CC sequence as opposed to prior art uses of developing potential anti-gene
 CC therapeutic agents or artificial restriction endonucleases

XX SQ Sequence 15 BP; 10 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743

DB 2 AGGTGAAAAGAGAA 14

RESULT 173

AAX33140/c
 ID AAX33140 standard; DNA; 15 BP.

XX AAX33140;

XX 24-JUN-1999 (first entry)

XX Beta-galactosidase targeting peptide nucleic acid SEQ ID NO:11.

KW Beta-galactosidase; peptide nucleic acid; PNA; antibacterial;
 KW growth inhibition; antibiotic; bacteria; infection; disinfectant; ss.
 XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..15

FT /tag= a
 FT /note= "N-acetyl (2-aminoethyl) glycine backbone"

FT modified_base 15

FT /tag= b

FT /note= "t is attached to an amidated lysine residue e.g.
 FT -t-Lys-NH2"

XX WO9913893-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-US019199.

XX 16-SEP-1997; 97US-00932140.

XX (ISIS-) ISIS PHARM INC.

XX (NIEL/) NIELSEN P E.

XX Nielsen PE, Good L;

XX WPI; 1999-254325/21.

XX Killing or inhibiting bacterial growth by using a peptide nucleic acid.

XX Example 5; Page 21; 97pp; English.

XX A method has been developed for killing or inhibiting the growth of
 CC bacteria by contacting the bacteria with a peptide nucleic acid (PNA).
 CC The PNA is targeted to messenger or ribosomal RNA. The antibacterial
 CC composition has bacteriostatic and bactericidal properties. The PNA can
 CC be used to treat a mammal suffering from a bacterial infection where the
 CC PNA is complementary to a region of ribosomal RNA and of mRNA of the
 CC bacteria. Further treatment may include concurrent treatment with an
 CC antibiotic. The PNA can also be used as a method of disinfection by
 CC selecting an object to be disinfected, contacting the object with PNA (in
 CC solution) and rinsing the object with a sterile liquid to remove the PNA.
 CC The invention provides new ways of tackling bacterial infections which
 CC have become resistant to frequently used antibiotics. The present
 CC sequence represents a PNA from an example of the present invention

XX SQ Sequence 15 BP; 2 A; 6 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743

DB 15 AGGAGAAAGAGTA 3


```

OS Hepatitis C virus.
XX
XX US2002082225-A1.
XX
XX PD 27-JUN-2002.
XX
XX PF 23-MAR-1999; 99US-00274553.
XX
XX PR 23-MAR-1999; 99US-00274553.
XX
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX
XX PI Blatt L, Meswigen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX
XX PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX replication and are useful to treat hepatitis C virus infections and
XX cirrhosis, liver failure or hepatocellular carcinoma.
XX
XX PS Claim 2; Page 59; 80pp; English.
XX
XX CC The present invention relates to enzymatic nucleic acids which
XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX (HP) motif where the binding arms comprise sequences complementary to one
XX of the substrate sequences defined in the specification. The HCV
XX ribozymes are useful for modulating the expression and/or replication of
XX HCV. They can be used to treat cirrhosis, liver failure and/or
XX hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX a condition associated with HCV infection in conjunction with one or more
XX other drug therapies, particularly type I interferon, especially
XX interferon alpha, beta or gamma or consensus interferon. The present
XX sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note:
XX Some of the sequence data for this patent did not form part of the
XX printed specification. The complete sequence data for this patent was
XX obtained in electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/psipsDIDEntry.html
XX
XX SQ Sequence 14 BP; 2 A; 5 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAACACGAC 744
DB |||||
13 GGTGAACAGTAC 1

RESULT 170
ABQ81011
ID ABQ81011 standard; DNA; 14 BP.
XX
XX AC ABQ81011;
XX
XX DT 10-JAN-2003 (first entry)
XX
XX DE Human alpha foetal protein gene oligonucleotide.
XX
XX KW Human; triple helix; alpha foetal protein; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO20027274-A2.
XX
XX PD 03-OCT-2002.
XX
XX PF 25-MAR-2002; 2002WO-FR001034.

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XX
XX PR 23-MAR-2001; 2001FR-00003953.
XX PR 23-APR-2001; 2001US-0285272P.
XX
XX PA (AVET ) AVENTIS PHARMA SA.
XX
XX PI Blanche F, Cameron B;
XX
XX DR WPI; 2003-018943/01.
XX
XX PT Purifying double-stranded DNA, useful e.g. for isolating plasmids or
XX therapeutic genes, by triple helix formation with oligonucleotide
XX directed to a specific target sequence.
XX
XX PS Claim 16; Page 10; 49pp; French.
XX
XX CC The present invention relates to novel double stranded (ds) DNA sequences
XX which can interact with a third strand to form a stable triple helix. The
XX invention also relates to a method for purifying a ds DNA molecule,
XX comprising contact with a third DNA strand that interacts with a target
XX sequence (TS) in the ds DNA to form a triple helix. The present sequence
XX is an oligonucleotide from human alpha foetal protein gene, used as the
XX ds DNA sequence in the method of the invention
XX
XX SQ Sequence 14 BP; 9 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACACGAA 743
DB |||||
2 AGGAGAACAGAA 14

RESULT 171
AAX31405/C
ID AAX31405 standard; DNA; 15 BP.
XX
XX AC AAX31405;
XX
XX DT 21-MAY-1999 (first entry)
XX
XX DE Tag sequence of a transcript decreased in colorectal cancer.
XX
XX KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9853319-A2.
XX
XX PD 26-NOV-1998.
XX
XX PF 20-MAY-1998; 98WO-US010277.
XX
XX PR 21-MAY-1997; 97US-0047352P.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PI Vogelstein B, Kinzler KW;
XX
XX DR WPI; 1999-070161/06.
XX
XX PT Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
XX pancreatic cancer.
XX
XX PS Claim 1; Page 49; 120pp; English.
XX
XX CC AAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the

```

RESULT 167
 AAX14799/C
 ID AAX14799 standard; DNA; 14 BP.
 AC AAX14799;
 XX
 XX 24-MAR-1999 (first entry)
 DT
 XX
 XX Triple helix third strand of Hepatitis B virus nucleotides 1810-1823.
 DE
 XX
 XX Triplex formation; DNA detection; triple helix; identification; bacteria;
 KW oncogene; virus; ss.
 XX
 OS Synthetic.
 OS Hepatitis B virus.
 XX
 PN US5861244-A.
 XX
 XX 19-JAN-1999.
 PD
 XX
 XX 22-DEC-1993; 93US-00173489.
 PF
 XX
 XX 29-OCT-1992; 92US-00968436.
 PR
 XX (PROP-) PROFILE DIAGNOSTIC SCI INC.
 PA
 XX Hepburn AG, Wang C;
 PI
 XX WPI; 1999-130384/11.
 DR
 XX Assay of genetic sequences based on triplex formation from double
 XX stranded analyte - and hybrid of anchor and reporter sequences, with
 PT reporter released if triplex formation occurs, used e.g. to identify
 PT bacteria.
 XX
 XX Disclosure; Col 19-20; 168pp; English.
 PS
 CC The present sequence represents a polynucleotide that is able to form a
 CC triple helix with a double stranded sequence. Cytosine bases in the
 CC present can be replaced with 5-methylcytosine for increased triplex
 CC stability. The present sequence is used in the assay of the invention,
 CC where it can be part of the anchor DNA or reporter DNA sequence. The
 CC assay comprises adding a sample containing double-stranded DNA test
 CC sequences to an aqueous medium containing at least one complex of anchor
 CC DNA, attached to a solid support, and reporter DNA, where either a part
 CC of the anchor DNA or reporter DNA is designed to form a triple-strand
 CC structure with part of the test sequence. Triplex formation results in
 CC displacement of the reporter DNA which is detected as an indication of
 CC the presence of the DNA test sequence. The method is used to detect DNA
 CC sequences, particularly for identification of bacteria (by detecting
 CC genes for ribosomal RNA) in clinical samples, but also detection of
 CC oncogenes and Hepatitis B virus
 XX
 XX Sequence 14 BP; 0 A; 6 C; 1 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.7e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 731 AGGAGAACAGAA 743
 Db 13 AGGAGAACAGAA 1
 RESULT 168
 AAZ64722/C
 ID AAZ64722 standard; RNA; 14 BP.
 XX
 AC AAZ64722;
 XX
 XX 28-MAR-2000 (first entry)
 DT
 XX Substrate for hairpin ribozyme which cleaves HCV at nt. 1863.
 DE

XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO9955847-A2.
 XX
 XX 04-NOV-1999.
 PD
 XX 26-APR-1999; 99WO-US009027.
 PF
 XX 27-APR-1998; 98US-0083217P.
 PR 18-SEP-1998; 98US-0100842P.
 PR 25-FEB-1999; 99US-00257608.
 PR 23-MAR-1999; 99US-00274553.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
 PI
 XX WPI; 2000-062023/05.
 DR
 XX Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection.
 PT
 XX Claim 2; Page 95; 123pp; English.
 PS
 CC The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the
 CC Hepatitis C virus (HCV) RNA sequence at the base position given in the
 CC descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer
 XX
 XX Sequence 14 BP; 2 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
 SQ
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.7e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 732 GGAGAACAGAAC 744
 Db 13 GGTGAACAGTAC 1
 RESULT 169
 ABX01559/C
 ID ABX01559 standard; RNA; 14 BP.
 XX
 XX ABX01559;
 AC
 XX 23-DEC-2002 (first entry)
 DT
 XX Hepatitis C virus substrate #44 for HCV hairpin ribozyme #44.
 DE
 XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cycostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hairpin ribozyme; HP ribozyme; ss.
 XX

CC beta 1. The sequences given in GENBSEQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 14 BP; 7 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCAGGAGAACACA 740
DB 2 GCAAGGAGAGCA 14

RESULT 165
AAV48481
ID AAV48481 standard; DNA; 14 BP.
XX
AC AAV48481;
XX
DT 15-OCT-1998 (first entry)
XX
DE TGF-beta-1 antisense oligonucleotide TGF-beta1-30.
XX
DE Transforming growth factor beta-1; TGF beta-1; antisense oligonucleotide;
KW modulate; gene expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN EP856579-A1.
XX
PD 05-AUG-1998.
XX
PF 31-JAN-1997; 97EP-00101531.
XX
PR 31-JAN-1997; 97EP-00101531.
XX
PA (BIOG-) BIOGOSTIK GBS BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiepen K, Brysch W;
XX
DR WPI; 1998-400910/35.
XX

PT Preparation of antisense oligonucleotide(s) which lack long runs of
PT consecutive guanosine or inosine - and have specific ratio of residues
PT able to form two or three hydrogen bonds, have greater activity and
PT reduced toxicity, used therapeutically or to modulate growth of cells in
PT culture.
XX
PS Claim 10; Fig 3b; 286pp; English.
XX
CC AAV48412-84 represent antisense oligonucleotides directed against
CC transforming growth factor beta-1 (TGF beta-1). The oligonucleotides
CC exemplify the invention. The specification describes oligonucleotides
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC can each form three hydrogen bonds to cytosine; do not contain four
CC consecutive nucleotides able to form three H-bonds each to four
CC consecutive cytosines; do not contain two sequences of three consecutive
CC nucleotides each able to form three H-bonds to three consecutive
CC cytosines, and the ratio between residues able to form two H-bonds each
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC oligonucleotides are used to modulate expression of genes, particularly
CC the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC oligonucleotides can also be used to analyse function of proteins (by
CC altering their expression or activity) and therapeutically, e.g. in cases
CC of cancer or (targeting TGF) for stimulating the immune system
XX
SQ Sequence 14 BP; 5 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAACACAG 741
DB 1 CCATGAGAGCAG 13

RESULT 166
AAX14811/C
ID AAX14811 standard; DNA; 14 BP.
XX
AC AAX14811;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix third strand of Hepatitis B virus nucleotides 274-287.
XX
KW Triplex formation; DNA detection; triple helix; identification; bacteria;
KW oncogene; virus; ss.
XX
OS Synthetic.
OS Hepatitis B virus.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROP-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX

PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 19-20; 168pp; English.
XX

CC The present sequence represents a polynucleotide that is able to form a
CC triple helix with a double stranded sequence. Cytosine bases in the
CC present can be replaced with 5-methylcytosine for increased triplex
CC stability. The present sequence is used in the assay of the invention,
CC where it can be part of the anchor DNA or reporter DNA sequence. The
CC assay comprises adding a sample containing double-stranded DNA test
CC sequences to an aqueous medium containing at least one complex of anchor
CC DNA, attached to a solid support, and reporter DNA, where either a part
CC of the anchor DNA or reporter DNA is designed to form a triple-strand
CC structure with part of the test sequence. Triplex formation results in
CC displacement of the reporter DNA which is detected as an indication of
CC the presence of the DNA test sequence. The method is used to detect DNA
CC sequences, particularly for identification of bacteria (by detecting
CC genes for ribosomal RNA) in clinical samples, but also detection of
CC oncogenes and Hepatitis B virus
XX
SQ Sequence 14 BP; 0 A; 6 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAA 743
DB 13 AGGAGAACAGCA 1

```

PF 06-APR-2001; 2001WO-IB000713.
XX
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WFI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 28052; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 734 AGAACAAGACAC 746
DB 1 AAAAAACAAGACAC 13

RESULT 163
AAQ40599
ID AAQ40599 standard; DNA; 14 BP.
XX
XX AAQ40599;
XX
XX 25-MAR-2003 (revised)
XX 10-AUG-1993 (first entry)
XX
XX Hypervariable region detection probe 14C5.
XX
XX HVR; human; animal; forensic science; paternity testing; diagnosis;
XX animal breeding; hereditary diseases; tumours; allele; loss;
XX chromosomal regions; tumour region identification; ss.
XX
XX Synthetic.
XX
XX FR2680520-A1.
XX
XX 26-FEB-1993.
XX
XX 22-AUG-1991; 91FR-00010516.
XX
XX 22-AUG-1991; 91FR-00010516.
XX
XX (ETFR ) ETAT FRANCAIS.
XX
XX Vergnaud G;
XX
XX WFI; 1993-136548/17.
XX
XX Detecting the hypervariable regions of DNA for diagnosing hereditary
PT illnesses and tumours - by hybridising labelled polynucleotides and

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PT analysing genomic DNA of individuals which react with restriction
PT fragments.
XX
XX Example; Page 13; 46pp; French.
XX
XX The sequence is that of a polynucleotide probe which may be used in the
XX detection of new hypervariable regions (HVR) in a DNA sequence. HVR
XX represent a fingerprint useful in e.g. forensic science, paternity
XX testing, animal breeding, etc. The probe may be used as part of a method
XX for the efficient detection in humans or other animals, without the use
XX of mini-satellites or primary enrichment. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX Sequence 14 BP; 8 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 733 GAGAAACAGACACA 745
DB 1 GACAAACAGACAGA 13

RESULT 164
AAQ78477
ID AAQ78477 standard; DNA; 14 BP.
XX
XX AAQ78477;
XX
XX 25-MAR-2003 (revised)
XX 27-JUN-1995 (first entry)
XX
XX TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
XX angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
XX carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
XX immunosuppression; oligonucleotide; ss.
XX
XX Synthetic.
XX
XX WO9425588-A2.
XX
XX 10-NOV-1994.
XX
XX 29-APR-1994; 94WO-EP001362.
XX
XX 30-APR-1993; 93EP-00107089.
XX 13-MAY-1993; 93EP-00107849.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
XX Bogdahn U;
XX
XX WFI; 1994-358266/44.
XX
XX New transforming growth factor beta anti-sense oligonucleotide(s) - for
XX treating immunosuppression, tumours, etc.
XX
XX Claim 6; Page 60; 74pp; English.
XX
XX The antisense oligonucleotides are useful in the treatment of tumours in
XX which expression of TGF-beta is of relevance for pathogenicity and/or
XX inhibition of pathological angiogenesis. They are used especially for the
XX treatment of the immunosuppressive effect of TGF-beta, augmentation of
XX the proliferation of cytotoxic lymphocytes, treatment of endogenous
XX hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
XX and malignant gliomas, including glioblastomas, treatment and prophylaxis
XX of skin carcinogenesis, and treatment of oesophageal and gastric
XX carcinomas. See AAQ78352-Q78486. The sequences given in GENESQ files
XX AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-

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XX	Oligonucleotide SEQ ID NO 263069 for detecting SNP TSC0063918.
DE	
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
OS	
XX	WO200177384-A2.
FN	
XX	18-OCT-2001.
PD	
XX	06-APR-2001; 2001WO-IB000713.
PF	
XX	07-APR-2000; 2000DE-01019173.
XX	(EPIG-) EPIGENOMICS AG.
PA	
XX	Olek A, Piepenbrock C, Berlin K;
PI	
XX	WPI; 2001-657177/75.
DR	
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single-nucleotide polymorphisms and cytosine
PT	methylation status.
XX	
XX	Claim 1; SEQ ID NO 263069; 29pp + Sequence Listing; German.
PS	
XX	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligoners are also used for detecting cell type differentiation. ABC00010
CC	-ABF9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073
CC	represent the oligomers described in the invention. NOTE: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 13 BP; 1 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
SQ	
Query Match 44.5%; Score 9.8; DB 1; Length 13;	
Best Local Similarity 84.6%; Pred. No. 3.6e+02;	
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	734 AGAACAGACAC 746
Db	13 ATAAACCGAACAC 1
RESULT 162	
ABC28035	
ID	ABC28035 standard; DNA; 13 BP.
XX	
AC	ABC28035;
AC	
XX	
DT	20-FEB-2002 (first entry)
XX	
XX	Oligonucleotide SEQ ID NO 28052 for detecting SNP TSC0007919.
DE	
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
OS	
XX	WO200177384-A2.
FN	
XX	18-OCT-2001.
PD	
XX	

DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 88771; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 10 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db 1 AGAGAGAAAAGAA 13

RESULT 158
ABH35192
ID ABH35192 standard; DNA; 13 BP.
AC ABH35192;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 235169 for detecting SNP TSC0057429.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 235169; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 10 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db 1 AGGAGAAAAGAA 13

RESULT 159
ABC52235/c
ID ABC52235 standard; DNA; 13 BP.
XX ABC52235;
AC ABC52235;
XX
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 52252 for detecting SNP TSC0014524.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 52252; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 10 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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ID ABC39719 standard; DNA; 13 BP.
XX
AC ABC39719;
XX
DT 20-FEB-2002 (first entry)
XX
DE DE Oligonucleotide SEQ ID NO 39736 for detecting SNP TSC0012134.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 39736; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACGACACCG 748
Db 1 AACACGACACCG 13
RESULT 156
ABH32901/C
ID ABH32901 standard; DNA; 13 BP.
XX
AC ABH32901;
XX
DT 22-FEB-2002 (first entry)
XX
DE DE Oligonucleotide SEQ ID NO 232878 for detecting SNP TSC0056815.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 39736; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACGACACCG 748
Db 1 AACACGACACCG 13
RESULT 156
ABH32901/C
ID ABH32901 standard; DNA; 13 BP.
XX
AC ABH32901;
XX
DT 22-FEB-2002 (first entry)
XX
DE DE Oligonucleotide SEQ ID NO 232878 for detecting SNP TSC0056815.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 232878; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 4 C; 0 G; 8 T; 0 U; 0 Other;
XX
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGAA 743
Db 13 AGGAGAAATAAGAA 1
RESULT 157
ABC88754
ID ABC88754 standard; DNA; 13 BP.
XX
AC ABC88754;
XX
DT 21-FEB-2002 (first entry)
XX
DE DE Oligonucleotide SEQ ID NO 88771 for detecting SNP TSC0022307.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
```

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 0 A; 3 C; 0 G; 10 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGAA 743
 Db 13 AGGAGAAACAGAA 1
 RESULT 153
 ABF97936
 ID ABF97936 standard; DNA; 13 BP.
 AC ABF97936;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 197933 for detecting SNP TSC0005346.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 PR
 XX
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 197933; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 8 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGAA 743
 Db 1 AGTAGAAATAGAA 13
 RESULT 154
 ABC52234
 ID ABC52234 standard; DNA; 13 BP.
 AC ABC52234;
 XX
 DT 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 52251 for detecting SNP TSC0014524.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 PR
 XX
 XX 07-APR-2000; 2000DE-01019173.
 PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 52251; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 9 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGAA 743
 Db 1 AGGAGAAATAGAA 13
 RESULT 155
 ABC39719

CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAACAGAAC 746
 | | | | | | | | | |
 Db 13 AAAAAACAAACAC 1

RESULT 148
 ABF97937/C
 ID ABF97937 standard; DNA; 13 BP.
 XX AC ABF97937;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 197934 for detecting SNP TSC0005346.
 XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX FS Claim 1; SEQ ID NO 197934; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 2 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
 | | | | | | | | | |

Db 13 AGTAGAAATAGAA 1

RESULT 149
 ABH32900
 ID ABH32900 standard; DNA; 13 BP.

XX AC ABH32900;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 232877 for detecting SNP TSC0056815.

XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX FS Claim 1; SEQ ID NO 232877; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
 | | | | | | | | | |
 Db 1 AGGAGAAATAGAA 13

RESULT 150
 ABC88755/C
 ID ABC88755 standard; DNA; 13 BP.

XX AC ABC88755;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 88772 for detecting SNP TSC0022307.

XX (UYJO) UNIV JOHNS HOPKINS.
 PA Vogelstein B, Kinzler KW, Zhang L, Zhou W;
 PI WPI; 2002-153821/20.
 XX
 XX New human nucleic acid containing specific SAGE tags, useful as
 PT diagnostic markers for cancer, also derived probes.
 XX
 XX Disclosure; Col 52; 161pp; English.
 XX
 XX The invention relates to an isolated, purified human nucleic acid (I)
 CC that has the same sequence as a mRNA found in humans and is a SAGE
 CC (serial analysis of gene expression) tag comprising a single stranded
 CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
 CC diagnostic and prognostic markers of cancer, especially of the colon and
 CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
 CC SAGE tags of the invention
 XX
 XX Sequence 15 BP; 6 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 45.5%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 732 GGAGAAACAG 741
 DB 5 GGAGAAACAG 14
 RESULT 146
 ABX00935/C
 ID ABX00935 standard; RNA; 15 BP.
 XX
 AC ABX00935;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Hepatitis C virus substrate #717 for HCV hammerhead ribozyme #717.
 XX
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.
 XX
 OS Hepatitis C virus.
 XX
 XX US2002082225-A1.
 PN
 XX 27-JUN-2002.
 PD
 XX 23-MAR-1999; 99US-00274553.
 PF
 XX 23-MAR-1999; 99US-00274553.
 PR
 XX (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA (ROBE/) ROBERTS B.
 PA (PVC/) PAVCO P A.
 PA (MACE/) MACEJACK D.
 XX
 XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
 PI WPI; 2002-617759/66.
 XX
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
 PT replication and are useful to treat hepatitis C virus infections and
 PT cirrhosis, liver failure or hepatocellular carcinoma.
 XX
 XX Claim 1; Page 42; 80pp; English.

XX The present invention relates to enzymatic nucleic acids which
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
 CC (HP) motif where the binding arms comprise sequences complementary to one
 CC of the substrate sequences defined in the specification. The HCV
 CC ribozymes are useful for modulating the expression and/or replication of
 CC HCV. They can be used to treat cirrhosis, liver failure and/or
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
 CC a condition associated with HCV infection in conjunction with one or more
 CC other drug therapies, particularly type I interferon, especially
 CC interferon alpha, beta or gamma or consensus interferon. The present
 CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
 CC Some of the sequence data for this patent did not form part of the
 CC printed specification. The complete sequence data for this patent was
 CC obtained in electronic format directly from the USPTO web site at
 XX seqdata.uspto.gov/psids/entry.html
 XX
 SQ Sequence 15 BP; 0 A; 6 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 45.5%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAA 737
 DB 13 GCCAGGAGAA 4
 RESULT 147
 ABC28034/C
 ID ABC28034 standard; DNA; 13 BP.
 XX
 AC ABC28034;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 28051 for detecting SNP TSC0007919.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 28051; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

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XX DT 13-AUG-2002 (first entry)
XX DE Human FOS gene allele-specific oligonucleotide sequencing primer #19.
XX KW Human FOS gene allele-specific oligonucleotide; primer;
XX KW Human; ss; allele specific oligonucleotide; primer;
XX KW single nucleotide polymorphism; SNP; lipase endothelial isogene; LIPG;
XX KW drug screening; atherosclerosis; cardiovascular disorder;
XX KW LIPG haplotyping; LIPG genotyping.
XX OS Homo sapiens.
XX PN WO200216397-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US026639.
XX PR 25-AUG-2000; 2000US-0227825P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Duda A, Kazemi A, Kliehm SE, Messer C;
XX DR WPI; 2002-292055/33.
XX DR Novel genetic variants of Lipase, Endothelial isogenes, useful for
XX PT improving efficiency and reliability in drug development for treating
XX PT diseases associated with LIPG activity, e.g. atherosclerosis.
XX PS Claim 16; Page 14; 134pp; English.
XX CC The invention relates to single nucleotide polymorphisms in the gene
XX CC encoding the human v-fos FBJ murine osteosarcoma viral oncogene homologue
XX CC (FOS) polypeptide. A method for haplotyping the FOS gene in an individual
XX CC comprises identifying the nucleotide at one or more polymorphic sites and
XX CC determining whether one of the copies of the gene is defined by one of
XX CC the FOS haplotypes given in the specification or whether both copies are
XX CC defined by a haplotype pair. This method is useful in genotyping, whereby
XX CC all possible haplotype pairs can be assigned to specific genotypes. An
XX CC association between a trait and a haplotype or haplotype pair of the FOS
XX CC gene can be identified by comparing the frequency of the haplotype or
XX CC haplotype pair in a population exhibiting the trait with the frequency of
XX CC the haplotype or haplotype pair in a reference population, where a higher
XX CC haplotype frequency in the trait population indicates the trait is
XX CC associated with the haplotype or haplotype pair. FOS and its
XX CC corresponding DNA are used for studying the expression and function of
XX CC FOS, for use in screening for candidate drugs to treat diseases related
XX CC to FOS activity, such as developmental bone disorders and tumours. The
XX CC sequences are also useful for studying the effect of variation on the
XX CC biological activity of FOS as well as on the binding affinity of
XX CC candidate drugs targeting FOS. Sequences ABK81338-ABK81357 represent
XX CC allele-specific oligonucleotide sequencing primers used for detecting FOS
XX CC gene polymorphisms
XX SQ Sequence 15 BP; 7 A; 2 C; 4 G; 1 T; 0 U; 1 Other;

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
DB 3 AGGAGAAACA 12
|||||
RESULT 144
ABL91826/c
ID ABL91826 standard; DNA; 15 BP.
XX AC ABL91826;
XX DT 11-JUL-2002 (first entry)

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XX DE Human LIPG gene allele specific oligonucleotide primer 5.
XX KW Human; ss; allele specific oligonucleotide; primer;
XX KW single nucleotide polymorphism; SNP; lipase endothelial isogene; LIPG;
XX KW drug screening; atherosclerosis; cardiovascular disorder;
XX KW LIPG haplotyping; LIPG genotyping.
XX OS Homo sapiens.
XX PN WO200216397-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US026639.
XX PR 25-AUG-2000; 2000US-0227825P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Duda A, Kazemi A, Kliehm SE, Messer C;
XX DR WPI; 2002-292055/33.
XX DR Novel genetic variants of Lipase, Endothelial isogenes, useful for
XX PT improving efficiency and reliability in drug development for treating
XX PT diseases associated with LIPG activity, e.g. atherosclerosis.
XX PS Claim 16; Page 14; 134pp; English.
XX CC The invention comprises the DNA and amino acid sequence of the human
XX CC lipase, endothelial (LIPG) isogene. Specifically, the invention relates
XX CC to the discovery of 20 novel polymorphic sites within the LIPG gene. The
XX CC LIPG coding sequence and protein are useful for screening drugs that can
XX CC be used to treat atherosclerosis and other cardiovascular disorders. The
XX CC LIPG coding sequence can also be used to haplotype and genotype the LIPG
XX CC gene of an individual. The DNA sequences ABL91822 - ABL91861 represent
XX CC LIPG gene allele specific oligonucleotide primers
XX SQ Sequence 15 BP; 2 A; 3 C; 2 G; 7 T; 0 U; 1 Other;

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
DB 13 AGAAACAGAA 4
|||||
RESULT 145
ABK32355
ID ABK32355 standard; DNA; 15 BP.
XX AC ABK32355;
XX DT 23-APR-2002 (first entry)
XX DE Human colon cancer SAGE tag #456.
XX KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
XX KW serial analysis of gene expression; diagnostic; prognostic; probe;
XX KW cancer marker; ss.
XX OS Homo sapiens.
XX PN US6333152-B1.
XX PD 25-DEC-2001.
XX PF 20-MAY-1998; 99US-00081646.
XX PR 20-MAY-1998; 98US-00081646.

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CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer

XX SQ Sequence 15 BP; 6 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 45.5%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
 |||||
 DB 5 GGAGAAACAG 14

RESULT 141
 AAZ63882/C
 ID AAZ63882 standard; RNA; 15 BP.

XX AC AAZ63882;

XX DT 28-MAR-2000 (first entry)

XX DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2516.
 XX ENzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 XX KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 XX KW autoimmune disease; ss.

XX OS Hepatitis C virus.

XX PN WO955847-A2.

XX PD 04-NOV-1999.

XX PF 26-APR-1999; 99WO-US009027.

XX PR 27-APR-1998; 98US-0083217P.

XX PR 18-SEP-1998; 98US-0100842P.

XX PR 25-FEB-1999; 99US-00257608.

XX PR 23-MAR-1999; 99US-00274553.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;

XX DR WPI; 2000-062023/05.

XX PT Novel ribozymes for the treatment of diseases and conditions related to

XX PS Hepatitis C infection.

XX PS Claim 1; Page 73; 123pp; English.
 CC The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesized to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer

XX SQ Sequence 15 BP; 0 A; 6 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 45.5%; Score 10; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
 |||||
 DB 13 GCCAGGAGAA 4

RESULT 142
 AAS14448
 ID AAS14448 standard; DNA; 15 BP.

XX AC AAS14448;

XX DT 23-APR-2002 (first entry)

XX DE ASO primer #11 to detect human SCY1 gene polymorphisms.

XX KW Human; single nucleotide polymorphism; SNP; SCY1; chromosome 17;
 XX KW small inducible cytokine A1-I-309; haplotyping; genotyping; gene;
 XX KW atherosclerosis; human immunodeficiency virus; HIV infection;
 XX KW allele-specific oligonucleotide; ASO; primer; ss.

XX OS Homo sapiens.

XX PN WO200179236-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US012305.

XX PR 14-APR-2000; 2000US-0197119P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Choi JY, Kiem SE, Koshy B, Sausker EA, Stephens JC;

XX DR WPI; 2002-075066/10.

XX PT Genotyping human small inducible cytokine A1-I-309, homologous to mouse
 XX PT Tca-3 gene of individual, involves determining identity of nucleotide
 XX PT pair at specific polymorphic sites for two copies of the gene.

XX PS Claim 15; Page 13; 58pp; English.

XX CC The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human small inducible cytokine A1-I-309 (SCY1) gene
 CC located on chromosome 17, and methods for haplotyping and/or genotyping
 CC the SCY1 gene. The methods of the invention make use of allele-specific
 CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
 CC oligonucleotides (ASOs) for detecting the SCY1 gene polymorphisms. The
 CC polynucleotides and screened compounds are useful for the treatment of
 CC diseases associated with SCY1 activity, such as atherosclerosis, human
 CC immunodeficiency virus (HIV) infection, and other inflammatory disorders.

XX CC AAS14438-AAS14455 represent ASO primers for detecting human SCY1 gene
 XX CC polymorphisms

XX SQ Sequence 15 BP; 6 A; 4 C; 4 G; 0 T; 0 U; 1 Other;

Query Match 45.5%; Score 10; DB 1; Length 15;

Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACCCG 748
 |||||
 DB 4 AACAGAACCCYG 15

RESULT 143

ABK81356
 ID ABK81356 standard; DNA; 15 BP.

XX AC ABK81356;

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9988, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI92073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pt_sequences
 CC
 XX Sequence 13 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 1 Other;
 SQ
 Query Match 45.5%; Score 10; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AATCAGAACACC 747
 :|||||
 Db 13 RAACAAACACC 2
 AAV93779;
 RESULT 139
 AAV93779/C
 ID AAV93779 standard; RNA; 14 BP.
 XX
 AC AAV93779;
 XX
 DT 18-FEB-1999 (first entry)
 XX
 DE Human B-raf target sequence nucleotide position 388.
 XX
 KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9850530-A2.
 XX
 PD 12-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-US009249.
 XX
 PR 09-MAY-1997; 97US-0046059P.
 PR 09-JUN-1997; 97US-0049002P.
 PR 03-JUL-1997; 97US-0051718P.
 PR 22-AUG-1997; 97US-0056808P.
 PR 02-OCT-1997; 97US-0061321P.
 PR 02-OCT-1997; 97US-0061324P.
 PR 05-NOV-1997; 97US-0064866P.
 PR 19-DEC-1997; 97US-0068212P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX
 DR WPI; 1999-009494/01.
 XX
 PT Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.
 XX
 PS Claim 179; Page 174; 259pp; English.
 XX
 CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method

CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene
 XX
 SQ Sequence 14 BP; 1 A; 3 C; 2 G; 0 T; 8 U; 0 Other;
 Query Match 45.5%; Score 10; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 734 AGAAACGAA 743
 :|||||
 Db 11 AGAAACGAA 2
 AAV93779;
 RESULT 140
 AAX31401
 ID AAX31401 standard; DNA; 15 BP.
 XX
 AC AAX31401;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Tag sequence of a transcript decreased in colorectal cancer.
 XX
 KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9853319-A2.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US010277.
 XX
 PR 21-MAY-1997; 97US-0047352P.
 XX
 PA (UJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW;
 XX
 DR WPI; 1999-070161/06.
 XX
 PT Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.
 XX
 PS Claim 1; Page 48; 120pp; English.
 XX
 CC AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
PN WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 264229; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 1 Other;
Query Match 45.5%; Score 10; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 736 AACACAGAACACC 747
DB 13 RACATACACC 2
RESULT 137
ABH64253
ID ABH64253 standard; DNA; 13 BP.
XX ABH64253;
AC
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 264230 for detecting SNP TSC0064030.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX

PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 264230; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 1 Other;
Query Match 45.5%; Score 10; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 736 AACACAGAACACC 747
DB 1 RACATACACC 12
RESULT 138
ABF80070/c
ID ABF80070 standard; DNA; 13 BP.
XX ABF80070;
AC
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 180067 for detecting SNP TSC0044584.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 180067; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC response to vaccination and/or therapy, in cancer immunoprophylaxis,
 CC immunotherapy and diagnosis, and monitoring of tumor progression or
 CC regression, and to produce large quantities of readily purified antigen
 XX

SQ Sequence 11 BP; 5 A; 2 C; 3 G; 0 T; 1 U; 0 Other;
 Query Match 45.5%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 CAGGAGAAAC 739
 |||||
 Db 2 CAGGAGAAAC 11

RESULT 134
 ABV65653
 ID ABV65653 standard; cDNA; 11 BP.

AC ABV65653;

DT 21-OCT-2002 (first entry)

DE Human skin EST 3439.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX Disclosure; Page 120; 1345pp; German.

XX The invention relates to in vitro identification (MI) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (MI) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 45.5%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
 |||||
 Db 1 GGAGAAACAG 10

RESULT 135
 ABF80071
 ID ABF80071 standard; DNA; 13 BP.

XX ABF80071;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 180068 for detecting SNP TSC0044584.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 180068; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 45.5%; Score 10; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
 :|||:||||
 Db 1 RAACAAACACC 12

RESULT 136
 ABH64252/c
 ID ABH64252 standard; DNA; 13 BP.

XX ABH64252;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 264229 for detecting SNP TSC0064030.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;


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PN WO2003032898-A2.
XX
PD 24-APR-2003.
XX
XX 23-JUL-2002; 2002WO-US023475.
XX
XX 23-JUL-2001; 2001US-0307345P.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Lyman SD, Van Ness KP, Paxton RJ;
XX
XX WPI: 2003-393470/37.
XX
XX P-PSDB; AAE37156.
XX
XX New modified human thymic stromal lymphopoietin (TSLP) protein and
PT polynucleotide, useful for stimulating lymphocyte proliferation of
PT lymphopoiesis, particularly as a vaccine for treating e.g. AIDS or
PT autoimmune diseases.
XX
XX Disclosure; Page 41; 52pp; English.
XX
XX The invention relates to modified human thymic stromal lymphopoietin
CC (TSLP) protein and polynucleotide sequences. TSLP protein is useful for
CC stimulating lymphocyte proliferation of lymphopoiesis, or inducing STARS.
CC TSLP DNA is useful for producing a furin-resistant polypeptide having at
CC least one functional human TSLP activity. The invention is useful in the
CC manufacture of a medicament for stimulating lymphocyte proliferation, for
CC promoting lymphopoiesis, or for inducing phosphorylation of STARS. It is
CC also useful as a vaccine for treating AIDS, autoimmune diseases (e.g.
CC transplant rejection), or bacterial or viral infections. The present
CC sequence is human TSLP furin cleavage site peptide encoding DNA
XX
XX Sequence 15 BP; 10 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGACACA 745
DB 1 AGGAGAAACAGGAAA 15
RESULT 132
ABL91866/c
ID ABL91866 standard; DNA; 10 BP.
XX
XX ABL91866;
XX
XX 11-JUL-2002 (first entry)
XX
XX Human LIPG gene primer extension oligonucleotide 5.
XX
XX Human; ss; primer; extension oligonucleotide;
XX single nucleotide polymorphism; SNP; lipase endothelial isogene; LIPG;
XX drug screening; atherosclerosis; cardiovascular disorder;
XX LIPG haplotyping; LIPG genotyping.
XX
XX Homo sapiens.
XX
XX WO200216397-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US026639.
XX
XX 25-AUG-2000; 2000US-0227825P.
XX
XX (GENA-) GENAISANCE PHARM INC.
XX
XX Duda A, Kazemi A, Klien SE, Messer C;
XX

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DR WPI; 2002-292055/33.
XX
XX Novel genetic variants of Lipase, Endothelial isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with LIPG activity, e.g. atherosclerosis.
XX
XX Claim 18; Page 14; 134pp; English.
XX
XX The invention comprises the DNA and amino acid sequence of the human
CC lipase, endothelial (LIPG) isogene. Specifically, the invention relates
CC to the discovery of 20 novel polymorphic sites within the LIPG gene. The
CC LIPG coding sequence and protein are useful for screening drugs that can
CC be used to treat atherosclerosis and other cardiovascular disorders. The
CC LIPG coding sequence can also be used to haplotype and genotype the LIPG
CC gene of an individual. The DNA sequences ABL91862 - ABL91901 represent
CC LIPG gene primer extension oligonucleotides
XX
XX Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;
SQ
Query Match 45.5%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 734 AGAAACAGAA 743
DB 10 AGAAACAGAA 1
RESULT 133
AAF28124
ID AAF28124 standard; RNA; 11 BP.
XX
XX AAF28124;
XX
XX 02-APR-2001 (first entry)
XX
XX Vesicular stomatitis virus gene junction #1.
XX
XX Vesiculovirus; vaccine; infection; cancer; ss.
XX
XX Vesicular stomatitis virus.
XX
XX US6168943-B1.
XX
XX 02-JAN-2001.
XX
XX 03-MAY-1996; 96US-00646695.
XX
XX 04-MAY-1995; 95US-00435032.
XX
XX (UYVA ) UNIV YALE.
XX
XX Rose JK;
XX
XX WPI; 2001-136716/14.
XX
XX Producing recombinant replicable vesiculovirus, useful as vaccines for
PT treating or preventing microbial infections, comprises culturing a cell
PT containing a nucleic acid for the expression of vesiculovirus antigenomic
PT RNA.
XX
XX Disclosure; Fig 3; 119pp; English.
XX
XX The present invention relates to producing a recombinant replicable
CC vesiculovirus. The method involves culturing a cell containing a first
CC recombinant nucleic acid that can be transcribed to produce an RNA
CC comprising a vesiculovirus antigenomic (+) RNA containing the
CC vesiculovirus promoter for replication and a ribozyme sequence
CC immediately downstream the antigenomic (+) RNA. The method is useful for
CC producing recombinant replicable vesiculoviruses, which can be used as
CC vaccines for the treatment or prevention of infections by a pathogenic
CC microorganism. The recombinant replicable vesiculoviruses are useful in
CC diagnosing and monitoring progression of infectious disorders, including

```

XX PD 27-JUN-2002.
XX PF 23-MAR-1999; 99US-00274553.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX replication and are useful to treat hepatitis C virus infections and
XX cirrhosis, liver failure or hepatocellular carcinoma.
XX PS Claim 1; Page 42; 80pp; English.
XX CC The present invention relates to enzymatic nucleic acids which
XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX (HP) motif where the binding arms comprise sequences complementary to one
XX of the substrate sequences defined in the specification. The HCV
XX ribozymes are useful for modulating the expression and/or replication of
XX HCV. They can be used to treat cirrhosis, liver failure and/or
XX hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX a condition associated with HCV infection in conjunction with one or more
XX other drug therapies, particularly type I interferon, especially
XX interferon alpha, beta or gamma or consensus interferon. The present
XX sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
XX Some of the sequence data for this patent did not form part of the
XX printed specification. The complete sequence data for this patent was
XX obtained in electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/psipsdIDentry.html
XX SQ Sequence 15 BP; 0 A; 5 C; 2 G; 0 T; 8 U; 0 Other;
Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 729 CCAGGAGAACAGAA 743
DB 15 CCAGGAGAGAGAAA 1
RESULT 130
ABX00934/C
ID ABX00934 standard; RNA; 15 BP.
XX AC ABX00934;
XX DT 23-DEC-2002 (first entry)
XX DE Hepatitis C virus substrate #716 for HCV hammerhead ribozyme #716.
XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
XX liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX type I interferon; interferon alpha; interferon beta; cytostatic;
XX interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX substrate; hammerhead ribozyme; HH ribozyme; ss.
XX OS Hepatitis C virus.
XX FN US2002082225-A1.
XX PD 27-JUN-2002.

XX 23-MAR-1999; 99US-00274553.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX replication and are useful to treat hepatitis C virus infections and
XX cirrhosis, liver failure or hepatocellular carcinoma.
XX PS Claim 1; Page 42; 80pp; English.
XX CC The present invention relates to enzymatic nucleic acids which
XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX (HP) motif where the binding arms comprise sequences complementary to one
XX of the substrate sequences defined in the specification. The HCV
XX ribozymes are useful for modulating the expression and/or replication of
XX HCV. They can be used to treat cirrhosis, liver failure and/or
XX hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX a condition associated with HCV infection in conjunction with one or more
XX other drug therapies, particularly type I interferon, especially
XX interferon alpha, beta or gamma or consensus interferon. The present
XX sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
XX Some of the sequence data for this patent did not form part of the
XX printed specification. The complete sequence data for this patent was
XX obtained in electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/psipsdIDentry.html
XX SQ Sequence 15 BP; 0 A; 6 C; 2 G; 0 T; 7 U; 0 Other;
Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 728 GCCAGGAGAACAGAA 742
DB 15 GCCAGGAGAGAGAAA 1
RESULT 131
AAD56173
ID AAD56173 standard; DNA; 15 BP.
XX AC AAD56173;
XX DT 07-AUG-2003 (first entry)
XX DE Human TSLP furin cleavage site peptide encoding DNA.
XX KW Thymic stromal lymphopoietin; TSLP; lymphopoiesis; STAT5; antibacterial;
XX furin-resistant protein; lymphocyte; vaccine; AIDS; autoimmune disease;
XX transplant rejection; infection; immunosuppressive; immunostimulant;
XX virucide; human; ds.
XX OS Homo sapiens.
XX FH Key
XX CDS Location/Qualifiers
1..15
/*tag= a
/product= "Human TSLP furin cleavage site peptide"
/note= "CDS does not include start and stop codon"
/partial
XX

DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2513.
 XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX
 OS Hepatitis C virus.
 XX
 XX WO955847-A2.
 XX
 XX 04-NOV-1999.
 XX
 XX 26-APR-1999; 99KO-US009027.
 XX
 XX 27-APR-1998; 98US-0083217P.
 PR 18-SEP-1998; 98US-0100842P.
 PR 25-FEB-1999; 99US-00257608.
 PR 23-MAR-1999; 99US-00274553.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
 PI WPI; 2000-062023/05.
 XX
 XX Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection.
 PT
 XX Claim 1; Page 73; 123pp; English.
 PS
 XX The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer
 XX
 SQ Sequence 15 BP; 0 A; 5 C; 2 G; 0 T; 8 U; 0 Other;
 Query Match 46.4%; Score 10.2; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 729 CCAGGAGAAACAGAA 743
 DB 15 CCAGGAGAGGAAAA 1
 RESULT 128
 AAF49128/c
 ID AAF49128 standard; DNA; 15 BP.
 XX
 XX AAF49128;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #88.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pteryiasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200078341-A1.
 XX
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 21-JUN-1999; 99US-0140345P.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 PT
 XX Example 8; Page 61; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pteryiasis, ruba, pilaris, serborrhoea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 0 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 46.4%; Score 10.2; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 733 GAGAACAGACACC 747
 DB 15 GAGAACAGAGGCC 1
 RESULT 129
 ABX00933/c
 ID ABX00933 standard; RNA; 15 BP.
 XX
 XX ABX00933;
 AC
 XX 23-DEC-2002 (first entry)
 DT
 XX Hepatitis C virus substrate #715 for HCV hammerhead ribozyme #715.
 DE
 XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.
 XX
 XX Hepatitis C virus.
 OS
 XX US2002082225-A1.
 PN

XX (IMMU-) IMMUSOL INC.
PA (BEGE/) BEGER C.
XX
XX PI Begier C, Barber J, Wong-Staal F;
XX
XX DR WPI; 2001-611503/70.
XX
XX Novel polypeptides that are the regulators of BRCA-1, useful for treating
PT cancer and diagnosing the presence of neoplastic cells in biological
PT sample.
XX
XX PS Disclosure; Page 26; 97pp; English.
XX
XX Sequences AAS56729-AAS56968 represent DNA encoding BRCA-1 regulators,
CC ribozyme target recognition RNA sequences, DNA fragments encoding the RNA
CC and primers used in the methods of the invention. Hybridisation of
CC ribozymes to their targets results in cleavage of the RNA target. The
CC ribozymes can be used to cleave regulators of the tumour suppressor BRCA-
CC 1, resulting in upregulation or downregulation of BRCA-1 in a cell. The
CC mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor
CC dominant negative 4 (ID4), breast basic conserved protein 1 (BBC1),
CC CHIR2, AF6, BR2 and BR3. Regulation of BRCA-1 is useful for treating and
CC diagnosing cancer and other proliferative disorders. The severity of an
CC incidence of cancer can be lessened by regulating tumour proliferation
CC through modulation of BRCA-1 expression. The sequences of the invention
CC are useful in the development of anti-cancer drugs
XX
XX SQ Sequence 16 BP; 7 A; 4 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGACACC 747
DB 5 AAAGAGACACC 16

RESULT 123
AAF56037/C
ID AAF56037 standard; DNA; 16 BP.
XX
XX AC AAF56037;
XX
XX DT 18-APR-2001 (first entry)
XX
XX DE HBV DNA polymerase gene L528M mutation probe HBPr274.
XX
XX KW HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
XX mutation detection; probe; ss.
XX
XX OS Hepatitis B virus.
XX
XX FN WO200104358-A2.
XX
XX PD 18-JAN-2001.
XX
XX PF 05-JUL-2000; 2000WO-BP006306.
XX
XX PR 08-JUL-1999; 99EP-00870148.
XX
XX PR 13-JUL-1999; 99US-0143546P.
XX
XX PA (INNO-) INNOGENETICS NV.
XX
XX PI Stuyver L, Maertens G, Van Geyt C;
XX
XX DR WPI; 2001-138370/14.
XX
XX Monitoring anti-HBV drug resistance by genetic detection of mutations in
PT DNA polymerase of HBV in patient's sample, involves hybridizing the
PT polynucleic acids of the sample with a probe and detecting the hybrid.
PT
XX

PS Claim 2; Page 9; 64pp; English.
XX
XX The present sequence is a probe used in a method for monitoring anti-
CC hepatitis B virus (HBV) drug resistance in a patient by genetic detection
CC of any one of mutations L528M, M552V/I and/or V/L/M555I in HBV DNA
CC polymerase in a biological sample from the patient. The method is useful
CC in the field of genetic detection of anti-HBV drug resistance during HBV
CC therapy. The method is rapid, reliable and precise.
XX
XX SQ Sequence 16 BP; 2 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGAGAGAAC 739
DB 13 GCCATGAGAGAAC 2

RESULT 124
ABN83342/C
ID ABN83342 standard; DNA; 16 BP.
XX
XX AC ABN83342;
XX
XX DT 29-AUG-2003 (revised)
XX
XX DT 12-AUG-2002 (first entry)
XX
XX DE Human rhinovirus PCR primer #2.
XX
XX KW PCR; primer; chronic obstructive pulmonary disease; COPD; RV1b; ss.
XX
XX OS Human rhinovirus sp.
XX
XX FN EP1211326-A2.
XX
XX PD 05-JUN-2002.
XX
XX PF 28-NOV-2001; 2001EP-00204552.
XX
XX PR 30-NOV-2000; 2000GB-00029270.
XX
XX PA (GLAX) GLAXO GROUP LTD.
XX
XX PI Blair ED, Snowden BW, Ward CL;
XX
XX DR WPI; 2002-464927/50.
XX
XX PT Predicting the likelihood of a patient suffering an onset of chronic
XX obstructive pulmonary disease exacerbation by assaying for a virus,
XX particularly a picornavirus allows management of the disease.
XX
XX PS Claim 6; Page 11; 19pp; English.
XX
XX The present invention relates to a method for predicting the likelihood
CC of a patient suffering an onset of chronic obstructive pulmonary disease
CC (COPD) exacerbation. The method comprises assaying for the presence of
CC human rhinovirus using a fluorogenic real time PCR assay. The present
CC sequence is a PCR primer for human rhinovirus, used to illustrate the
CC method of the invention. This sequence is complementary to the antisense
CC RNA at position 169 to 184 in the 5' non-coding region of RV1b. (Updated
CC on 29-AUG-2003 to standardise OS field)
XX
XX SQ Sequence 16 BP; 1 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAGAACAGAA 743
DB 16 GGGGAGAACAGAA 5

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XX 23-MAR-1999 (first entry)
DT PCR primer 1 used to amplify a 380 bp 5' UTR fragment.
DE RNA respiratory pathogen; common cold; multiple RNA pathogen infection;
XX single-stranded RNA virus; picornavirus; parainfluenza;
KW respiratory syncytial virus; pneumonia; EIB; asthma;
XX exercise induced bronchoconstriction; PCR primer; ss.
OS Synthetic.
OS Picornaviridae.
XX CA2231271-A.
XX 06-SEP-1998.
XX 05-MAR-1998; 98CA-02231271.
XX 06-MAR-1997; 97US-0040207P.
XX (UVR-) UNIV BRITISH COLUMBIA.
XX Hegele RG, Dakhama A;
XX WPI; 1999-071226/07.
XX Detection and diagnosis of multiple RNA respiratory pathogens - using
PT pooled random sequenced oligonucleotides as primers for reverse
PT transcription.
XX Example 1; Page 12; 30pp; English.
XX PCR primers AAX03274-75 were used in a RT-PCR to amplify a 380 bp
CC fragment of the 5' untranslated region (UTR) of Picornavirus, which can
CC detected using probe AAX03276. The primers are used in the method of the
CC invention. The specification describes a new method for obtaining cDNA
CC derived from multiple RNA respiratory pathogens present in cells from a
CC respiratory source. The method comprises extracting RNA from the cells,
CC producing cDNA by reverse transcribing the RNA using pooled short
CC oligonucleotides of random sequence and PCR amplifying the cDNA by using
CC oligonucleotide primers specific to two or more RNA respiratory
CC pathogens. The oligonucleotides are useful for obtaining and diagnosing
CC multiple RNA pathogen infections, especially single-stranded RNA viruses
CC including picornavirus, parainfluenza and respiratory syncytial viruses
CC which cause pneumonia, common cold, exercise induced bronchoconstriction
CC (EIB) and asthma
XX
XX
XX Sequence 16 BP; 1 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 732 GGAGAACACAA 743
DB 16 GGGGAACAGAA 5
RESULT 121
AAS56811
ID AAS56811 standard; DNA; 16 BP.
XX AAS56811;
AC
XX 16-JAN-2002 (first entry)
DT Target validation ribozyme TV30 DNA.
DE
XX Human; BRCA-1 regulator; ribozyme; BR1; RNA target recognition; probe;
KW cytosolic; RNA cleavage; tumour suppressor; PCR primer; CHLR2; AF6; BR2;
KW inhibitor dominant negative 4; breast basic conserved protein 1; BBC1;
XX BR3; ID4; cancer; proliferative disorder; tumour proliferation; ss.

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XX Homo sapiens.
OS WO200170982-A2;
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009559.
XX 23-MAR-2000; 2000US-00536058.
XX (IMMU-) IMMUSOL INC.
XX (BEGE/) BEGER C.
XX Beger C, Barber J, Wong-Staal F;
XX WPI; 2001-611503/70.
XX Novel polypeptides that are the regulators of BRCA-1, useful for treating
PT cancer and diagnosing the presence of neoplastic cells in biological
PT sample.
XX Example 6; Page 65; 97pp; English.
XX Sequences AAS56729-AAS56968 represent DNA encoding BRCA-1 regulators,
CC ribozyme target recognition RNA sequences, DNA fragments encoding the RNA
CC and primers used in the methods of the invention. Hybridisation of
CC ribozymes to their targets results in cleavage of the RNA target. The
CC ribozymes can be used to cleave regulators of the tumour suppressor BRCA-
CC 1, resulting in upregulation or downregulation of BRCA-1 in a cell. The
CC mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor
CC dominant negative 4 (ID4), breast basic conserved protein 1 (BBC1),
CC CHLR2, AF6, BR2 and BR3. Regulation of BRCA-1 is useful for treating and
CC diagnosing cancer and other proliferative disorders. The severity of an
CC incidence of cancer can be lessened by regulating tumour proliferation
CC through modulation of BRCA-1 expression. The sequences of the invention
CC are useful in the development of anti-cancer drugs
XX
XX Sequence 16 BP; 7 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AAACAGAACACC 747
DB 5 AAAGAGAACACC 16
RESULT 122
AAS56768
ID AAS56768 standard; RNA; 16 BP.
XX AAS56768;
AC
XX 16-JAN-2002 (first entry)
DT BR2 protein ribozyme sequence tag RNA #3.
XX
XX Human; BRCA-1 regulator; ribozyme; BR1; RNA target recognition; probe;
KW cytosolic; RNA cleavage; tumour suppressor; PCR primer; CHLR2; AF6; BR2;
KW inhibitor dominant negative 4; breast basic conserved protein 1; BBC1;
XX BR3; ID4; cancer; proliferative disorder; tumour proliferation; ss.
XX Homo sapiens.
OS WO200170982-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009559.
XX 23-MAR-2000; 2000US-00536058.

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```
Db          3 TGCAGGAGGAA 14
|||||
RESULT 118
ABK32031
ID ABK32031 standard; DNA; 15 BP.
XX
XX AC ABK32031;
XX
XX
DT 23-APR-2002 (first entry)
XX
DE Human colon cancer SAGE tag #132.
XX
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW serial analysis of gene expression; diagnostic; prognostic; probe;
KW cancer marker; ss.
XX
XX Homo sapiens.
OS
XX US6333152-B1.
FN
XX
XX 25-DEC-2001.
PD
XX
XX 20-MAY-1998; 98US-00081646.
PF
XX
XX 20-MAY-1998; 98US-00081646.
PR
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
PI
XX
XX WPI; 2002-153821/20.
DR
XX
XX New human nucleic acid containing specific SAGE tags, useful as
PT diagnostic markers for cancer, also derived probes.
PT
XX
XX Disclosure; Col 22; 161pp; English.
PS
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
CC
XX Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCAGGAGGAAA 738
|||||
Db 3 TGCAGGAGGAA 14
|||||
RESULT 119
ACD56204/C
ID ACD56204 standard; RNA; 15 BP.
XX
XX AC ACD56204;
XX
XX
DT 24-SEP-2003 (first entry)
XX
XX HBV enzymatic nucleic acid substrate sequence #93.
DE
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
degenerative; disease state; HBV infection; HCV infection; cirrhosis;
liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis B virus.
OS
XX WO200281494-A1.
FN
XX
XX 17-OCT-2002.
PD
XX
XX 26-MAR-2002; 2002WO-US009187.
PF
XX
XX 26-MAR-2001; 2001US-00817979.
PR
XX 08-JUN-2001; 2001US-00877478.
PR
XX 08-JUN-2001; 2001US-0296876P.
PR
XX 24-OCT-2001; 2001US-0335059P.
PR
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
DR
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
PT
XX
XX Example 1; Page 214; 387pp; English.
PS
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC enzymatic nucleic acid sequences disclosed in the present invention
XX
XX Sequence 15 BP; 1 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
SQ
Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGGAAAAC 739
|||||
Db 12 GCCAGGAGGAAAAC 1
|||||
RESULT 120
AAK03274/C
ID AAK03274 standard; DNA; 16 BP.
XX
XX AAK03274;
AC
```

XX PS Claim 16; Page 13; 79pp; English.

CC The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human dynein, axonemal light polypeptide chain 4 (DNAL4) gene located on chromosome 22q13.1, and methods for haplotyping and/or genotyping the DNAL4 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the DNAL4 gene polymorphisms. The polymorphisms and screened compounds are useful for the treatment of diseases associated with DNAL4 activity, such as neurological disorders. AAS1907-AAS1920 represent ASO probes for detecting human DNAL4 gene polymorphisms

XX SQ Sequence 15 BP; 1 A; 5 C; 2 G; 6 T; 0 U; 1 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 3.1e+02;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAACAGAA 743
|||||: |||
15 CAGGAGATCAGGA 2

Db

RESULT 116
ABK09887/c
ID ABK09887 standard; DNA; 15 BP.
XX AC
XX ABK09887;
XX
XX 14-MAR-2002 (first entry)
XX
XX P2RY1 gene allele-specific oligonucleotide #38.
XX
XX Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant; coagulant; platelet aggregation; haplotyping; drug screening; transgenic animal; human; allele-specific oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX WO200190117-A2.
XX
XX 29-NOV-2001.
XX
XX 21-MAY-2001; 2001WO-USO16432.
XX
XX 19-MAY-2000; 2000US-0205996P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Kazemi A, Koshiy B, Tanguay DA;
XX
XX WPI; 2002-083074/11.
XX
XX New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic variants, useful e.g. in studying the expression and function of P2RY1 and screening candidate drugs for treating diseases related to P2RY1 activity.

PS Claim 18; Page 13; 79pp; English.

XX The invention relates to a novel isolated polypeptide comprising a sequence which is a polymorphic variant of a reference sequence for the purinergic receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its fragment. The polymorphic variant comprises one or more variant amino acids selected from valine at a position 34 and glycine at a position 262. The polymorphic variants are useful in studying the expression and function of P2RY1, in expressing P2RY1 protein for use in screening for candidate drugs to treat diseases related to P2RY1 activity, in studying the effect of the variation on the biological activity of P2RY1, and the binding affinity of candidate drugs targeting P2RY1 for the treatment of disorders related to platelet aggregation. The haplotyping methods are

CC useful in validating P2RY1 as a candidate target for treating a specific condition or disease predicted to be associated with P2RY1 activity, or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with P2RY1 activity. The transgenic animals are useful for studying expression of the P2RY1 isogenes in vivo, for in vivo screening and testing of drugs targeted against P2RY1 protein, and for testing the efficacy of therapeutic agents and compounds for disorders related to platelet aggregation in a biological system. ABK09950-ABK09924 represent human purinergic receptor P2Y, G-coupled protein 1 (P2RY1) gene allele-specific oligonucleotides of the invention

XX SQ Sequence 15 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 1 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 3.1e+02;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAAC 744
|||||: |||
14 RGGGACACAGAAC 1

Db

RESULT 117
ABK32766
ID ABK32766 standard; DNA; 15 BP.
XX AC
XX ABK32766;
XX
XX 23-APR-2002 (first entry)
XX
XX Human colorectal and pancreatic cancer SAGE tag #133.
XX
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag; serial analysis of gene expression; diagnostic; prognostic; probe; cancer marker; ss.
XX
XX Homo sapiens.
XX
XX US6333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UJO) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 93; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer SAGE tags of the invention

XX SQ Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAA 738

CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer

XX SQ Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCAGGAGGAAA 738
 DB 3 TGCAGGAGGAAA 14
 |||||

RESULT 111

AAX31812
 ID AAX31812 standard; DNA; 15 BP.

XX AC AAX31812;
 XX AC

DT 21-MAY-1999 (first entry)

DE Transcript tag sequence increased in pancreatic and colorectal cancer.

XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.

XX Homo sapiens.

XX WO9853319-A2.

XX PD 26-NOV-1998.

XX PF 20-MAY-1998; 98WO-US010277.

XX PR 21-MAY-1997; 97US-0047352P.

XX PA (UJO) UNIV JOHNS HOPKINS.

XX PI Vogelstein B, Kinzler KW;

XX DR WPI; 1999-070161/06.

XX Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.
 XX Disclosure; Page 80; 120pp; English.

XX AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer

XX SQ Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCAGGAGGAAA 738
 DB 3 TGCAGGAGGAAA 14
 |||||

RESULT 112

AAS18254/C
 ID AAS18254 standard; DNA; 15 BP.

XX AC AAS18254;
 XX AC

DT 25-FEB-2002 (first entry)

XX ASO primer #1 to detect IMPDH2 gene polymorphisms.

XX Human; single nucleotide polymorphism; SNP; IMPDH2; chromosome 3p21.2;
 KW IMP dehydrogenase 2; haplotyping; genotyping; cancer; cytostatic;
 KW allele-specific oligonucleotide; ASO; primer; ss.

XX Homo sapiens.

XX WO200177363-A2.

XX PD 18-OCT-2001.

XX PF 11-APR-2001; 2001WO-US011851.

XX PR 11-APR-2000; 2000US-0196248P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Chew A, Choi JY, Koshy B, Lee HH, Stephens JC;

XX WPI; 2002-041297/05.

XX New isolated polynucleotide having polymorphic variant of IMP2
 PT dehydrogenase gene, useful for studying expression of the gene in vivo,
 PT and for testing efficacy of therapeutic agents for cancer in biological
 PT system.
 XX Claim 15; Page 13; 70pp; English.

XX The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human IMP dehydrogenase 2 (IMPDH2) gene located on
 CC chromosome 3p21.2, and methods for haplotyping and/or genotyping the
 CC IMPDH2 gene in an individual. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the IMPDH2 gene
 CC polymorphisms. The polynucleotides and screened compounds are useful for
 CC (developing) treatment of diseases associated with IMPDH2 activity, such
 CC as cancer. AAS18254-AAS18279 represent ASO primers for detecting IMPDH2
 CC gene polymorphisms

XX SQ Sequence 15 BP; 1 A; 3 C; 2 G; 8 T; 0 U; 1 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACAGA 742
 DB 12 AAGAGAACACAGA 1
 |||||

RESULT 113

ABQ88673
 ID ABQ88673 standard; DNA; 15 BP.

XX AC ABQ88673;
 XX AC

DT 23-SEP-2002 (first entry)

XX

XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves rRNA mRNA at the
 CC nucleotide base position indicated in the DE line. The rRNA gene product
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated
 CC specifically in the induction of inflammatory responses. Regions of the
 CC mRNA that do not form secondary folding structures and that contain
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified
 CC by computer analysis. Ribozymes directed against these mRNA sequences
 CC were designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit rRNA expression, making them potentially
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well
 CC as for increasing tolerance to transplanted tissues. The potential
 CC immunosuppressive properties of a ribozyme that cleaves rRNA means
 CC that uses are limited to local delivery, acute indications or ex vivo
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 15 BP; 2 A; 6 C; 1 G; 0 T; 0 U; 0 Other;
 SQ

Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACAGA 742
 Db 13 AGGGAAACAGA 2
 ||||| ||||| |||||

RESULT 109
 AAT50236/c
 ID AAT50236 standard; RNA; 15 BP.
 XX
 XX AAT50236;
 AC AAT50236;
 XX
 XX 07-MAR-1997 (first entry)
 DT
 XX Rabbit CERP HH ribozyme target sequence #797.
 DE
 XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypobetalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; rabbit;
 KW LDL; ss.
 XX
 XX Oryctolagus cuniculus.
 OS
 XX WO9620279-A1.
 PN
 XX 04-JUL-1996.
 PD
 XX 11-DEC-1995; 95WO-US016000.
 PF
 XX 23-DEC-1994; 94US-00363240.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
 PI
 XX WPI; 1996-321852/32.
 DR
 XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 PS
 XX Claim 4; Page 41; 72pp; English.
 PS
 XX AAT50138-T50359 represent target sequences for the rabbit cholesterol
 CC ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT50360-
 CC T50546). CERP is a 74 kD glycoprotein that facilitates neutral lipid

CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CERP. The ribozyme
 CC then binds to 5 nucleotides either side of this site. The ribozymes are
 CC able to cleave mRNA from the gene encoding CERP, thereby blocking
 CC synthesis and/or expression of the mRNA. By inhibiting CERP, the reverse
 CC cholesterol transport (RCT) pathway can be inhibited (or eliminated)
 CC thereby preventing the reduction in size density of the high density
 CC lipoproteins (HDL), prolonging HDL half life, and therefore increasing
 CC HDL levels. The ribozymes can be used to treat conditions associated with
 CC abnormal levels of CERP, specifically atherosclerosis, familial
 CC hypercholesterolaemia, peripheral vascular disease, dyslipidaemia,
 CC hyperbetalipoproteinaemia, hypobetalipoproteinaemia, vascular
 CC complications of diabetes, transplant, atherectomy and angioplastic
 CC restenosis. By inhibiting CERP, the levels of HDL and low density
 CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
 CC decrease in LDL levels, and a corresponding increase in HDL levels). The
 CC HH ribozymes can also be used diagnostically to study genetic drift and
 CC mutations in diseased cells, and to detect CERP mRNA. As the HH ribozymes
 CC target specific regions of the CERP gene, they have low non-specific
 CC activity
 XX
 XX Sequence 15 BP; 1 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
 SQ

Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACACAGAA 743
 Db 12 GGAGAACACAGAA 1
 ||||| ||||| |||||

RESULT 110
 AAX31078
 ID AAX31078 standard; DNA; 15 BP.
 XX
 XX AAX31078;
 AC AAX31078;
 XX
 XX 21-MAY-1999 (first entry)
 DT
 XX Tag sequence of a transcript increased in colorectal cancer.
 DE
 XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 KW
 OS Homo sapiens.
 XX
 XX WO9853319-A2.
 FN
 XX 26-NOV-1998.
 PD
 XX 20-MAY-1998; 98WO-US010277.
 PF
 XX 21-MAY-1997; 97US-0047352P.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Vogelstein B, Kinzler KW;
 PI
 XX WPI; 1999-070161/06.
 DR
 XX Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.
 PS
 XX Claim 2; Page 30; 120pp; English.
 PS
 XX AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a

XX AC ABZ72778;
 XX DT 09-APR-2003 (first entry)
 XX DE Rod opsin hairpin ribozyme target oligonucleotide SEQ ID NO:18.
 XX AC
 XX KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
 KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
 KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
 KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
 XX KW
 XX OS Homo sapiens.
 XX PN W0200288320-A2.
 XX PD 07-NOV-2002.
 XX PF 01-MAY-2002; 2002WO-US013679.
 XX PR 01-MAY-2001; 2001US-00847601.
 XX KW (UYFL) UNIV FLORIDA.
 XX PA
 XX PI Lewin AS, Shaw LC, Grant MB;
 XX DR WPI; 2003-111880/10.
 XX A recombinant adeno-associated virus-vectored ribozyme composition,
 PT useful for treating a disease or dysfunction of the mammalian eye e.g.
 PT retinal disease, e.g. diabetic retinopathy or age-related macular
 PT degeneration.
 XX Claim 1; Page 64; 115pp; English.
 XX CC The present invention describes a recombinant adeno-associated virus
 CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
 CC first ribozyme that specifically cleaves an mRNA encoding a protein,
 CC polypeptide, or peptide selected from the group of rod opsin, iNOS,
 CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
 CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
 CC vector comprising a polynucleotide encoding the ribozyme, where the
 CC polynucleotide operably positioned downstream of at least a first
 CC promoter that directs expression of the polynucleotide in a selected
 CC mammalian cell transformed with the vector; (c) a viral particle
 CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
 CC comprising the ribozyme or the polynucleotide; or (e) a host cell
 CC comprising the amount of mRNA encoding a selected polypeptide in a
 CC retinal cell of a mammalian eye, comprising providing to the eye the
 CC composition described above, and for a time effective to specifically
 CC cleave the mRNA in the cell. (II) has ophthalmological activity, and can
 CC be used in gene therapy. (I) can be used for treating a disease or
 CC dysfunction of the mammalian eye, such as a retinal disease or retinal
 CC dysfunction, (diabetic) retinopathy, or (age-related) macular
 CC degeneration. (II) is also useful for manufacturing a medicament for
 CC treating the diseases mentioned above, including autosomal dominant
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
 CC for treating, decreasing the severity, or ameliorating the symptoms of a
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
 CC blindness, a reduction in central or peripheral vision, or a reduction in
 CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
 CC exemplification of the present invention
 XX SQ Sequence 14 BP; 1 A; 4 C; 2 G; 0 T; 7 U; 0 Other;
 Query Match 47.3%; Score 10.4; DB 1; Length 14;
 Best Local Similarity 91.7%; Pred. No. 3e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGA 742
 DB 14 AGCAGAAACAGA 3

RESULT 108
 AAT54806/C
 ID AAT54806 standard; RNA; 15 BP.
 XX AC
 XX AC AAT54806;
 XX DT 25-MAR-2003 (revised)
 XX DT 07-APR-1997 (first entry)
 XX DE Mouse rela hammerhead ribozyme target sequence (nt. position 94).
 XX KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumor necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.
 XX OS Mus musculus.
 XX PN W09523225-A2.
 XX PD 31-AUG-1995.
 XX PF 23-FEB-1995; 95WO-IB000156.
 XX PR 23-FEB-1994; 94US-00201109.
 XX PR 29-MAR-1994; 94US-00218934.
 XX PR 04-APR-1994; 94US-00222795.
 XX PR 07-APR-1994; 94US-00224483.
 XX PR 15-APR-1994; 94US-00227958.
 XX PR 15-APR-1994; 94US-00228041.
 XX PR 18-MAY-1994; 94US-00245736.
 XX PR 06-JUL-1994; 94US-00271280.
 XX PR 15-AUG-1994; 94US-00291932.
 XX PR 16-AUG-1994; 94US-00291433.
 XX PR 17-AUG-1994; 94US-00292820.
 XX PR 19-AUG-1994; 94US-00293520.
 XX PR 02-SEP-1994; 94US-00300000.
 XX PR 08-SEP-1994; 94US-00303039.
 XX PR 23-SEP-1994; 94US-00311486.
 XX PR 23-SEP-1994; 94US-00311749.
 XX PR 28-SEP-1994; 94US-00314397.
 XX PR 03-OCT-1994; 94US-00316771.
 XX PR 07-OCT-1994; 94US-00319492.
 XX PR 11-OCT-1994; 94US-00321993.
 XX PR 04-NOV-1994; 94US-00334847.
 XX PR 10-NOV-1994; 94US-00337508.
 XX PR 28-NOV-1994; 94US-00345516.
 XX PR 16-DEC-1994; 94US-00357577.
 XX PR 23-DEC-1994; 94US-00363233.
 XX PR 30-JAN-1995; 95US-00380734.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Stinchcomb DT, Chowrira B, Dizenzo A, Draper KG, Dudycz LW;
 PI Gramm S, Karpelesky A, Kisich K, Matulic-Adamic J, Meswigen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott PE, Woolf T;
 XX WPI; 1995-351090/45.
 XX DR
 XX PT Ribozymes having modified bases and methods for producing them - for use
 XX PT in inhibiting disease related genes.
 XX PS Claim 2; Page 225; 407pp; English.

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 2.9e-02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 736 AAACAGAACACC 747
|||||
DB 2 AAACAGAACACC 13

RESULT 105

AAQ78476
ID AAQ78476 standard; DNA; 14 BP.

XX AAQ78476;

AC 25-MAR-2003 (revised)

DT 27-JUN-1995 (first entry)

DT

XX TGF-beta gene phosphorothioate antisense oligonucleotide.

DE

XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.

XX OS

XX Synthetic.

XX WO9425588-A2.

XX PN

XX 10-NOV-1994.

XX PD

XX 29-APR-1994; 94WO-EP001362.

XX PF

XX 30-APR-1993; 93EP-00107089.

XX PR

XX 13-MAY-1993; 93EP-00107849.

XX XX

PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI

XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;

XX PI

XX Bogdahn U;

XX XX

XX WPI; 1994-358266/44.

XX XX

XX New transforming growth factor beta anti-sense oligo:nucleotide(s) - for

XX PT

XX treating immunosuppression, tumours, etc.

XX PT

XX Claim 6; Page 60; 74pp; English.

XX PS

XX XX

XX The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENSEQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENSEQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)

XX XX

XX SQ

Sequence 14 BP; 6 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

RESULT 107

ABZ72778/C

ID ABZ72778 standard; RNA; 14 BP.

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3e-02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 731 AGGAGAACACAGA 742
|||||
DB 1 AGGAGAACACAGA 12

RESULT 106

AAV70179

ID AAV70179 standard; DNA; 14 BP.

XX AAV70179;

AC AAV70179;

XX DT

XX 03-FEB-1999 (first entry)

XX DE

XX Oligonucleotide SEQ ID NO:4 from Figure 14 of US5843661.

XX KW

XX Universal DNA based molecular Turing machine; circular DNA molecule;
KW computation; algorithm; ds.

XX XX

XX Synthetic.

XX OS

XX US5843661-A.

XX PN

XX 01-DEC-1998.

XX PD

XX 24-APR-1996; 96US-00639080.

XX PF

XX 24-APR-1996; 96US-00639080.

XX PR

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PA

XX Rothermund PMK;

XX PI

XX WPI; 1999-044569/04.

XX XX

XX Universal molecular Turing machine - based on circular DNA molecule.

XX PT

XX Disclosure; Fig 14; 90pp; English.

XX PS

XX The present invention describes a universal molecular Turing machine
CC comprising a circular DNA molecule, having sites representing information
CC storage of the Turing machine, the DNA molecule including: an invariant
CC (Inv) restriction site inside the circular DNA molecule; a state
CC restriction site also inside the circular DNA molecule; and adjacent to
CC the Inv restriction site; a current symbol, encoded on the circular DNA
CC molecule at a distance from the state restriction site that represents a
CC state of the Turing machine; a sequence of intervening nucleotides
CC between the state restriction site and the current symbol; a set of
CC asymmetric restriction enzymes; and a set of transition oligonucleotides,
CC which are inserted into the circular DNA molecule as additional symbols
CC to encode changes to the information storage caused by operation of the
CC Turing machine. The Turing machine is a model of computation. The
CC universal molecular Turing machine is capable of simulating any Turing
CC machine and hence any algorithm. AAV70176 to AAV70206 represent
CC oligonucleotides used to exemplify the present invention

XX SQ

Sequence 14 BP; 6 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3e-02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 735 GAAACAGAACAC 746
|||||
DB 2 GAAACAGTACAC 13

```

PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 240241; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 1 C; 6 G; 6 T; 0 U; 0 Other;
XX
Query Match 47.3%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 736 AACACGACACCC 747
Db 12 AACACGACACCC 1

RESULT 103
ABF73168/c
ID ABF73168 standard; DNA; 13 BP.
XX
AC ABF73168;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 173165 for detecting SNP TSC0006888.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 173166; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
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Db 12 AACACGACACCC 1

RESULT 104
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